Multiple-Group Factor Analysis Alignment

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Abstract

This paper 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 indices. Multiple-group CFA is not practical with many groups due to poor model fit of the scalar model and too many large modification indices. 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.

1   Introduction

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 indices (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 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 may 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 will return to this example at the end of the paper, using it to demonstrate the new approach that we propose.

Beierlein et al. (2012) analyzed data from the European Social Survey comprising 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.

[Table 1 about here.]

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-value $= 0.000$). A large part of this poor fit is due to the large sample size of $49,894$, but other fit indices also indicate very poor fit: $RMSEA = 0.148$, $CFI = 0.677$. In addition, there are many large modification indices: 83 in the range of 10-100, 15 in the range of 100-200, and 16 in the range of 200-457 (the largest value). The presence of so many large modification indices implies that a long sequence of model modifications is needed to reach a model with acceptable fit and the search for a good model may 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 paper we describe a radically different method: Alignment optimization. The alignment can be based on maximum-likelihood or Bayes estimation.

Section 2 presents the alignment method and Section 3 discusses its implementation in a Bayesian framework. Section 4 presents ideas for the secondary goal of finding measurement parameters that are significantly non-invariant. Section 5 discusses Monte Carlo simulation studies using both maximum-likelihood and Bayesian analysis. Section 6 returns to the application of tradition-conformity items measured in 26 countries. Section 7 concludes.

2 Alignment

Consider the multiple-group factor analysis model

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

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

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 indices are used to relax the measurement part of the model step by step, i.e., one parameter at a time. The problem with this approach is not only that the model modifications are done manually and many models have to be estimated before a well-fitting model is found. Another problem with this approach is that among the many well-fitting models the modification indices approach does not guarantee that the simplest, most interpretable model with the fewest number of non-invariant parameters is reached. Even with only three groups, the simplest path of model modification may 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 (1), i.e., 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 EFA analysis.

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 non-invariant measurement parameters and the amount of measurement non-invariance 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, i.e., despite the fact that the aligned model attempts to minimize the amount of non-invariance 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, i.e., has the same fit as the unrotated model.

Denote the estimates of model M0 by $\nu_{pg,0}$ and $\lambda_{pg,0}$. 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. These parameters can be obtained as follows

$$\lambda_{pg,1} = \frac{\lambda_{pg,0}}{\sqrt{\psi_g}}, \tag{2}$$

$$\nu_{pg,1} = \nu_{pg,0} - \alpha_g \frac{\lambda_{pg,0}}{\sqrt{\psi_g}}. \tag{3}$$

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

$$F = \sum_p \sum_{g_1 < g_2} w_{g_1,g_2} f(\lambda_{pg_1,1} - \lambda_{pg_2,1}) + \sum_p \sum_{g_1 < g_2} w_{g_1,g_2} f(\nu_{pg_1,1} - \nu_{pg_2,1}). \tag{4}$$

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 analysis, see for example 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 0.0001. 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 make 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 non-invariant measurement parameters and many approximately invariant measurement parameters rather than many medium-sized non-invariant measurement parameters. This is similar to the fact that EFA rotation functions aim for either large or small loadings, but not mid-sized 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

$$\psi_1 \times ... \times \psi_G = 1. \tag{5}$$

We also set $\alpha_1 = 0$, although this second constraint is generally not needed and in fact it may itself lead to biased parameter estimates. In principle the alignment optimization can identify $2G - 1$ of the parameters α_g and ψ_g, while the last

parameter is identified through equation (5). 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, i.e., $\psi_1 = 1$.[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 (2) and (3).

Minimizing the simplicity function F may 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 may 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 F with respect to those parameters yield identifying equations for

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[1]In fact in Mplus by default the parameters are indeed reported in that metric, however, the alignment optimization is carried out using (5) to ensure full symmetry between the different groups.

[2]By default Mplus uses 30 random starting values, however, more random starting values should be used if the global minimum is not replicated at least twice. Mplus 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 Mplus uses $-F$ instead of F as it maximizes the opposite of the fit function.

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 above 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.

3   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 non-informative priors. For the BSEM method the M0 model is a model where all measurement intercepts and loadings are held approximately equal/invariant across groups by specifying highly correlated priors, see Section 4 in Muthén and Asparouhov (2013), 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

$$\lambda_{pg,0} = \lambda_{pg,1}\sqrt{\psi_g}, \tag{6}$$

$$\nu_{pg,0} = \nu_{pg,1} + \alpha_g\lambda_{pg,1}, \tag{7}$$

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 (6) and (7) 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 (4) in each MCMC iteration. In other words, using the configural intercept and loadings values in each MCMC iteration we minimize the simplicity function (4) 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 of the advantages of the Bayesian alignment estimation over the ML alignment estimation is that it can easily accommodate binary indicator variables through the probit link function. In the MCMC estimation binary variables are used to generate the underlying normal variables with variance 1, see Asparouhov and Muthén (2010). Once the underlying variables are generated the estimation proceeds as with normally distributed indicator variables.

Another advantage of the Bayesian alignment estimation over the ML 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 may 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) may improve the model fit. In this way, the Baysian alignment model based on BSEM can have a better model fit than the ML 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, while the BSEM estimates are obtained by minimizing the variability of the estimates across groups. The alignment estimates will be simpler to interpret as fewer non-invariant parameters will be found.

Another advantage of the BSEM alignment estimation is that it can be used to resolve estimation problem within individual groups where there is 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.

4   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 bi-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 may work equally well. Here we do not provide a theoretical justification, rather, we provide details on the post-estimation algorithm that is used to determine invariance. This procedure works very well with simulated data, where the invariance and the non-invariant parameters are known by design. Thus we expect the procedure to work well in practical applications as well. Below we describe the details of the algorithm implemented in Mplus 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, i.e., multiple testing is done and to avoid false non-invariance discovery we use smaller p-values than the nominal 0.05.

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 0.01. 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 0.001 the group is added to the invariant set and 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. The above procedure is based on the delta method when the ML 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 1000 MCMC iterations will be sufficient. The above 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

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

invariant variable and use that as an anchor item in a multiple-group CFA, or to identify the most non-invariant variables which can then be revised or removed from the measurement instrument. The contribution to the simplicity function (4) from each variable can be isolated and reflects the level of non-invariance for the variable. The smaller the contribution is the more invariant the variables is.[4]

5   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 in Section 6.1, based on the analysis of the tradition-conformity data presented in Section 1.

5.1   Simulation Study 1: Bias and Coverage using ML

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 non-invariant intercept parameter and one non-invariant loading parameter. In all groups the invariant loadings and the residual variances of the indicator variables are set

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

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 3 groups, group 4 uses the same parameters as group 1, groups 5 uses the same parameters as group 2, etc. The non-invariant parameters in group 1 are $\nu_5 = 0.5$ and $\lambda_3 = 1.4$. The non-invariant parameters in group 2 are $\nu_1 = -0.5$ and $\lambda_5 = 0.5$. The non-invariant 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 v.s. FIXED, and the degree of non-invariance. 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 $N = 1000$ and we use four different number 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 non-invariance among the intercept and loading parameters. The generation scheme described above has $I = 20\%$ non-invariance because 1 out of 5 intercepts and 1 out of 5 loadings are non-invariant. To obtain different levels of non-invariance we modify the above generation scheme as follows. To obtain $I = 0\%$ we replace all the non-invariant values with invariant values

and to obtain $I = 10\%$ we remove the non-invariant loading parameter from each odd numbered group and we remove the non-invariant 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 non-invariance I, i.e., 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 1019 parameters.

Using the FIXED and FREE options, respectively, Tables 1 and 2 report the results for 6 parameters which are typical representatives for the rest of the model parameters. 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 non-invariant parameters in group 2, the first intercept $\nu_{1,2}$ and the fifth loading $\lambda_{5,2}$. ML estimation is used.

[Table 2 about here.]

[Table 3 about here.]

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=1000 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

17

biases are not large in most cases and tend to occur only when the amount of non-invariance is large, i.e., the combination of small sample size and large amount of non-invariance may lead to biased estimates. Third, we see that with many groups even a small degree of non-invariance requires a large sample size to avoid biases. Fourth, we see that the FREE alignment breaks down when there are only two groups, i.e., 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 non-invariance in the parameters, i.e., when $I = 0\%$. This is also as expected. If the parameters 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 non-invariance in the estimated model.[5]

Another conclusion that we can make is that the biases can increase as the amount of non-invariance increases. When the sample size is small and the non-invariance is relatively large we see the largest bias. In that case one can also expect that the simplicity function has multiple solutions and 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 analysis 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

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[5]Currently Mplus 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 non-invariance. The solution to that problem is to simply use the FIXED alignment method.

the sample size is small and there is a relatively large degree of non-invariance 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 non-invariance has been found.

5.2   Simulation Study 2: Parameter Variation using ML and Bayes

The coverage for most parameters in Tables 1 and 2 is somewhat 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% non-invariance and we vary only the sample size within each group. The FREE alignment approach is used together with both the ML and the Bayes estimator, where Bayes uses the configural method.

Table 3 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 3 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

19

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 ML estimator. The worst values for the ML estimator is 1.60 while 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, while the ML method relies on asymptotic theory but is independent of prior specifications.

[Table 4 about here.]

5.3 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 however is not true. 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% non-invariance, however, now we set the factor mean in the first group to 1. We report the simulation results for six parameters in Table 4. 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

20

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 this simulation results here. We also report in Table 4 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 non-invariant 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 sample size of $N = 1000$ and we only vary the number of groups. The results in Table 4 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 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 (4). The estimate α_2^* appears to be less biased that the original estimate for α_2 for small number of groups but it becomes more biased for larger number of groups. This simulations shows that whenever we have more than two groups and measurement non-invariance the FREE alignment parameter estimates are more accurate than the FIXED alignment estimates.

[Table 5 about here.]

6   A Multiple-Group Alignment Analysis of 26 Countries

This section continues the analysis of the tradition-conformity items for $49,894$ subjects in 26 European countries that was introduced in Section 1. 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 may be poorly identified as discussed in Section 2.[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 approach of Section 4. The countries that are deemed to have a significantly non-invariant measurement parameter are shown as bolded within parentheses. As seen in Table 6, most of the items show a large degree of measurement non-invariance for the measurement intercepts and, to a lesser extent, the loadings. The large degree of non-invariance 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 non-invariance and this item is therefore particularly useful for comparing these countries on the factor.

Table 7 shows the factor means as estimated by the alignment method. For

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[6]This is a warning provided by Mplus as mentioned in footnote 5

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 1 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 tradition-conformity and Cyprus (country 4) 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.

[Table 6 about here.]

[Table 7 about here.]

[Figure 1 about here.]

6.1 Monte Carlo Simulation Check of 26-Country Alignment

The Monte Carlo simulations of Section 5 studied how well the alignment method works under different conditions of varying number of groups, group sample size, and degree of measurement non-invariance. 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 Section 6 real-data analysis of the 26 countries indicates a larger percentage of non-invariant

measurement intercepts and loadings than was studied in the Monte Carlo simulations. The magnitudes of non-invariance for the loadings, however, are smaller. Relative to the Monte Carlo simulations, the 26 countries represent a mid-level 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, in order 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 8 for group sample sizes of $N_g = 100$, $N_g = 200$, $N_g = 500$, and $N_g = 2000$, the latter being close to the real-data group size. The table 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 non-invariance in this example. Interestingly, good recovery for all parameters except the factor variances is found already for $N_g = 100$. For sample size $N_g = 2000$ almost flawless results are seen.

[Table 8 about here.]

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

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

7 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 indices 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 followup 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 accommodates partial measurement non-invariance while still estimating group-specific factor means and variances.

Current limitations to this methodology are that indicator variables can load on only one factor, i.e., models with cross-loadings are not accommodated. In addition, CFA models with covariates can not be estimated with the alignment

method. Only continuous and binary variables are currently accommodated in the above framework, i.e., ordered polytomous variables are currently not included. 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 have to be studied further and the method has to be evaluated further with more practical applications. It is still unclear what amount of measurement non-invariance this methodology can accommodate. The fundamental assumption of the alignment method is that there is 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 in Section 6.1. The alignment method will always estimate the simplest model with the largest amount of non-invariance, but if the assumption of approximate measurement invariance is violated the simplest and most invariant model may 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 non-invariance, the alignment method will choose the non-invariant indicators as the invariant ones, singling out the other indicators as non-invariant.

The alignment method is unique in that there is no simple alternative for estimating factor means and variances in the context of measurement non-invariance given that these parameters are deemed unidentified by traditional methods accommodating measurement non-invariance. 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 Mplus Version 7.11 and scripts for all of the above analyses are available at www.statmodel.com.
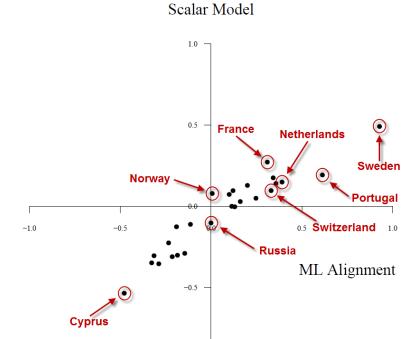
8 Acknowledgement

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List of Figures

Figure 1: Factor Means for Tradition-Conformity in 26 Countries: Alignment Method vs Scalar Model

List of Tables

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).

Table 2: Absolute Bias (Coverage) for the FIXED Alignment Estimates using ML

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	1000	0	.01(1.00)	.00(.98)	.00(.97)	.00(.99)	.00(.98)	.01(.99)
2	1000	10	.00(.98)	.02(.97)	.00(.97)	.00(.97)	.01(.96)	.00(.99)
2	1000	20	.00(.99)	.01(.98)	.00(.98)	.00(.96)	.01(.97)	.00(.98)
3	1000	0	.01(.99)	.00(.97)	.01(1.00)	.00(.99)	.00(.99)	.00(.96)
3	1000	10	.01(.99)	.01(.98)	.00(.98)	.00(.99)	.00(.98)	.01(.99)
3	1000	20	.02(.97)	.04(.95)	.01(.99)	.01(.99)	.01(.97)	.02(.97)
15	1000	0	.01(.97)	.00(.95)	.00(.98)	.00(.99)	.00(.96)	.00(.98)
15	1000	10	.01(.97)	.00(.96)	.00(.97)	.01(.99)	.00(.93)	.01(.99)
15	1000	20	.02(.97)	.03(.96)	.01(.98)	.01(.99)	.00(.97)	.01(.98)
60	1000	0	.01(0.97)	.01(.95)	.00(0.99)	.01(.96)	.01(.96)	.01(.99)
60	1000	10	.01(0.97)	.01(.95)	.00(0.99)	.01(.99)	.00(.94)	.01(.99)
60	1000	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 ML

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	1000	0	.00(1.00)	.00(.98)	.00(.97)	.00(1.00)	.00(.98)	.00(1.00)
2	1000	10	.99(.00)	.02(.97)	.00(.97)	.99(.00)	.01(.96)	.99(.00)
2	1000	20	.86(.08)	.02(.98)	.00(.97)	.87(.08)	.01(.96)	.86(.08)
3	1000	0	.39(.94)	.00(.97)	.01(1.00)	.38(0.94)	.00(.99)	.38(.95)
3	1000	10	.04(.94)	.01(.98)	.00(.98)	.05(0.93)	.00(.98)	.05(.94)
3	1000	20	.01(.96)	.04(.95)	.01(.99)	.00(1.00)	.01(.97)	.01(.98)
15	1000	0	.40(0.87)	.00(.95)	.00(.98)	.39(.90)	.00(.96)	.39(0.89)
15	1000	10	.02(0.98)	.00(.96)	.00(.97)	.01(.97)	.00(.93)	.01(0.96)
15	1000	20	.02(1.00)	.03(.96)	.01(.98)	.01(.98)	.00(.97)	.01(1.00)
60	1000	0	.39(0.09)	.01(.95)	.00(0.99)	.39(.09)	.01(.96)	.39(.12)
60	1000	10	.01(0.96)	.01(.95)	.00(0.99)	.01(.99)	.00(.94)	.01(.99)
60	1000	20	.01(0.99)	.02(.97)	.01(1.00)	.01(.98)	.00(.97)	.01(.99)

Table 4: Ratio between the Average Standard Errors and the Standard Deviation using ML 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	1000	1.12	1.26	1.44	1.19	1.10	1.20
Bayes	1000	1.09	1.19	1.27	1.10	1.06	1.16
ML	2000	1.14	1.52	1.60	1.06	1.15	1.10
Bayes	2000	1.05	1.13	1.10	1.06	0.99	0.97
ML	5000	1.02	1.13	1.19	1.00	1.12	1.02
Bayes	5000	0.96	1.09	1.18	0.94	0.99	0.97
ML	10000	1.05	1.08	1.22	1.00	1.05	0.99
Bayes	10000	0.94	1.13	1.08	0.96	0.99	0.97

Table 5: Comparing FIXED and FREE Alignment. Bias (Coverage)

	FREE	FREE	FIXED	FIXED	FREE	FIXED
G	α_1	α_2	α_2	α_2^*	$\nu_{1,1}$	$\nu_{1,1}$
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)

Table 6: ESS 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: ESS 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	

Table 8: Monte Carlo Simulation Check of 26-Country Alignment: True Values, Estimates, and Coverage (in parentheses) for Four Group Sizes

Parameter	True Value	$N_g = 100^1$	$N_g = 200$	$N_g = 500$	$N_g = 2000$
		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)

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