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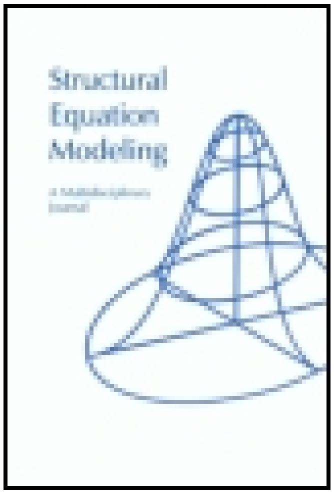

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Multiple-Group Factor Analysis Alignment

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This article presents a new method for multiple-group confirmatory factor analysis (CFA), referred to as the alignment method. The alignment method can be used to estimate group-specific factor means and variances without requiring exact measurement invariance. A strength of the method is the ability to conveniently estimate models for many groups. The method is a valuable alternative to the currently used multiple-group CFA methods for studying measurement invariance that require multiple manual model adjustments guided by modification indexes. Multiple-group CFA is not practical with many groups due to poor model fit of the scalar model and too many large modification indexes. In contrast, the alignment method is based on the configural model and essentially automates and greatly simplifies measurement invariance analysis. The method also provides a detailed account of parameter invariance for every model parameter in every group.

Keywords: measurement invariance, Mplus, multiple group factor analysis

Multiple-group confirmatory factor analysis (CFA) aims to compare latent variable means, variances, and covariances across groups while holding measurement parameters invariant. For factor means to be comparable, invariance of both factor loadings and measurement intercepts is required and is referred to as scalar invariance (see, e.g., Millsap, 2011). A model with such strict invariance is often rejected. This is typically followed by the use of modification indexes (Sörbom, 1989) to relax some of the invariance restrictions. Often, multiple-group applications involve the study of many groups based on surveys with a variety of aims: country comparisons of achievement such as Programme for International Student Assessment (PISA), Trends in International Mathematics and Science Study (TIMSS), and Progress in Literacy Study (PIRL); cross-cultural studies such as the International Social Survey Program (ISSP) and European Social Survey (ESS); and with research on organizations. With many groups, the usual multiple-group CFA approach is too cumbersome to be practical due to the many possible violations of invariance, and the modification index exploration could well lead to the wrong model due to the scalar model being far from the true model. Following is a typical example that illustrates the problem. We return to this example at the end of the article, using it to demonstrate the new approach that we propose.

Beierlein, Davidov, Schmidt, and Schwartz (2012) analyzed data from the European Social Survey including 26 countries and 49,894 subjects with an average country sample size of 1,919. The latent variable constructs of tradition and conformity are measured by four items presented in portrait format, where the scale of the items is such that a high value represents a low level of tradition conformity. The item wording is shown in Table 1.

The two constructs have been found to correlate highly and are here viewed as forming a single factor. Scalar invariance across the 26 countries for the one-factor model using maximum-likelihood estimation with a likelihood-ratio χ^2 test of model fit results in very poor fit, $\chi^2(202) = 8{,}654$ ($p = .000$). A large part of this poor fit is due to the large sample size of 49, 894, but other fit indexes also indicate very poor fit: root mean square error of approximation (RMSEA) $= 0.148$, comparative fit index (CFI) $= 0.677$. In addition, there are many large modification indexes: 83 in the range of 10 to 100, 15 in the range of 100 to 200, and 16 in the range of 200 to 457 (the largest value). The presence of so many large modification indexes implies that a long sequence of model modifications is needed to reach a model with acceptable fit and the search for a good model

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Color versions of one or more figures in the article can be found online at www.taylorandfrancis.com/hsem.

TABLE 1
Tradition Conformity Items From the European Social Survey

Tradition (TR):	9. It is important for him to be humble and modest. He tries not to draw attention to himself (ipmodst).
	20. Tradition is important to him. He tries to follow the customs handed down by his religion or family (imptrad).
Conformity (CO):	7. He believes that people should do what they're told. He thinks people should follow rules at all times, even when no one is watching (ipfrule).
	16. It is important for him to always behave properly. He wants to avoid doing anything people would say is wrong (ipbhprp).

could easily lead to the wrong model. We conclude that multiple-group CFA fails due to too many necessary model modifications. This is a typical outcome when a scalar invariance model is applied to many groups. It is then impossible to compare factor means across the groups. A new method is needed. In this article we describe a radically different method: alignment optimization. The alignment can be based on maximum-likelihood or Bayes estimation.

The first section presents the alignment method and the following section discusses its implementation in a Bayesian framework. Next, ideas for the secondary goal of finding measurement parameters that are significantly noninvariant are presented. The following that section discusses Monte Carlo simulation studies using both maximum-likelihood and Bayesian analysis. The topic then returns to the application of tradition-conformity items measured in 26 countries before the article concludes.

ALIGNMENT

Consider the multiple-group factor analysis model

$$y_{ipg} = \nu_{pg} + \lambda_{pg}\eta_{ig} + \epsilon_{ipg}, \tag{1}$$

where $p = 1, \ldots, P$ and P is the number of observed indicator variables, $g = 1, \ldots, G$ and G is the number of groups, $i = 1, \ldots, N_g$ where N_g is the number of independent observations in group g, η_{ig} is a latent variable, and we assume that $\epsilon_{ipg}\tilde{N}\left(0, \theta_{pg}\right), \eta_{ig}\tilde{N}\left(\alpha_g, \psi_g\right)$.

In the scalar invariance model the intercepts ν_{pg} and loading parameters λ_{pg} are held equal across groups, the factor mean in the first group is fixed to 0, and the factor variance in the first group is fixed to 1. As mentioned earlier, when the scalar model does not fit well, modification indexes are used to relax the measurement part of the model step by step, or one parameter at a time. One problem with this approach is that the model modifications are done manually and many models have to be estimated before a well-fitting model is found. Another problem is that among the many well-fitting models, the modification indexes approach does not guarantee that the simplest, most interpretable model with the fewest noninvariant parameters is reached. Even with only three groups, the simplest path of model modification might not be obvious.

If we instead estimate the model where all intercepts and loadings are unconstrained, the factor means and factor variances cannot be identified and are typically fixed to 0 and 1, respectively. This model is referred to as the configural model. Because the factor means and variances are not identified in the configural model, the factors η are not comparable across groups and will be on a different scale in each group. It is not possible to compare factor scores across individuals from different groups and it is not possible to compare factor means across groups.

Here we describe an alignment approach that can estimate the model of Equation 1; that is, it does not assume measurement invariance and can estimate the factor mean and variance parameters in each group while discovering the most optimal measurement invariance pattern. The method incorporates a simplicity function similar to the rotation criteria used with exploratory factor analysis (EFA).

The proposed alignment approach can estimate all of the parameters ν_{pg}, λ_{pg}, α_g, ψ_g by incorporating in the estimation the natural assumption that the number of noninvariant measurement parameters and the amount of measurement noninvariance can be held to a minimum. In the first step the alignment approach estimates the configural model where $\alpha_g = 0$, $\psi_g = 1$ for every g and all loading and intercept parameters are estimated as free and unequal. We call this model the base model M0. This is the best fitting model among all multiple-group factor analysis models as it has no across-group parameter restrictions. The final aligned model that we propose here has the same fit as the M0 model; that is, despite the fact that the aligned model attempts to minimize the amount of noninvariance, it does not compromise the fit. The relationship between M0 and the final aligned model parallels the relationship in EFA between the unrotated model (which has the best fit among all CFA models with a fixed number of factors) and the rotated model, which simplifies the loading matrix without compromising the fit of the model; that is, has the same fit as the unrotated model.

Denote the estimates of model M0 by $\nu_{pg,0}$, and $\lambda_{pg,0}$. The configural M0 model transforms the factor in each group to mean zero and variance one,

$$\eta_{g0} = \left(\eta_g - \alpha_g\right) \Big/ \sqrt{\psi_g}, \tag{2}$$

so that the variance and the mean of indicators can be reexpressed as

$$V\left(y_{pg}\right) = \lambda_{pg}^2 \psi_g = \lambda_{pg,0}^2, \tag{3}$$

$$E\left(y_{pg}\right) = \nu_{pg} + \lambda_{pg}\alpha_g = \nu_{pg,0}, \tag{4}$$

where

$$\lambda_{pg,0} = \lambda_{pg}\sqrt{\psi_g}, \tag{5}$$

$$\nu_{pg,0} = \nu_{pg} + \frac{\lambda_{pg,0}}{\sqrt{\psi_g}}\alpha_g. \tag{6}$$

For every set of parameters α_g and ψ_g there are intercept and loading parameters ν_{pg} and λ_{pg} that yield the same likelihood as the configural model. It follows from Equations 5 and 6 that these parameters can be obtained as

$$\lambda_{pg,1} = \frac{\lambda_{pg,0}}{\sqrt{\psi_g}}, \tag{7}$$

$$\nu_{pg,1} = \nu_{pg,0} - \alpha_g\frac{\lambda_{pg,0}}{\sqrt{\psi_g}}. \tag{8}$$

We want to choose α_g and ψ_g so that we minimize the amount of measurement noninvariance. To formalize this we minimize with respect to α_g and ψ_g the total loss/simplicity function F that accumulates the total measurement noninvariance

$$F = \sum_p \sum_{g_1<g_2} w_{g_1,g_2} f\left(\lambda_{pg_1,1} - \lambda_{pg_2,1}\right) + \sum_p \sum_{g_1<g_2} w_{g_1,g_2} f\left(\nu_{pg_1,1} - \nu_{pg_2,1}\right). \tag{9}$$

The function F implies that for every pair of groups and every intercept and loading parameter we add to the total loss function the difference between the parameters scaled via the component loss function (CLF) f. CLF has been used in EFA (see, e.g., Jennrich, 2006) and it is used similarly here. One good choice for the CLF is

$$f(x) = \sqrt{\sqrt{x^2 + \epsilon}}$$

where ϵ is a small number such as 0.01. The function is approximately equal to $\sqrt{|x|}$. It is exactly equal to $\sqrt{|x|}$ when the small number ϵ is set to 0. We use a positive ϵ so that we get a CLF that has a continuous first derivative, which makes the optimization of the total loss function F easier than if we use a CLF that has no continuous first derivative. This is because most optimization routines rely on continuous first derivatives. The choice of $f(x) = \sqrt{|x|}$ leads to no loss, if $x = 0$. If $x < 1$ the loss is amplified; that is, $f(x) > x$. If $x > 1$ the loss is attenuated; that is, $f(x) < x$. Thus the total loss function F will be minimized at a solution where there are a few large noninvariant measurement parameters and many approximately invariant measurement parameters rather than many medium-sized noninvariant measurement parameters. This is similar to the fact that EFA rotation functions aim for either large or small loadings, but not midsized loadings.

The weight factor w_{g_1,g_2} in F is set to reflect the group size and the amount of certainty we have in the group estimates for a particular group. We use

$$w_{g_1,g_2} = \sqrt{N_{g_1}N_{g_2}}.$$

With this weight factor, bigger groups will contribute more to the total loss function than smaller groups.

Minimizing the total loss function will generally identify the parameters α_g and ψ_g in all groups except the first group. To identify the parameters in the first group we use the parameter constraints

$$\psi_1 \times \ldots \times \psi_g = 1. \tag{10}$$

We also set $\alpha_1 = 0$, although this second constraint is generally not needed and in fact it might itself lead to biased parameter estimates. In principle the alignment optimization can identify $2G - 1$ of the parameters α_g and ψ_g, and the last parameter is identified through Equation 10. The two alignment optimizations are are referred to as FIXED and FREE. The FIXED alignment optimization assumes that $\alpha_1 = 0$. The FREE alignment optimization estimates α_1 as an additional parameter. Later on we illustrate with simulation studies the advantages and the disadvantages of the two different alignment methods. The parameters can also be standardized so that the factor metric is set in Group 1; that is, $\psi_1 = 1$.[1] In addition, the alignment optimization is conducted after the observed variables are standardized over the entire population so that all variables are on the same scale and the loss functions between the different indicator variables are comparable. Once the parameters α_g and ψ_g are obtained via the alignment optimization the loading and intercept parameters are obtained via Equations 7 and 8.

Minimizing the simplicity function F might be complicated due to multiple local optima and many random starting values should be used to ensure that the global minimum is obtained.[2] In many practical applications many local optima could be found. Often those local optima yield fit function values that are close to the global optimum fit function value and then typically the local optimum aligned parameters differ only slightly from the global optimum aligned parameters.

The standard errors for the aligned parameters can be computed using the delta method. The total loss function F has $2G$ — 1 independent parameters. The derivatives of

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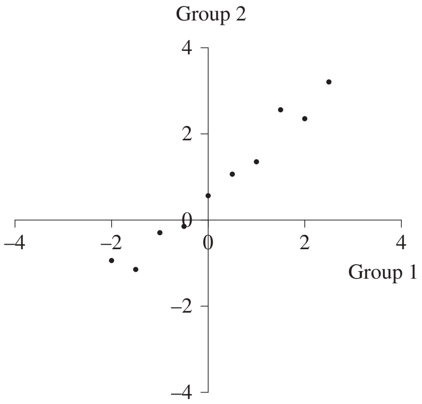
[1] In fact in M*plus* by default the parameters are indeed reported in that metric, however, the alignment optimization is carried out using Equation 10 to ensure full symmetry between the different groups.

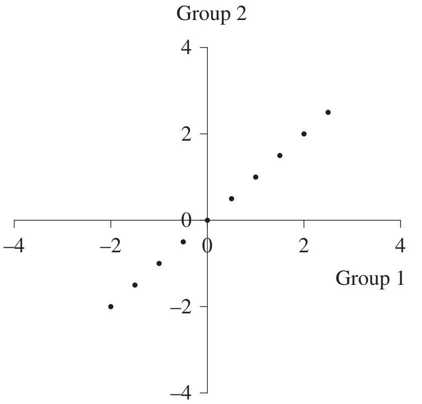
[2] By default M*plus* uses 30 random starting values; however, more random starting values should be used if the global minimum is not replicated at least twice. M*plus* will print a warning if this is the case. The technical 8 output can be used to see the fit function values obtained with the different random starting values. Note however that in the technical 8 output, M*plus* uses — F instead of F as it maximizes the opposite of the fit function.

F with respect to those parameters yield identifying equations for α_g and ψ_g. Those equations can be solved implicitly for α_g and ψ_g in terms of $\lambda_{pg,0}$ and $\nu_{pg,0}$ and using the asymptotic distribution for the parameter estimates of the configural model and these implicit equations one can obtain the asymptotic distribution of the aligned parameters. The technical details are given in the Appendix.

The reason for the choice of the term alignment for this new method is illustrated in Figure 1. Consider group-invariant intercepts and loadings for 10 items and two groups with factor means 0 and –1 and factor variances 1 and 2. The configural model of the first step of alignment fixes the factor means and variances to 0 and 1, respectively, in both groups. The formulas of Equations 5 and 6 show how the configural parameters, using the zero subscript, relate to the original parameters through the original factor means and variances. The plot at the top shows the configural intercept parameters that, due to group differences in factor means and variances, are not equal across the two groups despite the perfect measurement invariance of the original parameters. The plot at the bottom shows the invariance across groups of the original parameters where the correct factor means and variances have been taken into account. Going from the top to the bottom plot, the intercept parameters have been aligned.



Unaligned: Configural model (mean=0, variance=1 in both groups)



Aligned: Taking into account the group differences in means and variances

FIGURE 1 Unaligned and aligned intercept parameters.

The preceding discussion focuses on CFA models where an indicator loads on only one factor so that cases with multiple factors are aligned one factor at a time. Other current limitations that can be relaxed with further research include having covariates and using a full structural equation model.

BAYESIAN ESTIMATION

Two types of Bayesian alignment estimation methods are considered, the configural and the BSEM (Bayesian structural equation modeling; Muthén & Asparouhov, 2012) methods. Both methods first estimate a base model M0 using Markov Chain Monte Carlo (MCMC) methodology (see, e.g., Asparouhov & Muthén, 2010, and references therein). The difference between the two methods is in the model M0. For the configural method the model M0 is simply the configural model where all factor means are fixed to 0 and all factor variances are fixed to 1. The loading and intercept parameters are estimated as free and unequal parameters using noninformative priors. For the BSEM method the M0 model is a model where all measurement intercepts and loadings are held approximately equal or invariant across groups by specifying highly correlated priors (see Section 4 in Muthén & Asparouhov, 2013a), and the factor means and variances are estimated as free parameters in all but the first group. In the first group the factor variance is fixed to 1 and the factor mean is estimated if the FREE alignment is used and it is fixed to 0 if the FIXED alignment is used.

After the M0 model is estimated, the second half of the generated MCMC sequence is used to form the posterior distribution of the unaligned configural parameter estimates. That is, if the M0 model is the configural model we simply use the estimated posterior distribution of the M0 estimates. If the M0 model is the BSEM model we compute the posterior distribution for the configural loadings and intercepts parameters using the following formulas:

$$\lambda_{pg,0} = \lambda_{pg,1}\sqrt{\psi_g}, \tag{11}$$

$$\nu_{pg,0} = \nu_{pg,1} + \alpha_g \lambda_{pg,1}, \tag{12}$$

where $\lambda_{pg,0}$ and $\nu_{pg,0}$ are the configural loadings and intercepts and α_g, ψ_g, $\lambda_{pg,1}$, and $\nu_{pg,1}$ are the BSEM parameters. Using the BSEM parameters in each MCMC iteration we apply Equations 11 and 12 to obtain the configural loadings and intercepts for each MCMC iteration. We then use these values to form the posterior distribution for the configural intercept and loadings.

In a final step we obtain the posterior distribution of the aligned parameter estimates by minimizing the simplicity function (Equation 9) in each MCMC iteration. In other words, using the configural intercept and loadings values in each MCMC iteration we minimize the simplicity function

(Equation 9) to obtain aligned estimates in each MCMC iteration. The aligned values from all MCMC iterations are then used to estimate the aligned posterior distribution as well as the point estimates and the standard errors for the aligned parameters. To avoid problems with multiple local optima the aligned parameter values in one MCMC iteration are used as starting values for the next iteration. These starting values are usually quite good because the change in the configural estimates is somewhat gradual and thus the difference between the aligned values in consecutive MCMC iterations is not big.

One advantage of the Bayesian alignment estimation over the maximum-likelihood alignment estimation is that it can provide a more flexible model and a better fitting model due to the fact that it is based on the BSEM model. A multiple-group factor analysis model assuming configural invariance might not fit the data well In that case, using BSEM with small residual covariances among the indicator variables as suggested in Muthén and Asparouhov (2012) might improve the model fit. In this way, the Baysian alignment model based on BSEM can have a better model fit than the maximum-likelihood estimated multiple-group factor model.

The advantage of the BSEM model with the alignment estimation over the BSEM model without the alignment estimation is that it improves interpretability. The alignment estimates are obtained by minimizing the number of non-invariance items, whereas the BSEM estimates are obtained by minimizing the variability of the estimates across groups. The alignment estimates will be simpler to interpret as fewer noninvariant parameters will be found.

Another advantage of the BSEM alignment estimation is that it can be used to resolve estimation problems within individual groups where there is an insufficient amount of data or another data-related estimation problem arises. By holding the measurement parameters approximately equal across groups while allowing the group-specific factor means and variances to be estimated, we can stabilize the estimation by essentially incorporating a limited amount of information from other groups into the group-specific estimation.

INVARIANCE ANALYSIS

The primary goal of the alignment is to provide a comparison of factor means and factor variances across groups while allowing for approximate measurement invariance. As a by-product, information about the degree of measurement invariance can also be provided. After the alignment estimation is completed, a detailed analysis can be done to determine which measurement parameters are approximately invariant and which are not. The approach taken here is an ad-hoc procedure. Other ad-hoc procedures might work equally well. Here we do not provide a theoretical justification, rather, we provide details on the postestimation algorithm that is used to determine invariance. This procedure works very well with simulated data, where the invariance and the noninvariant parameters are known by design. Thus we expect the procedure to work well in practical applications as well. Later we describe the details of the algorithm implemented in M*plus* Version 7.11.

The idea behind the algorithm is as follows. For each measurement parameter the largest invariant set of groups is found where for each group in the invariant set of groups the measurement parameter in that group is not statistically significant from the average value for that parameter across all groups in the invariant set. For each group not in the invariant set the parameter is statistically significantly different from that average. The algorithm is based on multiple pairwise comparison; that is, multiple testing is done and to avoid false noninvariance discovery we use smaller p values than the nominal .05.

The first step in the algorithm is to determine a starting set of invariant groups. We conduct a pairwise test for each pair of groups and we "connect" two groups if the p value obtained by the pairwise comparison test is bigger than .01. Next we determine the largest connected set for that parameter. This will be the starting set of groups. The starting set will be modified using the following procedure. First the average parameter is computed using the current invariance set. Then for each group a test of significance is conducted to compare the parameter value for each group with the current average. If the p value is above .001, the group is added to the invariant set; if it is below that value, the group is removed from the invariance set. We then repeat that process until the invariant set stabilizes and no groups are added or removed from the invariance set. Additional rules are added to guarantee that the process indeed stabilizes. This procedure is based on the delta method when the maximum-likelihood estimation is used and with the Bayesian estimation the testing is done using the posterior distribution for the test statistic. With the Bayesian estimation it is recommended that a longer MCMC sequence is run so that small p values are more accurately estimated. Typically 1,000 MCMC iterations will be sufficient. This procedure uses small p values as cutoff values and thus it is important to accurately estimate small p values.[3]

Invariance analysis can be done not just for the individual parameters but also for the factor indicator variables. Such an analysis is useful to identify the most invariant variable and use that as an anchor item in a multiple-group CFA, or to identify the most noninvariant variables, which can then be revised or removed from the measurement instrument. The contribution to the simplicity function (Equation 9) from each variable can be isolated and reflects the level of

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[3] More details on the invariance analysis and various pairwise comparisons can be obtained in M*plus* using the ALIGN option of the OUTPUT command.

noninvariance for the variable. The smaller the contribution is, the more invariant the variables are. These values add up to the total optimized simplicity function value.[4]

An R^2 measure for each measurement parameter gives the parameter variation across groups in the configural model that is explained by variation in the factor mean and factor variance across groups. For intercepts and loadings the formulas are

$$R^2_{intercept} = 1 - V\left(\nu_0 - \nu - \alpha_g \lambda\right) \Big/ V\left(\nu_0\right), \tag{13}$$

$$R^2_{loading} = 1 - V\left(\lambda_0 - \sqrt{\psi_g}\lambda\right) \Big/ V\left(\lambda_0\right), \tag{14}$$

where ν is the average aligned intercept and λ is the average aligned loading. The R^2 measure gives a useful notion of the degree of noninvariance that can be absorbed by group-varying factor means and variances. A value close to 1 implies a high degree of invariance and a value close to 0 a low degree of invariance.

MONTE CARLO SIMULATIONS

In this section we study the quality of the alignment estimation methods. Simulation Study 1 considers the bias and coverage with the maximum-likelihood estimation, Simulation Study 2 considers the parameter sampling variability using the maximum-likelihood and the Bayes estimation methods, and Simulation Study 3 compares the FIXED and FREE alignment approaches. A further simulation study is presented later, based on the earlier analysis of the tradition-conformity data. Whereas these simulations focus on bias and coverage of each parameter in the model, Muthén and Asparouhov (2013b) discussed simulations where instead a more relaxed performance measure is used based on the correlation between the population factor means and variances and the corresponding estimated values. Such a performance measure focuses on the key aim of the alignment, namely the ordering of the groups with respect to factor means and variances.

Simulation Study 1: Bias and Coverage Using Maximum Likelihood

In this section we describe a basic simulation study that provides an overview of the quality of the aligned estimation. We generate data using a one-factor model with G groups each of size N. The factor is measured by five indicator variables. We generate data so that in each group there is one noninvariant intercept parameter and one noninvariant loading parameter. In all groups the invariant loadings and the residual variances of the indicator variables are set to 1 and the invariant intercepts of the indicator variables are set to 0. For simplicity there are three different types of groups in this simulation. In Group 1 the distribution of the factor is $N(0,1)$, in Group 2 the distribution is $N(0.3,1.5)$, and in Group 3 the distribution is $N(1,1.2)$. The remaining groups use the same parameter values as the first three groups: Group 4 uses the same parameters as Group 1, Group 5 uses the same parameters as Group 2, and so on. The noninvariant parameters in Group 1 are $\nu_5 = 0.5$ and $\lambda_3 = 1.4$. The noninvariant parameters in Group 2 are $\nu_1 = -0.5$ and $\lambda_5 = 0.5$. The noninvariant parameters in Group 3 are $\nu_2 = 0.5$and $\lambda_4 = 0.3$.

To illustrate the effect different features have on the alignment estimation, we vary the number of groups G, the number of observations in each group N, the alignment estimation method (FREE vs. FIXED), and the degree of noninvariance. The difference between these two methods is in the way the first group factor intercept α_1 is treated. With the FIXED alignment the parameter α_1 is fixed to 0 and with the FREE alignment that parameter is estimated as a free parameter. We use within-group sample size $N = 100$ or $N = 1{,}000$ and we use four different numbers of groups: 2, 3, 15, and 60. In this simulation the factor mean and variance in the first group are 0 and 1 and thus the default metric is the same as the metric used to generate the data. Therefore we expect the estimated results to match the generated values.

We also vary the percentage of noninvariance among the intercept and loading parameters. The generation scheme previously described has $I = 20\%$ noninvariance because one out of five intercepts and one out of five loadings are noninvariant. To obtain different levels of noninvariance we modify the generation scheme as follows. To obtain $I = 0\%$ we replace all the noninvariant values with invariant values and to obtain $I = 10\%$ we remove the noninvariant loading parameter from each odd-numbered group and we remove the noninvariant intercept parameter from each even-numbered group. Note here that this concerns only the data generation; the estimated model is the same regardless of the level of noninvariance I, so the estimated model includes for each group free and unequal loadings, intercepts, and residual variance, as well as factor means and variances, with the exception of the first group, where the factor variance is fixed to 1 and possibly the factor mean is fixed to 0. The total number of estimated parameters is $(3 \cdot P + 2) \cdot G - 1$ for the FREE alignment model and $(3 \cdot P + 2) \cdot G - 2$ for the FIXED alignment model. In our example with $P = 5$ indicators and with 60 groups, this amounts to 1,019 parameters.

Using the FIXED and FREE options, respectively, Tables 2 and 3 report the results for six parameters that are typical representatives for the rest of the model parameters.

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[4] M*plus* reports the contribution separately for the intercept and the loading component for each variable. Simplicity function contributions for indicator variables are obtained in M*plus* using the ALIGN option of the OUTPUT command.

The first two parameters are the factor mean α_2 and factor variance ψ_2 in Group 2. We also report two invariant parameters, the first loading $\lambda_{1,2}$ and the second intercept $\nu_{2,2}$ in Group 2. We also report two noninvariant parameters in Group 2, the first intercept $\nu_{1,2}$ and the fifth loading $\lambda_{5,2}$. Maximum-Likelihood estimation is used.

TABLE 2
Absolute Bias (Coverage) for the FIXED Alignment Estimates Using Maximum Likelihood

G	N	I	$\alpha_2 = 0.3$	$\psi_2 = 1.5$	$\lambda_{1,2} = 1$	$\nu_{2,2} = 0$	$\lambda_{5,2} = 0.5$	$\nu_{1,2} = -0.5$
2	100	0	.02 (.97)	.00 (.99)	.00 (0.98)	.01 (.96)	.01 (1.00)	.03 (.98)
2	100	10	.01 (.98)	.04 (.96)	.02 (0.96)	.01 (.97)	.00 (.96)	.00 (.96)
2	100	20	.06 (.96)	.20 (.86)	.09 (1.00)	.05 (.91)	.04 (.92)	.03 (.96)
3	100	0	.01 (.96)	.07 (.98)	.02 (.97)	.01 (.99)	.03 (.98)	.00 (.98)
3	100	10	.04 (.97)	.00 (.98)	.00 (.98)	.03 (.98)	.01 (.94)	.02 (.98)
3	100	20	.12 (.95)	.20 (.91)	.08 (.94)	.09 (.92)	.03 (.91)	.08 (.92)
15	100	0	.03 (.96)	.02 (.97)	.00 (.99)	.04 (.99)	.00 (1.00)	.04 (1.00)
15	100	10	.04 (.98)	.05 (.97)	.01 (1.00)	.05 (.98)	.01 (.97)	.04 (.98)
15	100	20	.10 (.94)	.17 (.89)	.06 (.98)	.09 (.99)	.03 (.96)	.09 (.98)
60	100	0	.18 (.97)	.02 (.99)	.00 (0.99)	.19 (0.98)	.01 (1.00)	.18 (.96)
60	100	10	.08 (.98)	.02 (.97)	.02 (1.00)	.09 (1.00)	.02 (.99)	.07 (1.00)
60	100	20	.10 (.97)	.12 (.93)	.05 (1.00)	.10 (1.00)	.04 (.98)	.08 (.98)
2	1,000	0	.01 (1.00)	.00 (.98)	.00 (.97)	.00 (.99)	.00 (.98)	.01 (.99)
2	1,000	10	.00 (.98)	.02 (.97)	.00 (.97)	.00 (.97)	.01 (.96)	.00 (.99)
2	1,000	20	.00 (.99)	.01 (.98)	.00 (.98)	.00 (.96)	.01 (.97)	.00 (.98)
3	1,000	0	.01 (.99)	.00 (.97)	.01 (1.00)	.00 (.99)	.00 (.99)	.00 (.96)
3	1,000	10	.01 (.99)	.01 (.98)	.00 (.98)	.00 (.99)	.00 (.98)	.01 (.99)
3	1,000	20	.02 (.97)	.04 (.95)	.01 (.99)	.01 (.99)	.01 (.97)	.02 (.97)
15	1,000	0	.01 (.97)	.00 (.95)	.00 (.98)	.00 (.99)	.00 (.96)	.00 (.98)
15	1,000	10	.01 (.97)	.00 (.96)	.00 (.97)	.01 (.99)	.00 (.93)	.01 (.99)
15	1,000	20	.02 (.97)	.03 (.96)	.01 (.98)	.01 (.99)	.00 (.97)	.01 (.98)
60	1,000	0	.01 (0.97)	.01 (.95)	.00 (0.99)	.01 (.96)	.01 (.96)	.01 (.99)
60	1,000	10	.01 (0.97)	.01 (.95)	.00 (0.99)	.01 (.99)	.00 (.94)	.01 (.99)
60	1,000	20	.01 (1.00)	.02 (.97)	.01 (1.00)	.01 (.99)	.00 (.97)	.01 (.99)

TABLE 3
Absolute Bias (Coverage) for the FREE Alignment Estimates Using Maximum Likelihood

G	N	I	$\alpha_2 = 0.3$	$\psi_2 = 1.5$	$\lambda_{1,2} = 1$	$\nu_{2,2} = 0$	$\lambda_{5,2} = 0.5$	$\nu_{1,2} = -0.5$
2	100	0	.08 (1.00)	.00 (.99)	.00 (0.98)	.08 (1.00)	.01 (1.00)	.08 (1.00)
2	100	10	.81 (.86)	.04 (.96)	.02 (0.96)	.82 (.83)	.00 (.96)	.85 (.83)
2	100	20	.42 (.93)	.20 (.86)	.09 (1.00)	.46 (.90)	.04 (.92)	.48 (.89)
3	100	0	.41 (.96)	.07 (.98)	.02 (.97)	.40 (.96)	.03 (.98)	.40 (.96)
3	100	10	.04 (.94)	.00 (.98)	.00 (.98)	.03 (.93)	.01 (.94)	.01 (.90)
3	100	20	.03 (.93)	.22 (.91)	.09 (.95)	.01 (.96)	.04 (.92)	.01 (.97)
15	100	0	.39 (.92)	.02 (.97)	.00 (.99)	.40 (.95)	.00 (1.00)	.39 (.94)
15	100	10	.07 (.98)	.05 (.97)	.01 (1.00)	.07 (.99)	.01 (.97)	.06 (.99)
15	100	20	.10 (.95)	.18 (.89)	.06 (.98)	.09 (.99)	.03 (.96)	.09 (.98)
60	100	0	.40 (.79)	.02 (.99)	.00 (0.99)	.41 (0.76)	.01 (1.00)	.39 (.69)
60	100	10	.09 (.99)	.03 (.98)	.02 (1.00)	.11 (0.98)	.02 (.99)	.09 (1.00)
60	100	20	.11 (.98)	.11 (.91)	.05 (1.00)	.09 (0.98)	.04 (.98)	.09 (.98)
2	1,000	0	.00 (1.00)	.00 (.98)	.00 (.97)	.00 (1.00)	.00 (.98)	.00 (1.00)
2	1,000	10	.99 (.00)	.02 (.97)	.00 (.97)	.99 (.00)	.01 (.96)	.99 (.00)
2	1,000	20	.86 (.08)	.02 (.98)	.00 (.97)	.87 (.08)	.01 (.96)	.86 (.08)
3	1,000	0	.39 (.94)	.00 (.97)	.01 (1.00)	.38 (0.94)	.00 (.99)	.38 (.95)
3	1,000	10	.04 (.94)	.01 (.98)	.00 (.98)	.05 (0.93)	.00 (.98)	.05 (.94)
3	1,000	20	.01 (.96)	.04 (.95)	.01 (.99)	.00 (1.00)	.01 (.97)	.01 (.98)
15	1,000	0	.40 (0.87)	.00 (.95)	.00 (.98)	.39 (.90)	.00 (.96)	.39 (0.89)
15	1,000	10	.02 (0.98)	.00 (.96)	.00 (.97)	.01 (.97)	.00 (.93)	.01 (0.96)
15	1,000	20	.02 (1.00)	.03 (.96)	.01 (.98)	.01 (.98)	.00 (.97)	.01 (1.00)
60	1,000	0	.39 (0.09)	.01 (.95)	.00 (0.99)	.39 (.09)	.01 (.96)	.39 (.12)
60	1,000	10	.01 (0.96)	.01 (.95)	.00 (0.99)	.01 (.99)	.00 (.94)	.01 (.99)
60	1,000	20	.01 (0.99)	.02 (.97)	.01 (1.00)	.01 (.98)	.00 (.97)	.01 (.99)

There are several conclusions that we can draw from these simulation results. First, we see that the methods work as expected, asymptotically. For sample size $N = 1,000$ the point estimates are unbiased and coverage is near or above 95%.

Second, we see that there are biases when the sample size is small although the biases are not large in most cases and tend to occur only when the amount of noninvariance is large; that is, the combination of small sample size and large amount of noninvariance could lead to biased estimates. Third, we see that with many groups even a small degree of noninvariance requires a large sample size to avoid biases. Fourth, we see that the FREE alignment breaks down when there are only two groups; that is, the factor intercept in the first group is not really identified with the FREE alignment when there are only two groups. If one intercept is not identified, all intercept parameters will not be identified. With three or more groups, however, the FREE alignment seems to work well and in some cases better than the FIXED alignment. The FREE alignment also breaks down when there is no noninvariance in the parameters, that is, when $I = 0\%$. This is also as expected. If the parameter estimates are nearly identical across the groups, the additional factor mean parameter in the FREE alignment will be poorly identified and the results will be biased. The parameter is well identified if there is some noninvariance in the estimated model.[5]

Another conclusion that we can make is that the biases can increase as the amount of noninvariance increases. When the sample size is small and the noninvariance is relatively large we see the largest bias. In that case one can also expect that the simplicity function has multiple solutions. Different solutions can be reached in the different replications and some of those solutions are not the same as the parameters used to generate the data. Just as in EFA using rotations, not all data-generating sets of parameters can be recovered in the estimation. Only those can be recovered that have no simpler alternatives. When the sample size is small and there is a relatively large degree of noninvariance in the parameters, the estimated configural model can be sufficiently far away from the generating configural model so that the simplest model estimates might not be near the original parameters just because a simpler solution with less noninvariance has been found.

Simulation Study 2: Parameter Variation Using Maximum Likelihood and Bayes

The coverage for most parameters in Tables 2 and 3 is too high. In the next simulation study we evaluate the quality of the standard errors by computing the ratio between the average standard errors and the standard deviation of the parameters across the replications. Ideally this ratio will be close to 1, although when the point estimates have finite sample size bias the nominal coverage would be achieved when the standard errors are bigger. The simulation study we conduct in this section is a modification of the simulation study described in the previous section. We use a three-group example using the 20% noninvariance and we vary only the sample size within each group. The FREE alignment approach is used together with both the maximum likelihood and the Bayes estimator, where Bayes uses the configural method.

Table 4 shows the ratio between the average standard errors and the standard deviation for same model parameters we used in the previous section. If the standard errors are correct, this ratio should be close to 1. The results in Table 4 show that in most cases the ratio is not far from 1 and it appears to be more often bigger than 1, which corresponds to the standard errors being overestimated. The overestimation appears to decrease as the sample size increases and the standard errors appear to be asymptotically correct. The Bayes estimator gives slightly more accurate standard errors with the average ratio being 1.09 compared to the average ratio of 1.14 for the maximum-likelihood estimator. The worst value for the maximum-likelihood estimator is 1.60, and the worst value for the Bayes estimator is 1.32. The comparison between the two types of standard errors is important, as the two use completely different computational methods. The Bayes method does not rely on asymptotic theory and is more empirically driven, whereas the ML method relies on asymptotic theory but is independent of prior specifications.

Simulation Study 3: Comparing FIXED and FREE Alignment

From the previous simulation studies it appears that the FIXED alignment is almost always better than the FREE alignment. That is not true, however. The appearance is simply due to all of the previous simulations generating data where the factor mean in the first group is 0. In the next simulation we again generate data with 20% noninvariance; however, now we set the factor mean in the first group to 1. We report the simulation results for six parameters in Table 5. First we report the α_1 and α_2 estimates for the FREE alignment estimation. Then we report the α_2 parameter under the FIXED alignment estimation as well as $\alpha_2^* = \alpha_2 + 1$. This second parameter is essentially the α_2 parameter scaled to the data-generating scale where the first factor mean is set to 1 instead of 0. If all the measurement parameters were invariant, then α_2^* would be an unbiased estimate for the true value of α_2. This can be illustrated with a different simulation study where all the measurement parameters are invariant, but we do not report these simulation results here. We also

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[5] Currently M*plus* will provide a standard error warning if it detects that the FREE alignment breakdown occurs due to a small number of groups or insufficient measurement noninvariance. The solution to that problem is to simply use the FIXED alignment method.

TABLE 4
Ratio Between the Average Standard Errors and the Standard Deviation Using Maximum Likelihood and Bayes for Three Groups

Estimator	*N*	$\alpha_2 = 0.3$	$\psi_2 = 1.5$	$\lambda_{1,2} = 1$	$\nu_{2,2} = 0$	$\lambda_{5,2} = 0.5$	$\nu_{1,2} = -0.5$
ML	300	1.11	1.11	1.11	1.16	1.01	1.04
Bayes	300	1.09	1.32	1.27	1.23	1.12	1.19
ML	1,000	1.12	1.26	1.44	1.19	1.10	1.20
Bayes	1,000	1.09	1.19	1.27	1.10	1.06	1.16
ML	2,000	1.14	1.52	1.60	1.06	1.15	1.10
Bayes	2,000	1.05	1.13	1.10	1.06	0.99	0.97
ML	5,000	1.02	1.13	1.19	1.00	1.12	1.02
Bayes	5,000	0.96	1.09	1.18	0.94	0.99	0.97
ML	10,000	1.05	1.08	1.22	1.00	1.05	0.99
Bayes	10,000	0.94	1.13	1.08	0.96	0.99	0.97

Note. ML = maximum likelihood.

TABLE 5
Comparing FIXED and FREE Alignment Bias (Coverage)

G	*FREE* α_1	*FREE* α_2	*FIXED* α_2	*FIXED* α_2^*	*FREE* $\nu_{1,1}$	*FIXED* $\nu_{1,1}$
3	.01 (1.00)	.01 (.94)	1.28 (.00)	0.28 (0.43)	.00 (.98)	1.00 (.00)
5	.01 (0.99)	.01 (.97)	1.23 (.00)	0.23 (0.46)	.02 (.97)	1.00 (.00)
10	.01 (1.00)	.01 (.99)	1.23 (.11)	0.23 (0.13)	.01 (1.00)	1.00 (.00)
15	.00 (1.00)	.02 (1.00)	0.05 (.94)	0.95 (0.00)	.00 (1.00)	1.00 (.00)
20	.00 (0.98)	.02 (.99)	0.04 (.96)	0.96 (0.00)	.01 (.98)	1.00 (.00)

report in Table 5 the results for the first intercept in the first group $\nu_{1,1}$ for both the FIXED and the FREE alignment.

In this simulation we focus on illustrating the advantages of the FREE alignment. In the previous simulation we showed that when the number of groups is two or when there are no noninvariant parameters, the FIXED alignment is the better choice. Now we will show that in most other cases the FREE alignment is the better choice. We use a sample size of $N = 1{,}000$ and we only vary the number of groups. The results in Table 5 show that for any number of groups the parameter estimates for $\nu_{1,1}$ are biased with the FIXED alignment and are unbiased with the FREE alignment. The factor mean estimates in the first two groups, α_1 and α_2, are unbiased with the FREE alignment and are biased with the FIXED alignment, although it appears that the FIXED alignment bias for α_2 decreases as the number of groups increases. That can be explained by the fact that as the number of groups increases the effect of the misspecification in the first group has a smaller effect on the estimates when the number of groups is larger. The change in the bias of the α_2 estimates with the FIXED alignment appears to be drastic. That indicates multiple local optima in the fit function (Equation 9). The estimate α_2^* appears to be less biased than the original estimate for α_2 for a small number of groups, but it becomes more biased for a larger number of groups. This simulation shows that whenever we have more than two groups and measurement noninvariance, the FREE alignment parameter estimates are more accurate than the FIXED alignment estimates.

A MULTIPLE-GROUP ALIGNMENT ANALYSIS OF 26 COUNTRIES

This section continues the analysis of the traditionconformity items for 49, 894 subjects in 26 European countries that was introduced earlier. It is shown how the alignment method resolves the problem of comparing factor means found with the traditional multiple-group factor analysis under scalar invariance. Maximum-likelihood estimation was used for the initial configural model. The FREE alignment approach was initially used but the standard error results indicated that it might be poorly identified as discussed previously.[6] Using the country with factor mean closest to zero, the FIXED approach is used with Country 22 chosen as the reference group with factor mean 0.

Table 6 shows the (non-) invariance results for the measurement intercepts and factor loadings using the previous approach. The countries that are deemed to have a significantly noninvariant measurement parameter are shown as bolded within parentheses. As seen in Table 6, most of the items show a large degree of measurement noninvariance for the measurement intercepts and, to a lesser extent, the loadings. The large degree of noninvariance is in line with the findings of the traditional approach using the scalar model. However, Table 6 also shows that item IPBHPRP has no significant measurement noninvariance and this item is therefore particularly useful for comparing these countries on the factor.

Table 7 shows each item's intercept and loading contribution to the optimized simplicity function. These values add up to the total optimized simplicity function value. In line with Table 6, it is seen that the item IPBHPRP contributes by far the least, whereas the items IPMODST, IMPTRAD, and IPFRULE contribute roughly the same. This implies that IPMODST, IMPTRAD, and IPFRULE have a similar degree of measurement noninvariance. The R^2 column of Table 7 also indicates that the IPBHPRP item is the most invariant in

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[6] This is a warning provided by M*plus* as mentioned in footnote 5.

TABLE 6
European Social Survey Tradition Conformity Items: Approximate Measurement (Non-) Invariance for Intercepts and Loadings Over 26 Countries

Intercepts	
IPMODST	(**1**) (**2**) (**3**) 4 (**5**) (**6**) (**7**) 8 (**9**) (**10**) (**11**) 12 13 (**14**) 15 16 (**17**) (**18**) (**19**) (**20**) (**21**) 22 23 (**24**) 25 (**26**)
IMPTRAD	(**1**) (**2**) (**3**) (**4**) 5 (**6**) 7 8 (**9**) 10 (**11**) 12 (**13**) (**14**) (**15**) (**16**) 17 (**18**) (**19**) (**20**) (**21**) (**22**) 23 24 (**25**) (**26**)
IPFRULE	(**1**) 2 (**3**) (**4**) 5 (**6**) (**7**) (**8**) (**9**) 10 (**11**) (**12**) (**13**) (**14**) (**15**) (**16**) 17 (**18**) (**19**) (**20**) 21 (**22**) 23 (**24**) 25 26
IPBHPRP	1 2 3 4 5 6 7 8 9 10 11 12 13 14 15 16 17 18 19 20 21 22 23 24 25 26
Loadings	
IPMODST	(**1**) 2 (**3**) 4 5 (**6**) (**7**) 8 (**9**) (**10**) (**11**) (**12**) 13 14 15 16 17 18 19 20 21 22 (**23**) (**24**) 25 26
IMPTRAD	1 2 3 4 5 6 (**7**) 8 9 10 11 12 13 14 15 16 17 18 19 20 (**21**) 22 (**23**) 24 (**25**) 26
IPFRULE	1 2 3 4 5 (**6**) 7 8 9 (**10**) (**11**) 12 13 14 15 16 17 18 19 20 21 22 23 24 25 26
IPBHPRP	1 2 3 4 5 6 7 8 9 10 11 12 13 14 15 16 17 18 19 20 21 22 23 24 25 26

TABLE 7
26-Country Example: Alignment Fit Statistics

	Intercepts			*Loadings*		
Item	*Fit Function Contribution*	R^2	*Variance*	*Fit Function Contribution*	R^2	*Variance*
IPMODST	−229.849	0.203	0.105	−158.121	0.000	0.020
IMPTRAD	−199.831	0.566	0.058	−134.042	0.000	0.014
IPFRULE	−213.806	0.198	0.103	−113.305	0.263	0.008
IPBHPRP	−32.836	1.000	0.000	−33.941	0.999	0.000

that essentially all the variation across groups in the configural model intercepts and loadings for this item is explained by variation in the factor mean and factor variance across groups. The variance column of Table 7 again shows the variation in the alignment parameters across groups and again indicates invariance for item IPBHPRP. Taken together, these three columns give an indication of the plausibility of the assumption underlying the alignment method, namely that an invariance pattern can be found. In this example, the inclusion of the IPBHPRP item makes this assumption plausible and ensures good performance of the alignment method. This is also supported by the earlier Monte Carlo simulation studies. Note, however, that our simulation studies show that to obtain good alignment performance, it is not necessary that any item has invariant measurement parameters across all groups.

Table 8 shows the factor means as estimated by the alignment method. For convenience in the presentation, the factor means are ordered from high to low and groups that have factor means significantly different on the 5% level are shown. Figure 2 compares the estimated factor means using the alignment method with the factor means of the scalar invariance model (without relaxing any invariance restrictions). Recalling the reversed scale, the two methods agree that Sweden (Country 23) has the lowest level of traditionconformity and Cyprus (Country 4) has the highest level. The alignment method, however, finds that Portugal (Country 21) has a significantly different mean from the Netherlands (Country 18), whereas the scalar method finds essentially no difference between these countries. Other discrepancies between the two methods are found for France compared to Switzerland and for Norway compared to Russia.

Monte Carlo Simulation Check of 26-Country Alignment

The earlier Monte Carlo simulations studied how well the alignment method works under different conditions of varying number of groups, group sample size, and degree of measurement noninvariance. Any given data set, however, has unique characteristics and it is useful to consider how well the methods work under conditions that more closely resemble those at hand. The preceding realdata analysis of the 26 countries indicates a larger percentage of noninvariant measurement intercepts and loadings than was studied in the Monte Carlo simulations. The magnitudes of noninvariance for the loadings, however, are smaller. Relative to the Monte Carlo simulations, the 26 countries represent a midlevel number of groups and a large number of observations per group, 1, 919. It is of interest to conduct a simulation based on these features, using the parameter estimates of the alignment method as data-generating population parameter values, to see how well population values can be recovered by the alignment method.[7]

The results of the simulation study for a selection of the model parameters are presented in Table 9 for group sample sizes of $N_g = 100$, $N_g = 200$, $N_g = 500$, and $N_g = 2,000$, the latter being close to the real-data group size. Table 9 contains the true values as well as the average estimates and coverage across 500 replications for the first five groups. Intercepts and loadings are shown for only the IPFRULE item. The variation across the groups of intercept and loadings gives an indication of the magnitude of noninvariance in this example. Interestingly, good recovery for all parameters except the factor variances is found already for $N_g = 100$. For sample size $N_g = 2,000$ almost flawless results are seen.

It is interesting that good recovery of measurement parameters as well as factor means and factor variances is possible even when there is a large degree of noninvariance.

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[7] This is conveniently carried out in M*plus* using the SVALUES option to save parameter estimates in a form suitable for input in a Monte Carlo run.

TABLE 8
European Social Survey Tradition Conformity Items: Factor Mean Comparisons of 26 Countries

Ranking	*Group*	*Value*	*Groups With Significantly Smaller Factor Mean*
1	23	0.928	21 18 6 10 3 11 26 7 5 16 8 1 12 19 22 14 20 25 15 17 9 2 13 24 4
2	21	0.613	18 6 10 3 11 26 7 5 16 8 1 12 19 22 14 20 25 15 17 9 2 13 24 4
3	18	0.391	26 7 5 16 8 1 12 19 22 14 20 25 15 17 9 2 13 24 4
4	6	0.357	26 7 5 16 8 1 12 19 22 14 20 25 15 17 9 2 13 24 4
5	10	0.342	7 5 16 8 1 12 19 22 14 20 25 15 17 9 2 13 24 4
6	3	0.331	7 5 16 8 1 12 19 22 14 20 25 15 17 9 2 13 24 4
7	11	0.310	5 16 8 1 12 19 22 14 20 25 15 17 9 2 13 24 4
8	26	0.247	16 8 1 12 19 22 14 20 25 15 17 9 2 13 24 4
9	7	0.200	12 19 22 14 20 25 15 17 9 2 13 24 4
10	5	0.161	19 22 14 20 25 15 17 9 2 13 24 4
11	16	0.130	19 22 14 20 25 15 17 9 2 13 24 4
12	8	0.121	19 22 14 20 25 15 17 9 2 13 24 4
13	1	0.114	19 22 14 20 25 15 17 9 2 13 24 4
14	12	0.100	22 14 20 25 15 17 9 2 13 24 4
15	19	0.007	14 20 25 15 17 9 2 13 24 4
16	22	0.000	14 20 25 15 17 9 2 13 24 4
17	14	−0.114	17 9 2 13 24 4
18	20	−0.145	9 2 13 24 4
19	25	−0.185	2 13 24 4
20	15	−0.190	2 13 24 4
21	17	−0.214	13 24 4
22	9	−0.234	13 24 4
23	2	−0.288	4
24	13	−0.314	4
25	24	−0.327	4
26	4	−0.478	

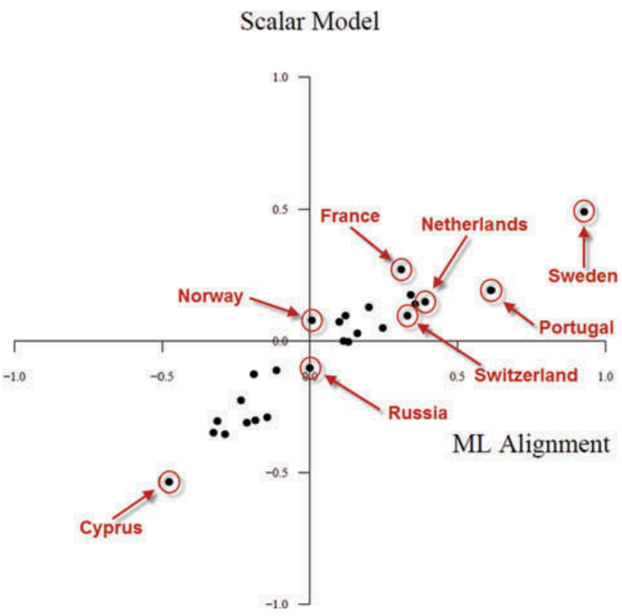

FIGURE 2 Factor means for tradition conformity in 26 countries: Alignment method versus scalar model. *Note*. ML = maximum likelihood.

It cannot be expected, however, that all real-data settings can give acceptable alignment results and Monte Carlo studies are therefore a useful complement to the alignment method.

CONCLUSIONS

The alignment method described in this article can be used to estimate group-specific factor means and variances without requiring exact measurement invariance. A strength of the method is the ability to conveniently estimate models for many groups. The method can be used to estimate models with multiple factors and many indicator variables. The method is a valuable alternative to the currently used multiple-group CFA methods for studying measurement invariance that require multiple manual model adjustments guided by imperfect modification indexes or other ad-hoc procedures based on multiple likelihood ratio tests. Multiple-group CFA is simply not practical with many groups. In contrast, the alignment method essentially automates and greatly simplifies measurement invariance analysis. The method provides a detailed account of parameter invariance for every model parameter in every group.

The alignment method can also be viewed as an exploratory method. Aligned factor analysis can be followed by an informed multiple-group CFA model similar to the way CFA models are used as a follow-up to an EFA model. The alignment method can be used to determine individual parameter invariance status, but it can also be used to determine the most invariant indicator variables in the measurement instrument. That information can be taken into account when constructing a well-fitting CFA model that

TABLE 9
Monte Carlo Simulation Check of 26-Country Alignment: True Values, Estimates, and Coverage (in Parentheses) for Four Group Sizes

Parameter	*True Value*	$N_g = 100^a$	$N_g = 200$	$N_g = 500$	$N_g = 2{,}000$
Group 1					
Factor mean	0.114	.01 (.99)	−.01 (.96)	−.01 (.99)	−.01 (.94)
Factor variance	0.902	−.09 (.93)	−.08 (.95)	.04 (.96)	.00 (.97)
Intercept	3.177	−.01 (.96)	−.01 (.96)	.01 (.96)	.00 (.96)
Loading	0.725	.10 (.99)	.06 (.99)	−.06 (.94)	.00 (.97)
Group 2					
Factor mean	−0.288	−.01 (.98)	.00 (.97)	.01 (.96)	.00 (.96)
Factor variance	1.059	.06 (.97)	.00 (.95)	−.06 (.96)	.00 (.95)
Intercept	2.741	.00 (.97)	.01 (.97)	.00 (.96)	.00 (.94)
Loading	0.704	.01 (.98)	.01 (.98)	.00 (.96)	.00 (.97)
Group 3					
Factor mean	0.331	−.02 (.95)	−.02 (.94)	.00 (.96)	−.01 (.95)
Factor variance	1.222	−.18 (.90)	−.19 (.91)	.04 (.93)	−.09 (.89)
Intercept	3.202	−.01 (.95)	.01 (.95)	.01 (.96)	.00 (.95)
Loading	0.654	.10 (.98)	.08 (.98)	−.05 (.91)	.03 (.94)
Group 4					
Factor mean	−0.478	.00 (.97)	.00 (.97)	.00 (.98)	.00 (.94)
Factor variance	0.881	.02 (.96)	−.04 (.97)	−.03 (.95)	−.01 (.96)
Intercept	3.197	.01 (.96)	.00 (.97)	.00 (.94)	.00 (.93)
Loading	0.716	.02 (.98)	.03 (.98)	−.01 (.97)	.00 (.96)
Group 5					
Factor mean	0.161	.01 (.98)	.00 (.99)	−.01 (.96)	.00 (.96)
Factor variance	1.065	−.05 (.94)	−.04 (.94)	.02 (.96)	−.01 (.95)
Intercept	2.699	−.02 (.97)	.00 (.96)	.02 (.95)	.00 (.94)
Loading	0.608	.05 (.97)	.03 (.96)	−.03 (.93)	.00 (.95)

[a] Only 488 out of 500 replications are reported because remaining replications did not replicate the best alignment fit function value.

accommodates partial measurement noninvariance while still estimating group-specific factor means and variances.

An alternative to the alignment method's handling of many groups is to treat the data as multilevel, viewing the groups as clusters and allowing random intercepts and loadings (see, e.g., De Jong, Steenkamp, & Fox, 2007; Fox, 2010). Muthén and Asparouhov (2013b) compared the two approaches and pointed out that the alignment method has many advantages. The advantages include better performance with a small number of factor indicators and better performance with a small number of groups. The alignment method also gives information about which groups contribute to noninvariance and is less computationally demanding. Disadvantages of the alignment method include handling a very large number of groups (e.g., greater than 100) and requiring a sufficiently clear measurement invariance pattern.

Current limitations to this methodology are that indicator variables can load on only one factor; that is, models with cross-loadings are not accommodated. In addition, CFA models with covariates cannot be estimated with the alignment method. These extensions can in principle be developed in the future using the same techniques. Alignment methods for multiple-group EFA models (referred to as ESEM; Asparouhov & Muthén, 2009) can also be developed in the future.

As our simulation studies illustrate, the aligned parameter estimates can have small biases in certain situations. The extent of these biases has to be studied further and the method has to be evaluated further with more practical applications. In this regard, Muthén and Asparouhov (2013b) suggested that the strength of the correlation between true and estimated factor means and variances might be more important than bias in individual parameters. The fundamental assumption of the alignment method is that there is a pattern of approximate measurement invariance in the data. Currently the method does not provide a clear instrument to indicate when this assumption is violated to a significant degree, although Monte Carlo studies are helpful as illustrated earlier. The alignment method will always estimate the simplest model with the largest amount of noninvariance, but if the assumption of approximate measurement invariance is violated, the simplest and most invariant model might not be the true model. For example, if data are generated where a minority of the factor indicators have invariant measurement parameters and the majority of the indicators have the same amount of noninvariance, the alignment method will choose the noninvariant indicators as the invariant ones, singling out the other indicators as noninvariant.

The alignment method is unique in that there is no simple alternative for estimating factor means and variances in the context of measurement noninvariance given that these parameters are deemed unidentified by traditional methods accommodating measurement noninvariance. The alignment method formalizes the analyst's assumption and belief that the measurement instrument should be similar across the groups while the actual factor distribution can vary across the groups. No other method automatically accommodates this intangible information within its estimation procedure. The alignment method is implemented in M*plus* Version 7.11 and scripts for all of the preceding analyses are available at www.statmodel.com

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APPENDIX

In this section we provide some details on the alignment estimation and the estimation of the standard errors for the aligned parameters. Denote by v_g

$$v_g = \frac{1}{\sqrt{\psi_g}}.$$

Then

$$\lambda_{pg,1} = v_g \lambda_{pg,0} \tag{A.1}$$

$$\nu_{pg,1} = \nu_{pg,0} - v_g \alpha_g \lambda_{pg,0}. \tag{A.2}$$

The simplicity function can be expressed in terms of v_g and α_g as

$$F\left(v_g, \alpha_g\right) = \sum_p \sum_{g_1<g_2} w_{g_1,g_2} f\left(v_{g_1}\lambda_{pg_1,0} - v_{g_2}\lambda_{pg_2,0}\right) + \sum_p \sum_{g_1<g_2} w_{g_1,g_2} f\left(\nu_{pg_1,0} - v_{g_1}\alpha_{g_1}\lambda_{pg_1,0} - \nu_{pg_2,0} + v_{g_2}\alpha_{g_2}\lambda_{pg_2,0}\right)$$

To minimize the simplicity function with respect to all v_g and α_g we can use a standard minimization algorithm based on the first derivative of F with respect to v_g and α_g.

As a first step we compute the derivative of F assuming that all v_g parameters are free and unconstrained. After that we accommodate the constraint $v_1 = (v_2 v_3 \ldots v_G)^{-1}$ as well as the constraint $\alpha_1 = 0$, which applies only for the FIXED alignment method. We denote the function F_0 to be the function F without the preceding constraints. Thus the function F_0 has as arguments

$$F_0\left(v_1, v_2, \ldots, v_G, \alpha_1, \alpha_2, \ldots, \alpha_G\right) = F$$

Now F can be expressed as

$$F(v2, \ldots, v_G, \alpha_1, \ldots, \alpha_G) = F_0\Big(\left(v_2 v_3 \ldots v_G\right)^{-1}, v2, \ldots, v_G, \alpha_1, \ldots, \alpha_G\Big)$$

To get the derivatives of F we use

$$\frac{\partial F}{\partial v_g} = \frac{\partial F_0}{\partial v_g} - \frac{\partial F_0}{\partial v_1}\frac{v_1}{v_g}$$

$$\frac{\partial F}{\partial \alpha_g} = \frac{\partial F_0}{\partial \alpha_g}.$$

Next we focus on the computation of the standard errors of the aligned parameters. An outline of this computation is as follows. Let us denote by m_1 all the parameters of the configural model: $\nu_{pg,0}$, $\lambda_{pg,0}$, and the residual variances $\theta_{pg,0}$. Let us denote by m_2 the aligned parameters α_g and v_g. The simplicity function F can be expressed as a function of both m_1 and m_2 parameters and the aligned parameters minimize the simplicity function

$$F = F\left(m_1, m_2\right).$$

Because F is optimized with respect to the m_2 parameters, the corresponding derivatives are all 0 and can be used as a set of equations that can be solved for m_2 with respect to m_1. Thus we have the equation

$$\frac{\partial F\left(m_1, m_2\right)}{\partial m_2} = 0,$$

which we use to solve implicitly for m_2 as a function of m_1, $m_2 = m_2(m_1)$. Thus

$$\frac{\partial F\left(m_1, m_2\left(m1\right)\right)}{\partial m_2} = 0.$$

If we differentiate the preceding equation with respect to m_1 we get

$$\frac{\partial^2 F\left(m_1, m_2\right)}{\left(\partial m_2\right)^2}\frac{\partial m_2}{\partial m_1} + \frac{\partial^2 F\left(m_1, m_2\right)}{\left(\partial m_2\right)\left(\partial m_1\right)} = 0.$$

From here we can derive the implicit derivatives of m_2 with respect to m_1

$$\frac{\partial m_2}{\partial m_1} = -\left(\frac{\partial^2 F\left(m_1, m_2\right)}{\left(\partial m_2\right)^2}\right)^{-1} \frac{\partial^2 F\left(m_1, m_2\right)}{\left(\partial m_2\right)\left(\partial m_1\right)}. \tag{A.3}$$

Now we can derive the asymptotic distribution of the aligned parameters m_2. Suppose the asymptotic variance covariance for the configural parameters m_1 is $Var(m_1) = H$. This matrix is obtained from the maximum-likelihood estimation of the configural model. The joint asymptotic variance covariance for all the parameters $m = (m_1, m_2)$ can be obtained as follows

$$Var\left(m\right) = AHA^T$$

where

$$A = \left(\frac{\partial m_2}{\partial m_1}, I\right)$$

and I is the identity matrix of size the size of the vector m_1. This joint distribution for the configural parameter m_1 and the aligned parameters m_2 will be needed to compute the asymptotic distribution of the aligned loadings and intercepts, which are themselves functions of m_1 and m_2. We compute the second derivatives used in Equation (A.3) similar to the way the first derivatives are computed. First we compute the second derivatives of F_0 and from there we can obtain the second derivatives of F. To get the asymptotic distribution for the aligned parameters parameters $\lambda_{pg,1}$ and $\nu_{\mathrm{pg};1}$ we use Equations 7 and 8 and the delta method.