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Finding clusters of groups with measurement invariance: Unraveling intercept non-invariance with mixture multigroup factor analysis

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Abstract

Comparisons of latent constructs across groups are ubiquitous in behavioral research and, nowadays, often numerous groups are involved. Measurement invariance of the constructs across the groups is imperative for valid comparisons and can be tested by multigroup factor analysis. For many groups, metric invariance (invariant factor loadings) often holds, whereas scalar invariance (invariant intercepts) is rarely supported. Scalar invariance is a prerequisite for comparing latent means, however. One may inspect group-specific intercepts to pinpoint non-invariances, but this is a daunting task in case of many groups. This paper presents mixture multigroup factor analysis (MMG-FA) for clustering groups based on their intercepts. Clusters of groups with scalar invariance are obtained by imposing cluster-specific intercepts and invariant loadings whereas unique variances, factor means and factor (co)variances can differ between groups. Thus, MMG-FA ties down the number of intercepts to inspect and generates clusters of groups wherein latent means can be validly compared.

Keywords: Measurement invariance, multigroup factor analysis, strong invariance, scalar invariance, mixture modeling.

1. Introduction

Behavioral researchers are commonly interested in latent constructs such as personality traits or attitudes, measured by questionnaire items (or other indicators). Often, the goal is to make between-group comparisons with regard to the constructs, for instance, to assess cross-cultural differences in human values (Inglehart, Basanez, Basanez, & Moreno, 1998). Before doing so, testing for measurement invariance (MI) across the groups is imperative (Meredith, 1993). Specifically, a 'measurement model' (MM) indicates how the constructs are measured by the

questionnaire items and measurement invariance holds when the MM is equal across groups. If so, the constructs are measured in exactly the same way across groups and are thus validly comparable. If not, between-group comparisons are invalidated (Chen, 2008; Greiff, & Scherer, 2018).

For continuous items, or items that are treated as such, the MM is traditionally evaluated with factor analysis (Lawley & Maxwell, 1962), where the extent to which an item measures a construct or 'factor' is indicated by a 'factor loading'. Confirmatory factor analysis (CFA) is used to impose a priori assumptions about which items are measuring which factors (by allowing a pre-specified subset of loadings to differ from zero) and evaluate the fit of this MM for a given data set. When such prior knowledge is lacking or one wants to explore the measured constructs without imposing zero loadings, exploratory factor analysis (EFA) is used. Regardless of the MM being assessed by CFA or EFA, measurement invariance pertains to the equality of certain parameters of the factor model across groups. Measurement invariance can be tested by multigroup factor analysis (MG-FA; Dolan, Oort, Stoel, & Wicherts, 2009; Jöreskog, 1971; Sörbom, 1974). Specifically, invariance of MM parameters holds when the decrease in model fit caused by imposing their equality across groups is non-significant (Cheung & Rensvold, 2002). In multigroup CFA, one first inspects the model fit for the baseline or 'configural invariance' model, to evaluate whether the number of factors and the imposed pattern of zero loadings holds across the groups (Meredith, 1993). In multigroup EFA, no specific zero loadings are imposed. In both approaches, the tenability of 'weak' or 'metric invariance' is evaluated by imposing equal factor loadings across groups. When metric invariance holds, latent structures (e.g., how values affect immigration attitudes; Beierlein, Kuntz, & Davidov, 2016) are comparable across groups. Next, 'strong' or 'scalar invariance' is tested by also restricting the item intercepts to be equal across

groups. Scalar invariance is a prerequisite for comparing latent means across groups. Finally, 'strict invariance' pertains to the invariance of the items' residual or 'unique' variances.

When a certain level of measurement invariance is rejected across groups, one may attempt to pinpoint sources of non-invariance – i.e., problematic parameters and/or groups – by comparing the group-specific factor models. However, the number of pairwise comparisons grows exponentially with an increasing number of groups and, nowadays, many studies involve a lot of groups (Kim, Cao, Wang, & Nguyen, 2017; Rutkowski & Svetina, 2014); for example, cross-national surveys such as the World Values Survey. The many comparisons make it hard to unravel invariant from non-invariant parameters and for which groups they apply (Byrne & van de Vijver, 2010) and elevates the chances of falsely detecting non-invariance (Rutkowski & Svetina, 2014).

The large number of groups makes it unlikely that all groups have the same MM, but it is equally unlikely that each group has its own MM. Realistically, some groups may have (near-)identical measurement parameters and, therefore, a few latent clusters of groups may emerge (Byrne & van de Vijver, 2010). To capture these latent clusters, De Roover, Vermunt and Ceulemans (2020) recently presented 'mixture multigroup factor analysis' (MMG-FA), which is an extension of MG-FA that performs a mixture clustering (McLachlan & Peel, 2000) of the groups based on (a specific subset of) the MM parameters. As described above, different levels of measurement (non-)invariance have different implications in terms of which comparisons are (in)valid (Meredith, 1993) and, therefore, MMG-FA clusters groups based on their MM parameters in a level-specific way. In fact, De Roover, Vermunt and Ceulemans (2020) focused on a variant of MMG-FA that clusters the groups on their factor loadings, to find clusters of groups for which metric invariance holds. For empirical data on many groups, scalar invariance is rarely supported, however, whereas metric invariance is established frequently. In cross-cultural research, for

instance, scalar non-invariance is more often a threat to valid cross-cultural comparisons than metric non-invariance (Boer, Hanke, & He, 2018; Davidov, Dülmer, Schlüter, Schmidt, & Meuleman, 2012). Therefore, this paper presents a variant of MMG-FA that clusters the groups on their intercepts specifically, whereas factor loadings are assumed to be invariant across groups.

By identifying clusters of groups with the same intercepts, MMG-FA (1) ties down the number of intercepts to compare, making it easier to identify non-invariant items, (2) indicates for which groups scalar invariance holds, allowing for valid comparisons of the latent means within each cluster, and (3) indicates potentially interesting between-group differences, for instance, cross-cultural differences in the functioning of an item. Obviously, the user somehow needs to determine the appropriate number of clusters for a given data set, but a solution to this model selection problem was already discussed by De Roover et al. (2020).

Note that clustering the groups based on all MM parameters at once (i.e., factor loadings, item intercepts and residual or 'unique' variances) would imply the stringent assumption that the same clustering is underlying all MM parameters, whereas some parameter differences may be explained by another clustering – possibly with more clusters. When this assumption does not hold, such a clustering may fail to capture any of the MM differences properly or would need many clusters to do so. For the same reason, MMG-FA also sets aside differences in 'structural' parameters, i.e., factor (co)variances and factor means, as they are irrelevant to the MI question. This is exactly what makes MMG-FA unique to other approaches for evaluating measurement (non-)invariance across many groups (for an overview, see Kim et al., 2017), i.e., it is the only method that clusters the groups exclusively on specific subsets of the MM parameters.

The remainder of this paper is organized as follows: Section 2 discusses MG-FA and its extension into MMG-FA for intercept non-invariance. Section 3 describes a simulation study to

evaluate the performance of MMG-FA, including model selection. Section 4 illustrates its empirical value by scrutinizing intercept non-invariance for human values data from the European Social Survey. Section 5 concludes with points of discussion and directions for future research.

2. Method

2.1. Multigroup factor analysis

Multigroup factor analysis (MG-FA) operates on data from multiple groups, for example, age groups, religions, patient groups, or countries. Formally, the groups are indicated by $g = 1, \ldots,$ G and the subjects within the groups by $n_g = 1, \ldots, N_g$. The item scores for subject n_g on the J items are denoted by the J-dimensional vector $\mathbf{x}_{n_g}$ and, per group g, they are gathered into an N_g $\times J$ matrix $\mathbf{X}_g$. The factor model for the scores in $\mathbf{x}_{n_g}$ is written as (Lawley & Maxwell, 1962):

$$\mathbf{x}_{n_g} = \mathbf{\tau}_g + \mathbf{\Lambda}_g \mathbf{\eta}_{n_g} + \mathbf{\varepsilon}_{n_g} \tag{1}$$

where $\mathbf{\tau}_g$ indicates a J-dimensional group-specific intercept vector, $\mathbf{\Lambda}_g$ denotes a $J \times Q$ matrix of group-specific factor loadings, $\mathbf{\eta}_{n_g}$ is a Q-dimensional vector of the subject's scores on the Q factors and $\mathbf{\varepsilon}_{n_g}$ is a J-dimensional vector of residuals. The factor loadings indicate how the factors are measured by the items. Per group, the factor scores are assumed to be identically and independently distributed (i.i.d.) as $MVN\left(\mathbf{\alpha}_g, \mathbf{\Phi}_g\right)$, independently of $\mathbf{\varepsilon}_{n_g}$, which are i.i.d. as $MVN\left(\mathbf{0}, \mathbf{\Psi}_g\right)$. The factor means of group g are denoted by $\mathbf{\alpha}_g$, whereas $\mathbf{\Phi}_g$ pertains to the group-specific factor (co)variances and $\mathbf{\Psi}_g$ to a diagonal matrix containing the group's unique variances. The model-implied covariance matrix for group g is $\mathbf{\Sigma}_g = \mathbf{\Lambda}_g \mathbf{\Phi}_g \mathbf{\Lambda}_g' + \mathbf{\Psi}_g$. Estimating Equation 1 for each group corresponds to the baseline model for MI testing. To partially identify the model, the factor means $\mathbf{\alpha}_g$ are fixed to zero and the factor variances on the diagonal of $\mathbf{\Phi}_g$ to one per group g.

Note that multigroup CFA (MG-CFA) tests invariance for an assumed MM by imposing specific zero loadings on $\mathbf{\Lambda}_g$. The tenability of this pattern of zero loadings across the groups is called 'configural invariance'. Note that, when configural invariance fails, resorting to EFA is often a better strategy (Gerbing & Hamilton, 1996) than elaborately respecifying CFA models, to avoid capitalization on chance (Browne, 2001; MacCallum, Roznowski, & Necowitz, 1992). Moreover, fixed zero loadings are often too restrictive (Asparouhov & Muthén, 2009; McCrae, Zonderman, Costa, Bond, & Paunonen, 1996; Muthén & Asparouhov, 2012) and model misspecifications can severely bias other parameter estimates (Anderson & Gerbing, 1982; Bollen, Kirby, Curran, Paxton, & Chen, 2007). As an alternative, multigroup EFA (MG-EFA) does not impose zero loadings, but includes rotational freedom of the factors (De Roover & Vermunt, 2019; Dolan, Oort, Stoel, & Wicherts, 2009; Hessen, Dolan, & Wicherts, 2006).

To test for weak or metric invariance, the fit of the model with invariant loadings, i.e., $\mathbf{\Lambda}_g = \mathbf{\Lambda}$ for $g = 1, \ldots, G$, is compared to that of the baseline model. For the metric invariance model, factor variances of one are imposed for one group or for the mean factor variances across groups; i.e., $diag\left(\dfrac{1}{N}\sum_{g=1}^{G} N_g \mathbf{\Phi}_g\right) = \mathbf{1}$ where $\mathbf{1}$ is a vector of ones and $N = \sum_{g=1}^{G} N_g$. To evaluate the comparability of latent means, strong or scalar invariance is tested by also restricting the intercepts to be invariant across groups, i.e., $\mathbf{\tau}_g = \mathbf{\tau}$ for $g = 1, \ldots, G$, while freely estimating factor means $\mathbf{\alpha}_g$ per group (Dolan et al., 2009; Meredith, 1993). For model identification, $\mathbf{\alpha}_g = \mathbf{0}$ for one group or $\dfrac{1}{N}\sum_{g=1}^{G} N_g \mathbf{\alpha}_g = \mathbf{0}$ across groups. Note that this paper focuses on the situation where metric invariance holds but scalar invariance fails. Therefore, the next step of evaluating strict invariance, i.e., $\mathbf{\Psi}_g = \mathbf{\Psi}$ for $g = 1, \ldots, G$, falls beyond the scope of this paper.

To evaluate whether the fit of MG-FA is significantly worse with invariant intercepts across groups, comparing fit indices such as the CFI and RMSEA – to evaluate 'practical' significance – is recommended since χ^2- difference tests for comparing nested models are strongly affected by sample size. Specifically, non-invariance of intercepts is indicated when the decrease in CFI (ΔCFI) exceeds .01 and the increase in RMSEA (ΔRMSEA) is larger than .01 when imposing invariant intercepts (Chen, 2007; Cheung & Rensvold, 2002). When scalar invariance indeed fails, one can return to the metric invariance model, i.e., with invariant loadings and group-specific intercepts, and compare the intercepts between groups to locate non-invariances. This quickly becomes cumbersome when more than a few groups are involved, however. For instance, comparing intercepts for five groups implies only 10 pairwise comparisons, but 10 groups already require 45 comparisons and 25 groups result in no less than 300 comparisons. In the next subsection, an extension of mixture multigroup factor analysis is presented to tie down the number of comparisons needed to identify intercept non-invariances.

2.2. Mixture multigroup factor analysis

2.2.1. Model specification

Mixture multigroup factor analysis (MMG-FA) aims to gather groups into a few clusters according to the equivalence of their MM parameters such that a specific level of measurement invariance holds within each cluster. This paper focuses on scalar (non-)invariance and, thus, on MMG-FA for finding clusters of groups with invariant intercepts. To this end, the observations $\mathbf{x}_{n_g}$ are assumed to be sampled from a mixture of K multivariate normal distributions where all observations of a group are sampled from the same normal distribution. Thus, the mixture clustering operates at the group level. In the remainder of the paper, the K mixture components are called 'clusters'. Formally, the MMG-FA model for group g is written as follows:

$$f\left(\mathbf{X}_g;\boldsymbol{\theta}\right)=\sum_{k=1}^{K}\pi_k f_{gk}\left(\mathbf{X}_g;\boldsymbol{\theta}_{gk}\right)=\sum_{k=1}^{K}\pi_k\prod_{n_g=1}^{N_g}MVN(\mathbf{x}_{n_g};\boldsymbol{\mu}_{gk},\boldsymbol{\Sigma}_g)$$

(2)

$$with \quad \boldsymbol{\Sigma}_g=\boldsymbol{\Lambda}\boldsymbol{\Phi}_g\boldsymbol{\Lambda}'+\boldsymbol{\Psi}_g \quad and \quad \boldsymbol{\mu}_{gk}=\boldsymbol{\tau}_k+\boldsymbol{\Lambda}\boldsymbol{\alpha}_{gk}$$

where f is the total population density function, and $\boldsymbol{\theta}$ refers to the total set of parameters. Similarly, f_{gk} refers to the kth cluster-specific density function for group g and $\boldsymbol{\theta}_{gk}$ refers to the corresponding set of parameters. The mixing proportions (i.e., prior probabilities of belonging to each of the clusters) are indicated by π_k, with $\sum_{k=1}^{K}\pi_k=1$. It is important to note that the covariance matrices are group-specific whereas the means are both group- and cluster-specific. Specifically, the covariance matrices are modeled by means of *invariant* factor loadings $\boldsymbol{\Lambda}$, *group-specific* factor (co)variances $\boldsymbol{\Phi}_g$, and *group-specific* unique variances $\boldsymbol{\Psi}_g$. The means are modeled by *cluster-specific* intercepts $\boldsymbol{\tau}_k$ and *group- and cluster-specific* factor means $\boldsymbol{\alpha}_{gk}$. This combination of invariant, group- and cluster-specific parameters assures that the clustering of groups is driven exclusively by intercept differences. It is notable that $\boldsymbol{\alpha}_{gk}$ is not only group-specific but also varies across clusters. Assuming the factor means of a group to be the same in all clusters would be too restrictive, because they depend on the cluster-specific intercepts. As shown in Appendix A, it is possible to estimate the factor means for every group-and-cluster combination despite the fact that the mixture model assumes that each group belongs to only one cluster. The resulting $\boldsymbol{\alpha}_{gk}$ are the factor means conditional on group g belonging to cluster k. For each group g, the factor means for the clusters the group does *not* belong to are nuisance parameters.

Thus, in MMG-FA, the factor model is conditional on the cluster membership of group g, indicated by z_{gk}, as follows:

$$\left[\mathbf{x}_{n_g}\mid z_{gk}=1\right]=\boldsymbol{\tau}_k+\boldsymbol{\Lambda}\boldsymbol{\eta}_{n_gk}+\boldsymbol{\varepsilon}_{n_g}$$

(3)

where $\boldsymbol{\eta}_{n_g k} \sim MVN\left(\boldsymbol{\alpha}_{gk}, \boldsymbol{\Phi}_g\right)$ and $\boldsymbol{\varepsilon}_{n_g} \sim MVN\left(\mathbf{0}, \boldsymbol{\Psi}_g\right)$. Note that, whereas De Roover et al. (2020) used EFA within clusters to scrutinize loading non-invariances, it is possible to use either CFA or EFA for modeling the invariant loadings $\boldsymbol{\Lambda}$ in the MMG-FA variant proposed in this paper. Indeed, when assumed zero loadings do not hold or are overly restrictive (see Section 2.1), MMG-EFA is a good alternative and, in that case, the factors can be rotated to facilitate interpretation and comparability. To set the scale of the factors, the means of the factor variances are fixed to one across all groups. Since it is unknown beforehand which groups belongs to which cluster, we refrain from imposing factor means of zero for one group per cluster. Instead, we restrict the factor means per cluster as follows: $\dfrac{1}{N_k}\displaystyle\sum_{g=1}^{G} N_g \hat{z}_{gk} \boldsymbol{\alpha}_{gk} = \mathbf{0}$ where $N_k = \displaystyle\sum_{g=1}^{G} N_g \hat{z}_{gk}$ and $\hat{z}_{gk}$ indicates the estimated cluster memberships or posterior classification probabilities (see Appendix A). Note that the factor means $\boldsymbol{\alpha}_{gk}$ can be compared among groups assigned to the same cluster, thus providing researchers with the latent mean comparisons they were looking for – albeit per cluster of groups.

Note that the existing method that is most similar to MMG-FA (as specified above) is multilevel factor mixture modeling (ML-FMM; Kim et al., 2017). Unlike MMG-FA, it clusters the groups based on measurement and structural parameters at the same time (and only allows to use CFA). When metric invariance holds and the aim is to trace intercept non-invariances, ML-FMM is specified such that the factor loadings are invariant across clusters and the mixture clustering is driven by intercept differences as well as differences in factor means, factor (co)variances and unique variances. This implies that factor means, factor (co)variances and unique variances are assumed to be the same for all groups within a cluster, which is too restrictive when looking for clusters of groups wherein scalar invariance holds. ML-FMM is thus less focused on intercept differences than MMG-FA.

2.2.2. Model estimation

The unknown parameters $\boldsymbol{\theta}$ of the MMG-FA model are estimated by means of maximum likelihood (ML) estimation. This involves maximizing the logarithm of the likelihood of the data:

$$
\begin{aligned}
\log L &= \log\left(\prod_{g=1}^{G} \sum_{k=1}^{K} \pi_k \prod_{n_g=1}^{N_g} \frac{1}{(2\pi)^{J/2} |\boldsymbol{\Sigma}_g|^{1/2}} \exp\left(-\frac{1}{2} \left(\mathbf{x}_{n_g} - \boldsymbol{\mu}_{gk} \right) \boldsymbol{\Sigma}_g^{-1} \left(\mathbf{x}_{n_g} - \boldsymbol{\mu}_{gk} \right)' \right) \right) \\
&= \sum_{g=1}^{G} \log\left(\sum_{k=1}^{K} \pi_k \prod_{n_g=1}^{N_g} \frac{1}{(2\pi)^{J/2} |\boldsymbol{\Sigma}_g|^{1/2}} \exp\left(-\frac{1}{2} \left(\mathbf{x}_{n_g} - \boldsymbol{\mu}_{gk} \right) \boldsymbol{\Sigma}_g^{-1} \left(\mathbf{x}_{n_g} - \boldsymbol{\mu}_{gk} \right)' \right) \right),
\end{aligned}
\tag{4}
$$

where $\boldsymbol{\mu}_{gk}$ and $\boldsymbol{\Sigma}_g$ are decomposed as specified in Equation 2. Note that obtaining the parameter estimates $\hat{\boldsymbol{\theta}}$ by means of Newton-Raphson, Fisher scoring or Quasi-Newton optimization methods – i.e., methods that are used in commercial software such as Latent Gold (Vermunt & Magidson, 2013, 2016) and Mplus (Muthén & Muthén, 2005) – is very slow due to the large number of parameters and sensitive to starting values. To find the parameter estimates in a time-efficient and stable manner, we developed an alternating expectation-conditional maximization (AECM) algorithm (Appendix A), which has been implemented in Matlab R2019b (Appendix A) and Latent Gold 6.0 (Appendix B). Because the algorithm may end up in a local maximum, it applies a multistart procedure to increase the probability of obtaining the global maximum. An R-package containing the AECM algorithm will be developed in the near future.

2.2.3. Model selection

In this paper, we focus on the case where the number of factors is assumed to be known. Thus, the model selection problem is confined to selecting the most appropriate number of clusters *K* for a given data set. For related mixture models, minimizing the Bayesian Information Criterion (BIC; Schwarz 1978) is often recommended (Nylund, Asparouhov, & Muthén, 2007; Tay, Diener, Drasgow, & Vermunt, 2011; Tein, Coxe, & Cham, 2013). The BIC balances the log *L* and model complexity by penalizing a model with more free parameters *fp* and larger sample size as follows:

$$\text{BIC} = -2\log L + fp \log(N) \tag{5}$$

For MMG-FA, *fp* is equal to the sum of the number of mixing proportions (minus one restriction), intercepts, factor loadings (minus *R* restrictions), factor variances (minus *Q* restrictions), factor covariances, factor means (minus *KQ* restrictions, excluding nuisance parameters), and unique variances: $fp = K - 1 + KJ + (JQ - R) + (G - 1)Q + GQ(Q - 1)/2 + (G - K)Q + GJ$. For CFA, '*R*' equals the number of imposed zero loadings and, for EFA, it equals $Q(Q - 1)$ (i.e., the correction for rotational freedom). Several authors (Kim, Joo, Lee, Wang, & Stark, 2016; Lukočienė, Varriale, & Vermunt, 2010) suggested that, for group-level clusters, one should use the number of groups *G* – instead of *N* – for the sample size in the BIC computation. For small sample sizes and low cluster separation in multilevel mixture modeling, the Akaike Information Criterion (AIC; Akaike, 1973) was found to outperform BIC (Kim et al., 2017; Lukočienė & Vermunt, 2010). For growth mixture models, Bauer (2007) and McNeish and Harring (2017) indicated that in less ideal but empirically realistic conditions (e.g., non-normality), BIC and AIC tend to overselect clusters.

On top of that, De Roover et al. (2020) showed that the Convex Hull procedure (CHull) is a valuable alternative to BIC and AIC for selecting the number of clusters in MMG-FA. The CHull (Ceulemans & Van Mechelen, 2005; Ceulemans & Kiers, 2006) is a generalization of the scree

test (Cattell, 1966) based on a plot of the log L versus fp of the obtained solutions. Note that, like a scree test, CHull cannot select the least complex model and thus selects at least two clusters. But when focusing on cases where scalar invariance was rejected, and intercept differences are thus expected to be present, this is not a problem. Furthermore, visual inspection of the CHull plot may still lead to the conclusion that no clear elbow is present and thus that an underlying clustering is unlikely. In the next section, these methods are compared in terms of their performance with regard to selecting the correct number of clusters underlying the between-group intercept differences.

3. Simulation Study

3.1. Problem

On the one hand, the goal of the simulation study is to evaluate the performance of MMG-FA with respect to the recovery of the clustering of the groups and of the parameters when the correct number of clusters is known. On the other hand, it is evaluated to what extent the model selection procedures described in Section 2.2.3 select the correct number of clusters for MMG-FA. We manipulated seven factors that were expected to affect the cluster separation and/or the stability of parameter estimates, and thus the performance of MMG-FA and its model selection: (1) the number of groups, (2) the group sizes, (3) the number of clusters, (4) the cluster sizes, (5) the number of factors, and the size (6) and number (7) of intercept differences.

Specifically, in terms of their effect, we hypothesize the following: The number of groups (1) on the one hand determines how many groups end up within each cluster. Because more groups within a cluster implies more information on the cluster-specific intercepts (i.e., a higher within-cluster sample size), the performance may improve with a higher number of groups. On the other hand, a higher number of groups implies more cluster memberships (posterior classification probabilities) to be estimated, which may be more intricate. More observations per group (2)

increase the within-cluster sample size and thus the performance. It also implies a higher cluster separation because more information is available for estimating each of the cluster memberships (Lukočienė, Varriale, & Vermunt, 2010). A higher number of clusters (3) lowers the within-cluster sample size (for a given number of groups) and is thus expected to lower the performance. It also increases the number of cluster memberships to be determined for each group, making their recovery more intricate. The cluster sizes (4), corresponding to the mixing proportions, pertain to the groups being equally or unequally divided across the clusters. In the unequal case, larger cluster(s) compete with smaller cluster(s) and the smaller ones may be much harder to recover both in terms of cluster memberships and intercepts. With respect to the number of factors (5), a higher number of factors – given the same number of variables – implies a lower factor overdetermination. In that case, more factor means need to be recovered as well, which may be more difficult. Finally, the size (6) and number (7) of intercept differences greatly determine the extent to which the cluster-specific intercepts differ from one another (i.e., cluster separation) and thus affects the recovery of the cluster memberships.

3.2. Design

These factors were systematically varied in a complete factorial design:

1. the *number of groups G* at 2 levels: 12, 60;
2. the *group sizes N_g* (i.e., number of subjects per group) at 4 levels: 50, 100, 300, 500;
3. the *number of clusters K* at 2 levels: 2, 4;
4. the *cluster sizes* at 2 levels: equal, unequal;
5. the *number of factors Q* at 2 levels: 2, 4;
6. the *size of intercept differences* at 2 levels: .60, .30;
7. the *number of intercept differences* at 2 levels: 8 or 2 per pair of clusters.

The number of variables *J* was fixed at 20 and the invariant factor loading matrix Λ was manipulated as follows:

$$\Lambda' = \begin{bmatrix} \sqrt{.6} & \sqrt{.6} & \sqrt{.6} & \sqrt{.6} & \sqrt{.6} & \sqrt{.6} & \sqrt{.6} & \sqrt{.6} & \sqrt{.6} & \sqrt{.6} & 0 & 0 & 0 & 0 & 0 & 0 & 0 & 0 & 0 & 0 \\ 0 & 0 & 0 & 0 & 0 & 0 & 0 & 0 & 0 & 0 & \sqrt{.6} & \sqrt{.6} & \sqrt{.6} & \sqrt{.6} & \sqrt{.6} & \sqrt{.6} & \sqrt{.6} & \sqrt{.6} & \sqrt{.6} & \sqrt{.6} \end{bmatrix}$$

or

$$\Lambda' = \begin{bmatrix} \sqrt{.6} & \sqrt{.6} & \sqrt{.6} & \sqrt{.6} & \sqrt{.6} & 0 & 0 & 0 & 0 & 0 & 0 & 0 & 0 & 0 & 0 & 0 & 0 & 0 & 0 & 0 \\ 0 & 0 & 0 & 0 & 0 & \sqrt{.6} & \sqrt{.6} & \sqrt{.6} & \sqrt{.6} & \sqrt{.6} & 0 & 0 & 0 & 0 & 0 & 0 & 0 & 0 & 0 & 0 \\ 0 & 0 & 0 & 0 & 0 & 0 & 0 & 0 & 0 & 0 & \sqrt{.6} & \sqrt{.6} & \sqrt{.6} & \sqrt{.6} & \sqrt{.6} & 0 & 0 & 0 & 0 & 0 \\ 0 & 0 & 0 & 0 & 0 & 0 & 0 & 0 & 0 & 0 & 0 & 0 & 0 & 0 & 0 & \sqrt{.6} & \sqrt{.6} & \sqrt{.6} & \sqrt{.6} & \sqrt{.6} \end{bmatrix}$$

for two and four factors, respectively. The non-zero loadings are equal to $\sqrt{.60}$ in order to obtain total variances that vary around one, since the unique variances vary around .40 (see below).

The numbers of groups of 12 and 60 correspond to the range of group numbers that are generally encountered in large-scale surveys (Rutkowski & Svetina, 2014). To obtain equal cluster sizes, the groups are equally divided across clusters, i.e., each cluster contains 50% of the groups when $K = 2$, and 25% when $K = 4$. In the unequal cluster size conditions, the groups are divided over the clusters such that one cluster contains 75% of the groups, whereas the rest is equally divided over the remaining clusters. Thus, in case of two clusters, 75% of the groups are in one cluster and 25% in the other one. When $K = 4$, the three smaller clusters contain 8.33% of the groups each, which implies that they are singleton clusters (i.e., including only one group) in case of 12 groups. In case of 60 groups, they hold five groups each. The group sizes range from 50 to 500, which correspond to very small and large sample sizes for factor analysis, respectively (Fabrigar, MacCallum, Wegener, & Strahan, 1999; MacCallum, Widaman, Zhang, & Hong, 1999). In the current study, MMG-FA focuses on differences in intercepts and the factor loadings are invariant across groups. Therefore, the accuracy of the cluster-specific intercept estimates is determined by the sample size of a cluster of groups, rather than of a single group, whereas the accuracy of the factor loadings depends on the total sample size across all groups. The precision of the group- and cluster-specific factor means still depends on the group sizes, however.

The cluster-specific intercepts $\boldsymbol{\tau}_k$ are zero for the invariant items and equal to .60 or .30 for the non-invariant items. An intercept difference of .60 is considered to be a large non-invariance (Meade, Johnson, & Braddy, 2008; Stark, Chernyshenko, & Drasgow, 2006; Woods, 2009) that, when ignored, can lead to incorrect statistical inferences and biased parameter estimates (Hancock, Lawrence, & Nevitt, 2000; Kim & Willson, 2014). To obtain two intercept differences for each pair of clusters, the intercept was increased to .60 or .30 for one item per cluster. Similarly, altering four intercepts per cluster led to eight differences per cluster pair. The set of non-invariant items differs across the clusters: e.g., in case of eight differences per cluster pair and four clusters, the non-invariant items are [1, 6, 11, 16] for cluster 1, [2, 7, 12, 17] for cluster 2, [3, 8, 13, 18] for cluster 3 and [4, 9, 14, 19] for cluster 4. The group- and cluster-specific factor means $\boldsymbol{\alpha}_{gk}$ are randomly sampled from a uniform distribution between −.50 and .50, i.e., from $U\left(-.50,.50\right)$. To make sure that the clustering is driven only by the manipulated intercept differences, the factor means are 'centered' for each cluster k such that $\frac{1}{N_k}\sum_{g=1}^{G}N_{gk}\boldsymbol{\alpha}_{gk}=\mathbf{0}$. Note that, for a given pair of groups, the factor mean differences range from 0 to 1.00, whereas a factor mean difference of .50 is considered to be substantial (Kim et al., 2017). The group-specific factor correlations are sampled from $U\left(-.50,.50\right)$ and factor variances from $U\left(.50,1.50\right)$. Whenever a resulting $\boldsymbol{\Phi}_g$ is not positive definite, the sampling is repeated. Group-specific unique variances (i.e., the diagonal of $\boldsymbol{\Psi}_g$) are sampled from $U\left(.20,.60\right)$. Finally, factor scores are sampled from $MVN\left(\boldsymbol{\alpha}_{gk},\boldsymbol{\Phi}_g\right)$ and residuals from $MVN\left(\mathbf{0},\boldsymbol{\Psi}_g\right)$ and the simulated data are created according to Equation 3.

According to this procedure, 50 data sets were generated per cell of the design, using Matlab R2019b. Thus, 2 (number of groups) × 4 (group sizes) × 2 (number of clusters) × 2 (cluster

sizes) $\times$ 2 (number of factors) $\times$ 2 (size of intercept differences) $\times$ 2 (number of intercept

differences) $\times$ 50 (replications) = 12,800 data sets were generated. The data were analyzed by the

AECM algorithm for MMG-FA detailed in Appendix A, using CFA with the correct number of

factors Q, the correct pattern of zero loadings and using 10 starts (i.e., starting from 10 random

partitions of the groups). On the one hand, the correct number of clusters K was specified to

evaluate the performance of the MMG-CFA algorithm itself. On the other hand, for the first five

replications of each cell of the design (i.e., for 1,280 data sets), MMG-CFA analyses were

performed with numbers of clusters between one and six to evaluate the performance of the model

selection procedures described in Section 2.2.3. To check the performance of the EFA-based

algorithm, the first five replications of each cell of the design were also analyzed with MMG-EFA

with the correct Q and K. To compare the performance of MMG-CFA to that of ML-FMM, each

data set was also analyzed by ML-FMM with the correct K and Q and 10 starts. All analyses

converged within the imposed maximum of 1000 iterations. The mean CPU time for MMG-FA

with the correct K was 48 seconds, both for the CFA- and EFA-based algorithms, on an i5

processor with a clock frequency of 2.4 GHz and 8GB RAM. For the model selection procedure,

estimating the six models with an increasing number of clusters took about 5 minutes on average.

3.3. Results

Detailed results for the MMG-CFA analyses are discussed in Sections 3.3.1 to 3.3.5,

whereas Section 3.3.6 gives a short overview of the performance of MMG-EFA. Finally, the model

selection results are discussed in Section 3.3.7.

3.3.1. Sensitivity to local maxima

To evaluate the frequency of local maximum solutions, we should compare the log L value

of the best solution obtained by the multistart procedure (i.e., starting from 10 random partitions;

see Appendix A2) with the global ML solution for each simulated data set. Because of sampling

fluctuations, the global maximum is unknown, however. Therefore, we make use of a 'proxy' of

the global ML solution; i.e., the solution that is obtained when the algorithm starts from the true

clustering of the groups. The best solution from the multistart procedure is then considered to be a

local maximum when its log L value is smaller than the one from the proxy. To exclude mere

calculation precision differences, we only considered such differences with an absolute value

higher than .0001 to indicate a local maximum. By this definition, 1,296 (10.1%) local maxima

were detected over all 12,800 simulated data sets. Not surprisingly, most of these occur in the more

difficult conditions; e.g., 1,264 of the 1,296 local maxima are found in the conditions with four

unequal clusters (i.e., with three very small clusters). Note that, for 919 out of these 1,296 data

sets, re-running the analysis with 50 starts (i.e., starting from 50 random partitions) was sufficient

to avoid the local maxima, reducing the percentage of local maxima to 2.9% across all data sets.

3.3.2. Goodness of cluster recovery

To examine the goodness of recovery of the groups' cluster memberships, we compare the

modal clustering (i.e., assigning each group to the cluster for which the posterior classification

probability is the highest) to the true clustering by means of the *Adjusted Rand Index* (*ARI*; Hubert

& Arabie, 1985). The *ARI* equals 1 if the two partitions are identical, and equals 0 when the overlap

between the two partitions is at chance level. The mean *ARI* over all data sets amounted to .95 (*SD*

= .14) and the *ARI* was equal to 1 for no less than 86% of the data sets, which indicates a very

good recovery. Out of the 1,766 solutions with at least one incorrect cluster assignment, 1,296

were in fact a local maximum. After replacing the 1,296 local maxima (obtained with 10 starts) by

the solutions obtained with 50 starts (see Section 3.3.1), the number of data sets with incorrect

assignments reduced from 1,766 to 912 and the overall mean of the *ARI* amounted to .98 (*SD* =

.10). Table 1 presents the mean *ARI* values in function of the simulated conditions. In addition to

the ones for MMG-CFA with 10 random starts, it also includes the *ARI* results after replacing the

1,296 local maxima by the solutions obtained with 50 starts. When inspecting the latter results, we

find that the *ARI* was affected most by the group sizes, but also by the number and size of intercept

differences and the cluster sizes (i.e., number of clusters and whether cluster sizes are equal or

unequal). Specifically, the cluster recovery was excellent in all conditions according to the

guidelines provided by Steinley (2004), but even better in case of larger groups, larger or more

intercept differences, less clusters or equal cluster sizes.

[Insert Table 1 about here]

To examine the occurrence of classification uncertainty, we computed the minimum

posterior probability with which a group was assigned to a cluster (according to the modal

assignments), i.e., the minimum 'classification certainty' or 'CC_{min}', for each data set. For the data

sets with a perfect cluster recovery (i.e., *ARI* = 1) after 10 starts, CC_{min} varied between .55 and

1.00, with a mean of .9979 (*SD* = .02). For the data sets with at least one misclassification, CC_{min}

varied between .41 and 1.00 with a mean of .80 (*SD* = .19). Thus, for the simulated conditions,

classification uncertainty seems to be somewhat related to misclassification.

Finally, we compared the cluster recovery of MMG-CFA to that of ML-FMM. Over all

data sets, the mean *ARI* of ML-FMM amounted to .75 (*SD* = .36) and the *ARI* was equal to 1 for

65% of the data sets. Thus, the performance of MSFA is clearly inferior to that of MMG-CFA

when it comes to recovering the clustering that is underlying the intercept differences. Table 1

includes the mean *ARI* values for ML-FMM in function of the simulated conditions. It is obvious

that ML-FMM performs reasonably well when it comes to picking up larger and/or more intercept

differences, but that its performance drops in case of smaller or fewer intercept differences, probably because the clustering then focuses on differences in factor means.

3.3.3. Goodness of intercept recovery

To quantify how well the cluster-specific intercepts $\boldsymbol{\tau}_k$ are recovered, we calculated the mean absolute difference (*MAD*) between the true and estimated intercepts:

$$MAD_{intercepts} = \frac{\sum_{k=1}^{K}\sum_{j=1}^{J}\left|\tau_{kj} - \hat{\tau}_{kj}\right|}{KJ} \quad (6)$$

To account for the permutational freedom of the cluster labels (i.e., 'label switching'; Tueller, Drotar, & Lubke, 2011), the permutation was chosen that maximizes *MAD*$_{intercepts}$. On average, *MAD*$_{intercepts}$ was equal to .03 (*SD* = .03). The mean *MAD*$_{intercepts}$ values in function of the simulated conditions, both for 10 starts and after replacing the local maxima with the best solution after 50 starts, are given in Table 2. The intercept recovery depends most on the within-cluster sample size; i.e., it improves with more groups, larger groups, less clusters and equal cluster sizes.

[Insert Table 2 about here]

3.3.4. Goodness of loading recovery

To evaluate the recovery of the invariant factor loadings, we obtained a *goodness-of-loading-recovery statistic* (*GOLR*) by computing congruence coefficients φ (Tucker, 1951) between the loadings of the true and estimated factors and averaging across factors as follows:

$$GOLR = \frac{1}{Q}\sum_{q=1}^{Q}\varphi\left(\boldsymbol{\lambda}_q, \hat{\boldsymbol{\lambda}}_q\right) \quad (7)$$

where $\boldsymbol{\lambda}_q$ and $\hat{\boldsymbol{\lambda}}_q$ indicate the true and estimated loadings of the q-th factor, respectively. The *GOLR* statistic takes values between 0 (no recovery at all) and 1 (perfect recovery). For the MMG-

CFA analyses with 10 starts, the average *GOLR* is .9999 (*SD* = .00), which corresponds to an excellent recovery that is hardly affected by the manipulated conditions – probably because the total sample size is always large (i.e., at least 600).

3.3.5. Goodness of factor mean recovery

To quantify the recovery of the group- and cluster-specific factor means $\boldsymbol{\alpha}_{gk}$, we computed the mean absolute difference between the true and estimated factor means as follows:

$$MAD_{factormeans} = \frac{\sum\limits_{g=1}^{G} \hat{z}_{gk}^{*} \sum\limits_{k=1}^{K} \sum\limits_{q=1}^{Q} \left| \alpha_{gkq} - \hat{\alpha}_{gkq} \right|}{GQ} \tag{8}$$

where $\hat{z}_{gk}^{*}$ indicates the modal cluster memberships. With respect to the permutation of the cluster labels, we applied the best permutation of the estimated clusters obtained in Section 3.3.3. (i.e., the one maximizing *MAD_{intercepts}*). Note that, due to the identification restriction on the factor means per cluster, i.e., $\frac{1}{N_k} \sum\limits_{g=1}^{G} N_g \hat{z}_{gk} \hat{\boldsymbol{\alpha}}_{gk} = \boldsymbol{0}$, the so-called 'alignment' (Asparouhov & Muthén, 2014) of the factor means within a cluster depends on the posterior classification probabilities for that particular cluster. Thus, misclassification and classification uncertainty cause the estimated factor means for the corresponding cluster to be 'misalignment' and not directly comparable to the true factor means. Therefore, we exclude the 912 data sets with an *ARI* < 1 (after 10 or 50 starts, see Section 3.3.2) and recall that classification uncertainty was rare among the data sets with an *ARI* = 1. When averaged across the 11,888 data sets with a correct clustering, *MAD_{factormeans}* amounts to .06 (*SD* = .02), which indicates a good recovery. Not surprisingly, *MAD_{factormeans}* depends most on the size of the groups; specifically, group sizes of 50, 100, 300 and 500 result in mean values of .11, .08, .04, and .03, respectively.

3.3.6. Sensitivity to local maxima and goodness-of-recovery for MMG-EFA

To evaluate whether the performance is affected by using EFA instead of CFA to model the factors, we present the overall results for the 1,280 data sets analyzed by MMG-EFA (with 10 starts). Out of these 1,280 solutions, 137 (10.7%) were found to be local maxima. The mean *ARI* was equal to .95 (*SD* = .15) and the *ARI* was equal to one for 1,094 (85%) of the data sets. The mean $MAD_{intercepts}$ amounted to .03 (*SD* = .03) and the $MAD_{factormeans}$ was, on average across the 1,094 data sets with *ARI* = 1, equal to .06 (*SD* = .03). The mean *GOLR* was .9996 (*SD* = .00), upon resolving the factors' rotational freedom by an oblique procrustes rotation of the estimated towards the true loadings. Thus, overall, MMG-EFA and MMG-CFA perform equally well.

3.3.7. Model selection

Per data set, MMG-CFA analyses with one to six clusters were performed and the number of clusters with the optimal balance between log *L* and the number of free parameters *fp* was determined according to four model selection procedures (Section 2.2.3): BIC using the number of subjects *N* as the sample size (BIC_N), BIC using the number of groups *G* as the sample size (BIC_G), AIC and CHull. For BIC_N and BIC_G, the percentage of data sets for which the correct number of clusters was chosen amounts to 79.8% and 87.8%, respectively. AIC selects the correct number of clusters for 84.3% of the data sets and CHull for 87.3% of the data sets. For BIC_N, the majority of the model selection mistakes pertain to the number of clusters being underestimated, whereas AIC often selects too many clusters. For BIC_G and CHull, under- and overselection of clusters occurs about equally often.

The main effects of the simulated conditions on the performance of these four criteria are given in Table 3. Clearly, BIC_G, AIC and CHull show comparable performances in most conditions and, overall, BIC_G performs best with CHull as a close second. Their performance

was affected most by unequal cluster sizes and the number of clusters being four rather than two. Recall that these are the conditions with the most local maxima. To determine whether some model selection mistakes are due to local maxima, we repeated the faulty model selections for analyses with one to six clusters performed with 50 random starts instead of 10. Doing so avoids 63 mistakes for BIC_N, 75 for BIC_G, 69 for AIC and 84 for CHull, bringing their overall accuracy to 84.8%, 93.7%, 89.7% and 93.9%, respectively.

[Insert Table 3 about here]

3.4. Conclusion

Regarding the sensitivity to local maxima, we conclude that the multistart procedure of MMG-CFA with 10 starts is sufficient to largely avoid local maxima, but that it is certainly advisable to increase the number of starts in case of more clusters and/or very unequal cluster sizes. The recovery of the cluster memberships of the groups was excellent for all simulated conditions, but, of course, it helps to have larger groups, less clusters, equally sized clusters, or a higher separability of the clusters in terms of number and size of intercept differences. The cluster-specific intercepts were well recovered and even more so in case of more groups, larger groups, less clusters and equal cluster sizes. The recovery of the invariant factor loadings was excellent overall. With respect to the recovery of the factor means, we found a good recovery that improves with a larger group size. Note that, even though in the simulation study the factor means were not comparable – i.e., 'misaligned' – to the true ones in case of misclassification, the factor mean *differences* between groups within a cluster – and thus the latent mean comparisons that are of main interest to the researcher – are unaffected by this so-called misalignment. Overall, MMG-EFA performed equally well, indicating that one can scrutinize intercept non-invariance without imposing zero loadings that require a priori knowledge on the MM and may be overly restrictive.

For selecting the number of clusters, BIC_G, AIC and CHull were found to perform similarly, at least for the simulated conditions. BIC_G and AIC have the added value that they can automatically distinguish between one cluster (i.e., scalar invariance across all groups) and more clusters, but CHull makes no distributional assumptions and, thus, may perform better for empirical data. Furthermore, visual inspection of the CHull plot may still suggest one cluster, i.e., in case of no clear elbow. Therefore, combining BIC_G and/or AIC with CHull is recommended. For CHull, one can use the free software developed by Wilderjans, Ceulemans, and Meers (2013) or the R-package that is available from https://cran.r-project.org/package=multichull.

4. Application

In this section, we illustrate the performance of MMG-FA for unraveling intercept non-invariance for data on human values measured by the 21 items Portrait Value Questionnaire (PVQ-21) during round 6 of the European Social Survey (ESS). The PVQ-21 measures 10 basic values which form four higher-order values: self-enhancement (i.e., including achievement and power), self-transcendence (i.e., benevolence and universalism), conservation (i.e., conformity, tradition, and security), and openness to change (i.e., self-direction, stimulation, and hedonism) (Schwartz, 2006). Cieciuch, Davidov, Algesheimer, and Schmidt (2018) tested the cross-country invariance of the PVQ-21 for 15 countries included in rounds 1 to 6 of the ESS: Belgium, Switserland, Germany, Denmark, Spain, Finland, United Kingdom, Hungary, Ireland, the Netherlands, Norway, Poland, Portugal, Sweden, and Slovenia. Specifically, they tested MI per higher-order value and showed that approximate invariance (Muthén & Asparouhov, 2013) could be established for openness to change and self-enhancement, whereas, for conservation and self-transcendence, this could be established only for a subset of the countries. Non-invariance pertained mostly to the intercepts. To focus on these intercept non-invariances, we looked for a subset of countries with

invariant loadings to start from. Based on the so-called 'difference output' (provided by Mplus) in the online appendices of Cieciuch et al. (2018), we inspected which countries had loadings that significantly deviated from the average. For round 6, only a few countries had significantly deviating loadings; i.e., Spain, Hungary, Portugal and Slovenia for conservation and Norway for self-transcendence. Hence, we continued with 11 countries for conservation and 14 for self-transcendence. After excluding respondents with missing values, we retained a sample size of 21,672 for the conservation data and 27,512 for self-transcendence.

To scrutinize the intercept non-invariances for the six conservation items (listed in Appendix C), we performed MMG-FA analyses with one factor and 1 to 11 clusters (where the latter corresponds to MG-FA with group-specific intercepts). BIC_G and AIC suggest 11 clusters (Table 4), which may be an overselection (see Section 2.2.3). According to CHull, the best number of clusters is four, with a scree ratio of 3.21. Indeed, the CHull plot (Figure 1) has a first elbow for two clusters, but really levels off after four clusters. The clustering of the four-cluster model is given in Table 5. Cluster 1 contains Belgium and Sweden, whereas Switzerland, Germany, United Kingdom and Ireland are gathered in Cluster 2. Norway and Denmark make out Cluster 3 and Finland, the Netherlands, and Poland are assigned to Cluster 4. The cluster-specific intercepts and invariant factor loadings are given in Table 6. Note that, due to the identification constraints on the factor means per cluster (Section 2.2.1), the intercepts pertain to the cluster-specific item means. The intercept for the conformity item 'ipfrule' (i.e., about following rules) is higher in Cluster 1 and 2 (i.e., for Belgium, Sweden, Switzerland, Germany, United Kingdom, and Ireland), whereas the intercept for the tradition item 'ipmodst' (i.e., being humble and modest) is higher in Cluster 3 and 4 (i.e., for Denmark, Norway, Finland, the Netherlands, and Poland). The security items 'impsafe' and 'ipstrgv' (i.e., about secure surroundings and the government ensuring safety)

have a higher intercept in Clusters 1 and 3 (i.e., for Belgium, Sweden, Denmark and Norway). The group- and cluster-specific means on the 'conservation' factor are in Table 7. These latent means are validly comparable within each cluster. For Cluster 1, we conclude that conservation is, on average, valued more in Sweden that it is in Belgium. In Cluster 2, it is valued most in Germany. In Cluster 3, there is hardly a difference among Denmark and Norway. In Cluster 4, the respondents of Poland value conservation the most.

[Insert Tables 4, 5, 6, and 7 about here]

For the five self-transcendence items (Appendix C), we performed MMG-FA analyses with one factor and 1 to 14 clusters (where the latter implies group-specific intercepts). BIC_G and AIC indicate 14 clusters (Table 4), again likely to be an overselection, whereas CHull selects three clusters, with a scree ratio of 2.22 and a clear elbow in Figure 1. The assignments into three clusters are given in Table 5. Specifically, Belgium, Switzerland, Germany, Denmark are assigned to Cluster 1. Spain, United Kingdom, Ireland, the Netherlands, Portugal, and Sweden are in Cluster 2. Hungary, Poland, and Slovenia make out Cluster 3. Table 8 contains the factor loadings and cluster-specific intercepts. The intercept for the benevolence item 'iplylfr' (i.e., about loyalty to friends) is highest for the countries in Cluster 2 and lowest in Cluster 1. The intercept for the universalism item 'impenv' (i.e., about looking after the environment) is highest in Cluster 2 and lowest in Cluster 3. For the other items, the differences are very subtle.

In general, we conclude that the intercept non-invariances for conservation could be evaluated by assigning the 11 countries to four clusters and inspecting four sets of cluster-specific intercepts, whereas for the self-transcendence items the non-invariances across 14 countries were captured by three clusters and three sets of cluster-specific intercepts. This implies only a few pairwise comparisons of cluster-specific intercepts, which is clearly more efficient and insightful

than resorting to 55 and 91 pairwise comparisons of the country-specific intercepts, respectively. Based on the MMG-FA solutions, latent mean comparisons could be made per cluster.

5. Discussion

Mixture multigroup factor analysis is an efficient and insightful way to trace MM differences across many groups. This paper focused on comparing intercepts across groups for which metric invariance holds (i.e., invariant factor loadings) but scalar invariance fails. Specifically, groups with (near-)identical intercepts end up in the same mixture cluster and are modeled with one set of cluster-specific intercepts. Since other MM or structural parameters are either invariant or allowed to differ across groups, the clustering is only affected by the intercepts. As a result, MMG-FA not only drastically reduces the number of intercepts to compare but also takes an essential step towards finding clusters of groups for which latent mean comparisons are valid. Indeed, the resulting factor means can be compared among groups in the same cluster.

When one aims to make valid comparisons across all groups, instead of per cluster, the MMG-FA solution provides the user with useful clues on how to continue. Firstly, the comparison of the cluster-specific intercepts may indicate that one or a few items are causing the non-invariance and, thus, that excluding these items – or making their intercepts non-invariant to continue with partial invariance (Byrne, Shavelson, & Muthén, 1989) – allows for valid comparisons across all groups in the data set. Secondly, the clustering may identify a few problematic groups and, then, excluding these groups is an option. Thirdly, a combination of non-invariant items and groups may be found. In any case, one should consider which (combination of) items or groups to remove based on substantive considerations and the amount of retained data.

The cluster-specific intercepts – and the differences between them – depend on the 'alignment' of intercepts and factor means within each cluster. Thus, in order to optimally compare

intercepts across clusters and disentangle invariances from non-invariances, the cluster-specific solutions should be aligned to maximize the between-cluster agreement of intercepts. Currently, in case of no crossloadings and no (or hardly any) classification uncertainty, one can take the clusters obtained by MMG-FA and use them as the grouping variable in multigroup factor alignment (Asparouhov & Muthén, 2014), imposing invariant loadings across groups. In the future, MMG-FA will be extended with an alignment that allows for crossloadings.

To explore predictors of the non-invariances captured by the clustering, MMG-FA can be extended to allow for group-level covariates explaining the cluster memberships (Lubke & Muthén, 2005, 2007). Alternately, covariates can be added after estimating MMG-FA by using the three-step approach (Vermunt, 2010). This would enable researchers, for instance, to use economic, political or cultural indicators to explain between-country differences in intercepts.

Since partial invariance of loadings does not preclude latent mean comparisons (Byrne, Shavelson, & Muthén, 1989), MMG-FA should be able to build on partial metric invariance. Therefore, in the future, it will be extended to allow for loadings that are partially group-specific. For the time being, one could remove items with non-invariant loadings before applying MMG-FA for tracing intercept non-invariances and potentially combine it with the standard multigroup factor analysis with partially invariant loadings and group-specific intercepts.

Finally, exact and full invariance of the intercepts within a cluster may be too restrictive and unrealistic, especially in case of many groups. While awaiting MMG-FA extensions capturing partial or approximate invariance within the clusters, one can use existing approaches – such as modification indices (Sörbom, 1989), item-deletion strategies (Byrne & van de Vijver, 2010) and multigroup Bayesian structural equation modeling (Muthén & Asparouhov, 2013) – within each cluster of the MMG-FA solution.

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Table 1. Mean Adjusted Rand Index (*ARI*) of the estimated clustering of the groups in comparison to the true clustering, in function of the simulated conditions, for MMG-CFA with 10 random starts (left) and with 10 or 50 starts (i.e., 50 starts when 10 starts resulted in a local maximum; middle), and for ML-FMM with 10 starts (right).

	ARI MMG-CFA 10 starts	*ARI* MMG-CFA 10 or 50 starts	*ARI* ML-FMM 10 starts
$G = 12$	.97	.98	.73
$G = 60$	.94	.98	.78
$N_g = 50$	.91	.94	.70
$N_g = 100$	.95	.98	.75
$N_g = 300$	.97	.99	.78
$N_g = 500$	.98	.99	.79
$K = 2$	.99	.99	.87
$K = 4$	.91	.96	.63
equal clusters	.99	.99	.86
unequal clusters	.91	.96	.65
$Q = 2$	.95	.98	.79
$Q = 4$	.95	.98	.72
intercept differences of .60	.97	.99	.90
intercept differences of .30	.93	.96	.60
8 intercept differences	.97	.99	.90
2 intercept differences	.93	.96	.60
overall	.95	.98	.75

Table 2. Mean Absolute Difference (*MAD*) between the estimated and true cluster-specific intercepts, in function of the simulated conditions, for MMG-CFA with 10 random starts (left) and 10 or 50 random starts (i.e., 50 starts when 10 starts resulted in a local maximum; right).

	MMG-CFA 10 starts	MMG-CFA 10 or 50 starts
$G = 12$	.04	.04
$G = 60$	.03	.02
$N_g = 50$	.05	.05
$N_g = 100$	.04	.03
$N_g = 300$	.02	.02
$N_g = 500$	.02	.02
$K = 2$	.02	.02
$K = 4$	.04	.04
equal clusters	.02	.02
unequal clusters	.04	.03
$Q = 2$	.03	.03
$Q = 4$	.03	.03
intercept differences of .60	.03	.03
intercept differences of .30	.03	.03
8 intercept differences	.03	.03
2 intercept differences	.03	.03
overall	.03	.03

Table 3. Percentage of data sets for which BIC_N, BIC_G, AIC and CHull select the correct

number of clusters K, in function of the simulated conditions.

	BIC_N	BIC_G	AIC	CHull
$G = 12$	78.0	91.9	92.5	90.9
$G = 60$	81.7	83.8	76.1	83.8
$N_g = 50$	65.3	80.3	76.3	82.5
$N_g = 100$	75.3	87.2	81.6	86.6
$N_g = 300$	89.7	91.9	90.9	89.7
$N_g = 500$	89.1	91.9	88.4	90.6
$K = 2$	95.2	98.9	93.9	98.4
$K = 4$	64.5	76.7	74.7	76.3
equal clusters	91.7	98.1	93.0	97.5
unequal clusters	68.0	77.5	75.6	77.2
$Q = 2$	80.6	88.4	85.2	88.4
$Q = 4$	79.1	87.2	83.4	86.3
intercept differences of .60	88.6	91.6	87.5	90.0
intercept differences of .30	71.1	84.1	81.1	84.7
8 intercept differences	88.1	90.9	87.0	89.1
2 intercept differences	71.6	84.7	81.6	85.6
overall	79.8	87.8	84.3	87.3

Table 4. Loglikelihood (log *L*), number of free parameters (fp), BIC_G, AIC and CHull scree

ratio for MMG-CFA models for the ESS human values data, with 1 to 11 clusters for conservation

(above) and with 1 to 14 clusters for self-transcendence (below), where the latter models imply

group-specific intercepts. Note that the models with no scree ratio (i.e., indicated by '-') were not

on the convex hull. For each criterion, the value for the best model is in bold face.

Number of clusters	log *L*	fp	BIC_G	AIC	CHull scree ratio
$K = 1$	-202976.2	98	406187.3	406148.4	0.00
$K = 2$	-201886.0	104	404021.4	403980.0	2.80
$K = 3$	-201497.1	110	403258.0	403214.3	1.54
$K = 4$	-201244.0	116	402766.2	402720.1	**3.21**
$K = 5$	-201187.3	122	402667.1	402618.5	-
$K = 6$	-201095.4	128	402497.7	402446.7	-
$K = 7$	-201007.5	134	402336.3	402283.0	1.50
$K = 8$	-200958.7	140	402253.2	402197.5	-
$K = 9$	-200902.5	146	402155.1	402097.0	2.69
$K = 10$	-200883.0	152	402130.4	402070.0	1.17
$K = 11$	-200866.3	158	**402111.4**	**402048.6**	0.00
Number of clusters	log *L*	fp	BIC_G	AIC	CHull scree ratio
$K = 1$	-172820.7	106	345921.1	345853.3	/
$K = 2$	-172461.9	111	345216.8	345145.8	1.38
$K = 3$	-172201.8	116	344709.8	344635.7	**2.22**
$K = 4$	-172084.5	121	344488.2	344410.9	1.78
$K = 5$	-172032.8	126	344398.2	344317.7	-
$K = 6$	-171973.8	131	344293.3	344209.6	-
$K = 7$	-171886.6	136	344132.1	344045.2	1.97
$K = 8$	-171861.6	141	344095.3	344005.2	-
$K = 9$	-171819.6	146	344024.5	343931.2	1.50
$K = 10$	-171811.9	151	344022.3	343925.9	-
$K = 11$	-171774.9	156	343961.4	343861.8	1.88
$K = 12$	-171763.8	161	343952.4	343849.5	-
$K = 13$	-171751.1	166	343940.2	343834.2	1.75
$K = 14$	-171744.3	171	**343939.8**	**343830.5**	/

Table 5. Clustering of MMG-FA models for the ESS human values data on conservation and

self-transcendence. All countries are assigned to the clusters with posterior probability $\hat{z}_{gk} = 1$.

Country	Clustering for conservation	Clustering for self-transcendence
Belgium	1	1
Switzerland	2	1
Germany	2	1
Denmark	3	1
Spain	/	2
Finland	4	1
United Kingdom	2	2
Hungary	/	3
Ireland	2	2
Netherlands	4	2
Norway	3	/
Poland	4	3
Portugal	/	2
Sweden	1	2
Slovenia	/	3

Table 6. Invariant loadings and cluster-specific intercepts of the MMG-FA model for the six

conservation items. Intercepts that are at least .30 higher than in one of the other clusters are

indicated in bold face.

Item	Loadings Conservation	Intercepts Cluster 1	Intercepts Cluster 2	Intercepts Cluster 3	Intercepts Cluster 4
ipfrule	0.76	**3.21**	**3.28**	2.82	2.78
ipbhprp	0.80	2.75	2.67	2.55	2.66
ipmodst	0.51	2.55	2.56	**3.30**	**2.86**
imptrad	0.66	2.83	2.73	2.85	2.62
impsafe	0.66	**2.64**	2.21	**2.86**	2.35
ipstrgv	0.59	**2.61**	2.19	**2.74**	2.35

Table 7. Group- and cluster-specific means on the 'conservation' factor, for each country and for the cluster that country is assigned to.

Country	Cluster 1	Cluster 2	Cluster 3	Cluster 4
Belgium	-0.28			
Switzerland		0.03		
Germany		0.17		
Denmark			0.03	
Finland				0.25
United Kingdom		-0.12		
Ireland		-0.11		
Netherlands				0.30
Norway			-0.03	
Poland				-0.58
Sweden	0.29			

Table 8. Invariant loadings and cluster-specific intercepts of the MMG-FA model for the five self-transcendence items. Intercepts that are at least .30 higher than in one of the other clusters are indicated in bold face.

Item	Loadings Self-Transcendence	Intercepts Cluster 1	Intercepts Cluster 2	Intercepts Cluster 3
iphlppl	0.58	2.00	2.05	2.09
iplylfr	0.50	1.66	1.93	1.86
ipeqopt	0.45	1.98	1.93	1.84
ipudrst	0.54	2.17	2.34	2.30
impenv	0.49	2.01	**2.16**	1.82

Table 9. Group- and cluster-specific means on the 'self-transcendence' factor, for each country

and for the cluster that country is assigned to.

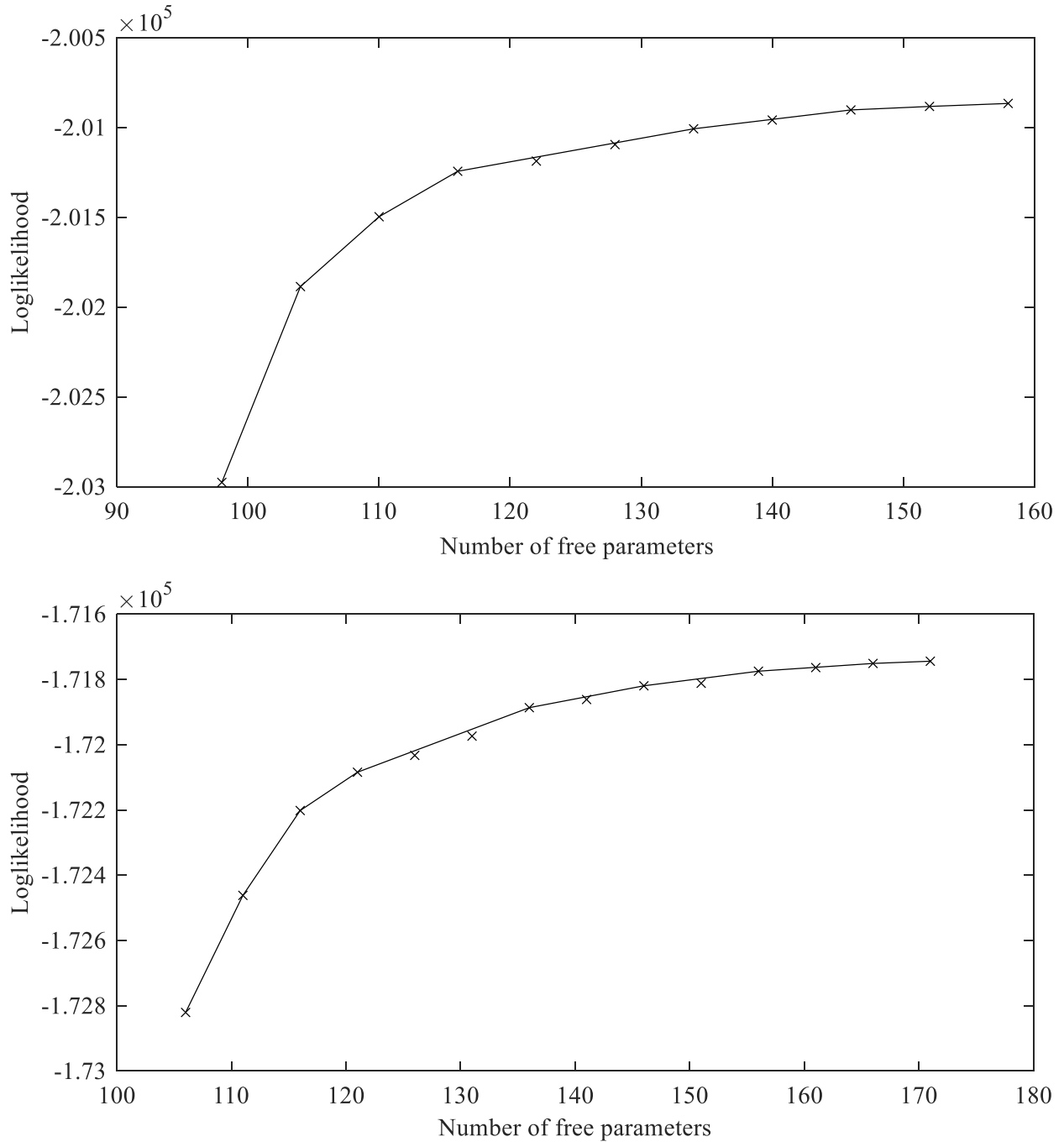| Country	Cluster 1	Cluster 2	Cluster 3
Belgium	0.11		
Switzerland	-0.17		
Germany	-0.06		
Denmark	-0.01		
Spain		-0.57	
Finland	0.11		
United Kingdom		-0.14	
Hungary			0.13
Ireland		-0.03	
Netherlands		0.13	
Poland			0.08
Portugal		0.71	
Sweden		-0.16	
Slovenia			-0.32

Figure 1. Convex Hull (CHull) plot of the loglikelihood in function of the number of free parameters for MMG-FA models for the ESS human values data, with 1 to 11 clusters for conservation (above) and with 1 to 14 clusters for self-transcendence (below), where the latter models correspond to MG-FA with group-specific intercepts.

Appendix A: AECM algorithm and multistart procedure MMG-FA

As in all mixture models, log L (Equation 4) – also referred to as the 'observed-data loglikelihood' – is complicated by the latent clustering of the groups, making it hard to maximize log L directly. Therefore, the EM algorithm makes use of the so-called 'complete-data loglikelihood', i.e., the loglikelihood when the latent (or 'missing') data is assumed to be known (i.e., the joint distribution of the observed and latent data). For estimating MMG-FA as specified in Section 2.2.1, we make use of an alternating expectation conditional maximization (AECM) algorithm (Meng, & Van Dyk, 1997), where two cycles are alternated. In cycle 1, only the groups' cluster memberships z_{gk} are considered as missing data, which leads to the following log L_c:

$$
\begin{aligned}
\log L_c^1 &= \log\left[\prod_{k=1}^{K}\prod_{g=1}^{G}\prod_{n_g=1}^{N_g}\left(f\left(z_{gk}\right)f\left(\mathbf{x}_{n_g}\mid z_{gk}\right)\right)\right]\\[2mm]
&= \log\left[\prod_{k=1}^{K}\prod_{g=1}^{G}\left(\pi_k\prod_{n_g=1}^{N_g}MVN\left(\mathbf{x}_{n_g};\boldsymbol{\tau}_k+\boldsymbol{\Lambda}\boldsymbol{\alpha}_{gk},\boldsymbol{\Sigma}_g\right)\right)^{z_{gk}}\right]\\[2mm]
&= \sum_{g=1}^{G}\sum_{k=1}^{K}z_{gk}\left(\log\left(\pi_k\right)+\sum_{n_g=1}^{N_g}\log\left(\frac{1}{\left(2\pi\right)^{J/2}\left|\boldsymbol{\Sigma}_g\right|^{1/2}}\exp\left(-\frac{1}{2}\tilde{\mathbf{x}}_{n_gk}'\boldsymbol{\Sigma}_g^{-1}\tilde{\mathbf{x}}_{n_gk}\right)\right)\right)\\[2mm]
&= \sum_{g=1}^{G}\sum_{k=1}^{K}z_{gk}\log\left(\pi_k\right)-\frac{NJ}{2}\log\left(2\pi\right)-\frac{1}{2}\sum_{g=1}^{G}N_g\log\left(\left|\boldsymbol{\Sigma}_g\right|\right)-\frac{1}{2}\sum_{g=1}^{G}\sum_{k=1}^{K}z_{gk}\left(\sum_{n_g=1}^{N_g}\left(tr\left(\tilde{\mathbf{x}}_{n_gk}\tilde{\mathbf{x}}_{n_gk}'\boldsymbol{\Sigma}_g^{-1}\right)\right)\right)
\end{aligned}
\tag{9}
$$

where $\tilde{\mathbf{x}}_{n_gk}=\mathbf{x}_{n_g}-\boldsymbol{\tau}_k-\boldsymbol{\Lambda}\boldsymbol{\alpha}_{gk}$ and $\boldsymbol{\Sigma}_g=\boldsymbol{\Lambda}\boldsymbol{\Phi}_g\boldsymbol{\Lambda}'+\boldsymbol{\Psi}_g$. By inserting the expected values of the missing cluster memberships (Equation 10), also referred to as the posterior classification probabilities, the expected value of $\log L_c^1$ is obtained (Equation 11):

$$
\hat{z}_{gk}=E\left[z_{gk}=1\mid\mathbf{X}_g\right]=\frac{\pi_k f_{gk}\left(\mathbf{X}_g;\boldsymbol{\theta}_{gk}\right)}{\sum_{k'=1}^{K}\pi_{k'}f_{gk'}\left(\mathbf{X}_g;\boldsymbol{\theta}_{gk'}\right)},
\tag{10}
$$

$$E\left[\log L_c^1\right] = \sum_{g=1}^{G}\sum_{k=1}^{K}\hat{z}_{gk}\log\left(\pi_k\right) - \frac{NJ}{2}\log\left(2\pi\right) - \frac{1}{2}\sum_{g=1}^{G}N_g\log\left(\left|\Sigma_g\right|\right) - \frac{1}{2}\sum_{g=1}^{G}\sum_{k=1}^{K}N_{gk}tr\left(\mathbf{S}_{gk}\Sigma_g^{-1}\right). \quad (11)$$

Note that, in Equation 11, $N_{gk} = \hat{z}_{gk}N_g$ and $\mathbf{S}_{gk} = \frac{1}{N_g}\sum_{n_g=1}^{N_g}\tilde{\mathbf{x}}_{n_g k}\tilde{\mathbf{x}}'_{n_g k}$. By taking the derivative of

$E\left[\log L_c^1\right]$ and equating it to zero – using the lagrange multiplier method for imposing $\sum_{k=1}^{K}\hat{\pi}_k = 1$

– we obtain the following parameter updates (i.e., conditional maximization steps) for cycle 1:

$$\hat{\pi}_k = \frac{1}{G}\sum_{g=1}^{G}\hat{z}_{gk}, \quad (12)$$

$$\hat{\tau}_k = \left(\sum_{g=1}^{G}N_{gk}\Sigma_g^{-1}\right)^{-1}\left(\sum_{g=1}^{G}N_{gk}\Sigma_g^{-1}\left(\overline{\mathbf{x}}_g - \Lambda\alpha_{gk}\right)\right), \quad (13)$$

$$\hat{\alpha}_{gk} = \left(\Lambda'\Sigma_g^{-1}\Lambda\right)^{-1}\Lambda'\Sigma_g^{-1}\left(\overline{\mathbf{x}}_g - \tau_k\right). \quad (14)$$

In cycle 2, both the cluster memberships z_{gk} and the factor scores $\eta_{n_g k}$ are considered as

missing data and the complete-data loglikelihood becomes:

$$\log L_c^2 = \log \left[\prod_{k=1}^{K} \prod_{g=1}^{G} \prod_{n_g=1}^{N_g} \left(f\left(z_{gk}\right) f\left(\boldsymbol{\eta}_{n_{gk}} \mid z_{gk}\right) f\left(\mathbf{x}_{n_g} \mid \boldsymbol{\eta}_{n_{gk}}, z_{gk}\right) \right) \right]$$

$$= \log \left[\prod_{k=1}^{K} \prod_{g=1}^{G} \left(\pi_k \prod_{n_g=1}^{N_g} \left(MVN\left(\boldsymbol{\eta}_{n_gk}; \boldsymbol{\alpha}_{gk}, \boldsymbol{\Phi}_g\right) MVN\left(\mathbf{x}_{n_g}; \boldsymbol{\tau}_k + \boldsymbol{\Lambda}\boldsymbol{\eta}_{n_gk}, \boldsymbol{\Psi}_g\right) \right) \right)^{z_{gk}} \right]$$

$$= \sum_{g=1}^{G} \sum_{k=1}^{K} z_{gk} \left(\begin{array}{l} \log\left(\pi_k\right) + \sum_{n_g=1}^{N_g} \log\left(\dfrac{1}{\left(2\pi\right)^{Q/2}\left|\boldsymbol{\Phi}_g\right|^{1/2}} \exp\left(-\dfrac{1}{2}\left(\boldsymbol{\eta}_{n_gk} - \boldsymbol{\alpha}_{gk}\right)' \boldsymbol{\Phi}_g^{-1}\left(\boldsymbol{\eta}_{n_gk} - \boldsymbol{\alpha}_{gk}\right)\right) \right) \\ + \sum_{n_g=1}^{N_g} \log\left(\dfrac{1}{\left(2\pi\right)^{J/2}\left|\boldsymbol{\Psi}_g\right|^{1/2}} \exp\left(-\dfrac{1}{2}\left(\mathbf{x}_{n_g} - \boldsymbol{\tau}_k - \boldsymbol{\Lambda}\boldsymbol{\eta}_{n_gk}\right)' \boldsymbol{\Psi}_g^{-1}\left(\mathbf{x}_{n_g} - \boldsymbol{\tau}_k - \boldsymbol{\Lambda}\boldsymbol{\eta}_{n_gk}\right)\right) \right) \end{array} \right)$$

$$= \sum_{g=1}^{G} \sum_{k=1}^{K} z_{gk} \log\left(\pi_k\right) - \frac{N(J+Q)}{2}\log\left(2\pi\right) - \frac{1}{2}\sum_{g=1}^{G} N_g \log\left(\left|\boldsymbol{\Phi}_g\right|\right) - \frac{1}{2}\sum_{g=1}^{G} N_g \log\left(\left|\boldsymbol{\Psi}_g\right|\right)$$

$$- \frac{1}{2}\sum_{g=1}^{G} \sum_{k=1}^{K} z_{gk} \left(\sum_{n_g=1}^{N_g} \left(\begin{array}{l} tr\left(\tilde{\boldsymbol{\eta}}_{n_gk}\tilde{\boldsymbol{\eta}}_{n_gk}'\boldsymbol{\Phi}_g^{-1}\right) + tr\left(\tilde{\mathbf{x}}_{n_gk}\tilde{\mathbf{x}}_{n_gk}'\boldsymbol{\Psi}_g^{-1}\right) - \tilde{\mathbf{x}}_{n_gk}'\boldsymbol{\Psi}_g^{-1}\boldsymbol{\Lambda}\tilde{\boldsymbol{\eta}}_{n_gk} \\ -\left(\boldsymbol{\Lambda}\tilde{\boldsymbol{\eta}}_{n_gk}\right)'\boldsymbol{\Psi}_g^{-1}\tilde{\mathbf{x}}_{n_gk} + tr\left(\boldsymbol{\Lambda}'\boldsymbol{\Psi}_g^{-1}\boldsymbol{\Lambda}\tilde{\boldsymbol{\eta}}_{n_gk}\tilde{\boldsymbol{\eta}}_{n_gk}'\right) \end{array} \right) \right) \tag{15}$$

where $\tilde{\boldsymbol{\eta}}_{n_gk} = \boldsymbol{\eta}_{n_gk} - \boldsymbol{\alpha}_{gk}$ and $\tilde{\mathbf{x}}_{n_gk} = \mathbf{x}_{n_g} - \boldsymbol{\tau}_k$. The expected values of z_{gk}, $\tilde{\boldsymbol{\eta}}_{n_gk}$ and $\tilde{\boldsymbol{\eta}}_{n_gk}\tilde{\boldsymbol{\eta}}_{n_gk}'$ are

inserted in Equation 15, which yields the following expected value of $\log L_c^2$:

$$E\left[\log L_c^2\right] = \sum_{g=1}^{G} \sum_{k=1}^{K} \hat{z}_{gk} \log\left(\pi_k\right) - \frac{N(J+Q)}{2}\log\left(2\pi\right) - \frac{1}{2}\sum_{g=1}^{G} N_g \log\left(\left|\boldsymbol{\Phi}_g\right|\right)$$

$$- \frac{1}{2}\sum_{g=1}^{G} N_g \log\left(\left|\boldsymbol{\Psi}_g\right|\right) - \frac{1}{2}\sum_{g=1}^{G} \sum_{k=1}^{K} \hat{z}_{gk} tr\left(\boldsymbol{\Phi}_g^{-1} \sum_{n_g=1}^{N_g} E\left[\tilde{\boldsymbol{\eta}}_{n_gk}\tilde{\boldsymbol{\eta}}_{n_gk}'\right] \right) - \frac{1}{2}\sum_{g=1}^{G} \sum_{k=1}^{K} N_{gk} tr\left(\mathbf{S}_{gk}\boldsymbol{\Psi}_g^{-1}\right)$$

$$+ \frac{1}{2}\sum_{g=1}^{G} \sum_{k=1}^{K} \hat{z}_{gk} tr\left(\boldsymbol{\Lambda}'\boldsymbol{\Psi}_g^{-1}\tilde{\mathbf{x}}_{n_gk} \sum_{n_g=1}^{N_g} E\left[\tilde{\boldsymbol{\eta}}_{n_gk}\right]' \right) + \frac{1}{2}\sum_{g=1}^{G} \sum_{k=1}^{K} \hat{z}_{gk} tr\left(\tilde{\mathbf{x}}_{n_gk}'\boldsymbol{\Psi}_g^{-1}\boldsymbol{\Lambda} \sum_{n_g=1}^{N_g} E\left[\tilde{\boldsymbol{\eta}}_{n_gk}\right] \right) \tag{16}$$

$$- \frac{1}{2}\sum_{g=1}^{G} \sum_{k=1}^{K} \hat{z}_{gk} tr\left(\boldsymbol{\Lambda}'\boldsymbol{\Psi}_g^{-1}\boldsymbol{\Lambda} \sum_{n_g=1}^{N_g} E\left[\tilde{\boldsymbol{\eta}}_{n_gk}\tilde{\boldsymbol{\eta}}_{n_gk}'\right] \right)$$

where $\hat{z}_{gk}$ corresponds to the posterior classification probability (Equation 10) and $E\left[\tilde{\boldsymbol{\eta}}_{n_gk}\right]$ and

$E\left[\tilde{\boldsymbol{\eta}}_{n_gk}\tilde{\boldsymbol{\eta}}_{n_gk}'\right]$ are equal to (McLachlan & Krishnan, 2007):

$$E\left[\tilde{\mathbf{\eta}}_{n_g k}\right] = E\left[\tilde{\mathbf{\eta}}_{n_g k} \mid \mathbf{x}_{n_g}, z_{gk} = 1\right] = \mathbf{\beta}_g \tilde{\mathbf{x}}_{n_g k} \quad with \quad \mathbf{\beta}_g = \mathbf{\Phi}_g \mathbf{\Lambda}' \left(\mathbf{\Lambda}\mathbf{\Phi}_g \mathbf{\Lambda}' + \mathbf{\Psi}_g\right)^{-1}, \quad (17)$$

$$E\left[\tilde{\mathbf{\eta}}_{n_g k}\tilde{\mathbf{\eta}}'_{n_g k}\right] = E\left[\tilde{\mathbf{\eta}}_{n_g k}\tilde{\mathbf{\eta}}'_{n_g k} \mid \mathbf{x}_{n_g}, z_{gk} = 1\right] = \mathbf{\Phi}_g - \mathbf{\beta}_g \mathbf{\Lambda}\mathbf{\Phi}_g + \mathbf{\beta}_g \tilde{\mathbf{x}}_{n_g k} \tilde{\mathbf{x}}_{n_g k}' \mathbf{\beta}_g'. \quad (18)$$

where $\tilde{\mathbf{x}}_{n_g k} = \mathbf{x}_{n_g k} - \mathbf{\mu}_{gk}$ and $\mathbf{\mu}_{gk} = \mathbf{\tau}_k + \mathbf{\Lambda}\mathbf{\alpha}_{gk}$. By taking the derivative of $E\left[\log L_c^2\right]$ and equating

it to zero – again imposing $\sum_{k=1}^{K}\hat{\pi}_k = 1$ – we obtain the conditional maximization steps for cycle 2:

$$\hat{\pi}_k = \frac{1}{G}\sum_{g=1}^{G}\hat{z}_{gk} \quad (19)$$

$$\hat{\mathbf{\tau}}_k = \left(\sum_{g=1}^{G} N_{gk}\mathbf{\Psi}_g^{-1}\right)^{-1}\left(\sum_{g=1}^{G} N_{gk}\mathbf{\Psi}_g^{-1}\left(\bar{\mathbf{x}}_g - \mathbf{\Lambda}\mathbf{\alpha}_{gk} - \mathbf{\Lambda}\mathbf{\beta}_g\left(\bar{\mathbf{x}}_g - \mathbf{\mu}_{gk}\right)\right)\right) \quad (20)$$

$$\hat{\mathbf{\alpha}}_{gk} = \left(\mathbf{\Lambda}'\mathbf{\Psi}_g^{-1}\mathbf{\Lambda}\right)^{-1}\mathbf{\Lambda}'\mathbf{\Psi}_g^{-1}\left(\bar{\mathbf{x}}_g - \mathbf{\tau}_k - \mathbf{\Lambda}\mathbf{\beta}_g\left(\bar{\mathbf{x}}_g - \mathbf{\mu}_{gk}\right)\right) \quad (21)$$

$$\hat{\mathbf{\lambda}}_j^{nz} = \left(\sum_{g,k=1}^{G,K}\frac{N_{gk}}{d_{gj}}\left(\mathbf{S}_{gk}\mathbf{\beta}_g^{nz'} + \left(\bar{\mathbf{x}}_g - \mathbf{\tau}_k\right)\mathbf{\alpha}_{gk}^{nz'}\right)_{j.}\right)\left(\sum_{g,k=1}^{G,K}\frac{N_{gk}}{d_{gj}}\left(\mathbf{\Theta}_{gk}^{nz} + \mathbf{\alpha}_{gk}^{nz}\mathbf{\alpha}_{gk}^{nz'} + \mathbf{\beta}_g^{nz}\left(\bar{\mathbf{x}}_g - \mathbf{\mu}_{gk}\right)\mathbf{\alpha}_{gk}^{nz'}\right)\right)^{-1} \quad (22)$$

$$diag\left(\hat{\mathbf{\Psi}}_g\right) = diag\left(\frac{1}{N_g}\sum_{k=1}^{K}N_{gk}\left(\mathbf{S}_{gk} - \left(2\mathbf{\Lambda}\mathbf{\beta}_g\mathbf{S}_{gk} - \mathbf{\Lambda}\mathbf{\Theta}_{gk}\mathbf{\Lambda}'\right)\right)\right) \quad (23)$$

$$\hat{\mathbf{\Phi}}_g = \frac{1}{N_g}\sum_{k=1}^{K}N_{gk}\mathbf{\Theta}_{gk} \quad (24)$$

where $\bar{\mathbf{x}}_g$ is the observed mean for group g and $\mathbf{\Theta}_{gk} = \mathbf{\Phi}_g - \mathbf{\beta}_g\mathbf{\Lambda}\mathbf{\Phi}_g + \mathbf{\beta}_g\mathbf{S}_{gk}\mathbf{\beta}_g'$. Note that the factor

loadings (Equation 22) are updated per variable j and that the 'nz' superscript refers to the fact

that, for MMG-CFA, the update only concerns the non-zero (nz) loadings for variable j – whereas

the other loadings, obviously, remain zero. For MMG-EFA, all loadings are non-zero for all

variables $j = 1, \ldots, J$. When defining a binary 'design' matrix $\mathbf{B}$ of size $J \times Q$, with ones for the

non-zero loading positions, the reduced matrices in Equation 22 are obtained as follows: $\boldsymbol{\beta}_g^{nz}$ is

equal to the columns of $\boldsymbol{\beta}_g$ corresponding to the ones in row j of matrix $\mathbf{B}$ (i.e., $\mathbf{b}_j$), $\boldsymbol{\alpha}_{gk}^{nz}$ contains

the elements of $\boldsymbol{\alpha}_{gk}$ corresponding to the ones in $\mathbf{b}_j$, and $\boldsymbol{\Theta}_{gk}^{nz}$ is obtained by selecting rows and

columns $\boldsymbol{\Theta}_{gk}$ as indicated by the ones in $\mathbf{b}_j$.

To set the scale of the factors, the mean factor variances are fixed to one over all groups,

i.e., $diag\left(\boldsymbol{\Phi}\right) = diag\left(\dfrac{1}{N}\sum\limits_{g=1}^{G} N_g \boldsymbol{\Phi}_g\right) = \mathbf{1}$. Note that, for MMG-EFA, the factor covariances are also

fixed to zero over all groups, which implies that the initial rotation is orthogonal. Afterwards, one

can choose to rotate the exploratory factors according to an orthogonal or oblique rotation criterion

and counterrotate the group-specific factor covariances accordingly. Additionally, the factor

means are restricted per cluster as follows: $\dfrac{1}{N_k}\sum\limits_{g=1}^{G} N_g \hat{z}_{gk}\boldsymbol{\alpha}_{gk} = \mathbf{0}$ for $k = 1, \ldots, K$. To impose these

restrictions, the factor (co)variances, loadings, factor means and intercepts are transformed as

follows:

$$\hat{\boldsymbol{\Phi}}_g^* = \left(\boldsymbol{\Theta}\right)^{-\frac{1}{2}} \hat{\boldsymbol{\Phi}}_g \left(\boldsymbol{\Theta}\right)^{-\frac{1}{2}} \quad with \quad \boldsymbol{\Theta} = \frac{1}{N}\left(\sum_{g'=1}^{G}\sum_{k=1}^{K} N_{g'k}\boldsymbol{\Theta}_{g'k}\right) \tag{25}$$

$$\hat{\boldsymbol{\Lambda}}^* = \hat{\boldsymbol{\Lambda}}\left(\boldsymbol{\Theta}\right)^{\frac{1}{2}} . \tag{26}$$

$$\hat{\boldsymbol{\alpha}}_{gk}^* = \hat{\boldsymbol{\alpha}}_{gk} - \hat{\boldsymbol{\alpha}}_k \quad with \quad \hat{\boldsymbol{\alpha}}_k \frac{1}{N_k}\sum_{g'=1}^{G} N_{g'}\hat{z}_{g'k}\hat{\boldsymbol{\alpha}}_{g'k} = \mathbf{0} \tag{27}$$

$$\hat{\boldsymbol{\tau}}_k^* = \left(\sum_{g=1}^{G} N_{gk}\boldsymbol{\Sigma}_g^{-1}\right)^{-1}\left(\sum_{g=1}^{G} N_{gk}\boldsymbol{\Sigma}_g^{-1}\left(\overline{\mathbf{x}}_g - \boldsymbol{\Lambda}\boldsymbol{\alpha}_{gk}^*\right)\right) \tag{28}$$

where the offdiagonal elements of $\boldsymbol{\Theta}$ are fixed to zero in case of MMG-CFA. Note that this is done

in the final iteration only (i.e., upon convergence).

A1. Algorithm

For a user-specified number of starts, perform the following steps for each start:

1. Start from a pre-selected random partition (Section A2), i.e., with binary values for $\hat{z}_{gk}$.

2. For each cluster k of the random partition, initialize $\boldsymbol{\tau}_k$ as follows: $\boldsymbol{\tau}_k = \dfrac{1}{N_k} \sum_{g=1}^{G} \hat{z}_{gk} \sum_{n_g=1}^{N_g} \mathbf{x}_{n_g}$.

3. Initialize $\boldsymbol{\Lambda}$, $\boldsymbol{\Psi}_g$ and $\boldsymbol{\Phi}_g$, based on probabilistic principal component analysis (Tipping

   & Bishop, 1999), as follows[1]: $\boldsymbol{\Lambda} = \mathbf{U}_Q \sqrt{\left(\mathbf{V}_Q - \hat{\sigma}^2 \mathbf{I}_Q\right)}$ and $\boldsymbol{\Psi}_g = \hat{\sigma}^2 \mathbf{I}_J$ for $g = 1, \ldots, G$,

   where the columns of $\mathbf{U}_Q$ correspond to the first Q eigenvectors and the diagonal matrix

   $\mathbf{V}_Q$ contains the first Q eigenvalues of the eigenvalue decomposition of

   $\mathbf{S} = \dfrac{1}{N} \sum_{k=1}^{K} \sum_{g=1}^{G} \hat{z}_{gk} \left(\sum_{n_g=1}^{N_g} \tilde{\mathbf{x}}_{n_g k} \tilde{\mathbf{x}}'_{n_g k} \right)$ with $\tilde{\mathbf{x}}_{n_g k} = \mathbf{x}_{n_g} - \boldsymbol{\tau}_k$, $\hat{\sigma}^2$ is the average variance in the $J - Q$

   discarded dimensions, and $\mathbf{I}_Q$ and $\mathbf{I}_J$ are $Q \times Q$ and $J \times J$ identity matrices, respectively. In

   case of MMG-CFA, the thus obtained loadings $\boldsymbol{\Lambda}$ are orthogonally Procrustes rotated

   towards the design matrix $\mathbf{B}$ and then the zero loadings are fixed to zero. The factor

   (co)variance matrices $\boldsymbol{\Phi}_g$ are initialized as $\mathbf{I}_Q$.

4. Initialize $\boldsymbol{\alpha}_{gk}$ for $g = 1, \ldots, G$ and $k = 1, \ldots, K$ based on the singular value decomposition

   $\tilde{\mathbf{X}}_{gk} \boldsymbol{\Lambda} = \mathbf{U}_{gk} \mathbf{D}_{gk} \mathbf{V}'_{gk}$ where $\tilde{\mathbf{X}}_{gk}$ contains the group-specific deviations around $\boldsymbol{\tau}_k$ and $\mathbf{U}_{gk}$

   and $\mathbf{V}_{gk}$ contain the left and right singular vectors, respectively: Group- and cluster-

   specific component scores are obtained by $\mathbf{F}_{gk} = \left(\mathbf{U}_{gk}\right)_Q \mathbf{V}'_{gk}$ (ten Berge, 1993) where

---

[1] These starting values are similar to the maximum likelihood estimates of image factor analysis described by Jöreskog (1969).

$\left(\mathbf{U}_{gk}\right)_Q$ corresponds to the first Q columns of $\mathbf{U}_{gk}$. After rescaling $\mathbf{F}_{gk}$ to have a variance

of one, $\boldsymbol{\alpha}_{gk}$ is initialized as the mean of $\mathbf{F}_{gk}$.

5. Iterate the following steps while δ_1 & $\delta_2 > 1 \times 10^{-4}$ and $v \leq 100$:

    a. Update the iteration number: $v = v + 1$.

    b. Cycle 1, E-step: Update the posterior classification probabilities $\hat{z}_{gk}$ (Equation 10)

        for $g = 1, \ldots, G$ and $k = 1, \ldots, K$.

    c. Cycle 1, conditional M-steps:

        i. Update $\hat{\pi}_k$ (Equation 12) for $k = 1, \ldots, K$.

        ii. Update $\hat{\boldsymbol{\tau}}_k$ (Equation 13) for $k = 1, \ldots, K$.

        iii. Update $\hat{\boldsymbol{\alpha}}_{gk}$ (Equation 14) for $g = 1, \ldots, G$ and $k = 1, \ldots, K$.

    d. Cycle 2: E-step: Update the posterior classification probabilities $\hat{z}_{gk}$ (Equation 10)

        for $g = 1, \ldots, G$ and $k = 1, \ldots, K$.

    e. Cycle 2: Conditional M-steps:

        i. Update $\hat{\pi}_k$ (Equation 19) for $k = 1, \ldots, K$.

        ii. Update $\hat{\boldsymbol{\tau}}_k$ (Equation 20) for $k = 1, \ldots, K$.

        iii. Update $\hat{\boldsymbol{\alpha}}_{gk}$ (Equation 21) for $g = 1, \ldots, G$ and $k = 1, \ldots, K$.

        iv. Update the factor loadings $\boldsymbol{\Lambda}$ (Equation 22), the unique variances $\boldsymbol{\Psi}_g$ for

           $g = 1, \ldots, G$ (Equation 23) and the factor (co)variance matrices $\boldsymbol{\Phi}_g$ for $g =$

           $1, \ldots, G$ (Equation 24). To remedy Heywood cases, fix unique variances to

           .0001 when they are smaller than this number.

    f. Compute $\log L^v$ value (Equation 4).

g. Evaluate convergence with respect to $\log L^v$ and the parameter estimates $\hat{\theta}_p^v$:

$$\delta_1 = \sum_{p=1}^{P} \left| \frac{\hat{\theta}_p^v - \hat{\theta}_p^{v-1}}{\hat{\theta}_p^{v-1}} \right| \text{ and } \delta_2 = \log L^v - \log L^{v-1}.$$

6. After (preliminary) convergence is reached (or 100 iterations), check whether the obtained solution is the best one in terms of $\log L$ (across all starts up to now) and, if so, save the parameter estimates $\hat{\theta}_p^{best} = \hat{\theta}_p^v$ and iteration number $v^{best} = v$.

After performing this procedure for all starts, iterate further until full convergence is reached for the best solution: i.e., starting from $\hat{\theta}_p^v = \hat{\theta}_p^{best}$ and $v = v^{best}$, iterate Steps 5a to 5g while δ_1 & $\delta_2 >$ 1×10^{-6} and $v \leq 1000$ (or another user-specified maximal number of iterations). Finally, the model identification constraints are imposed by means of Equations 25 to 28.

A2. Multistart procedure

Because the AECM algorithm described in Section A1 is not guaranteed to converge to the global maximum, a multistart procedure is used to increase the probability of finding the global maximum. The multistart procedure applies a tiered testing strategy with respect to several sets of starting values. Specifically, given the user-specified number of starts (e.g., 10), it starts from 10 times as many random partitions of the groups (e.g., 10×10 partitions). For each of these partitions, the parameter estimates are initialized as described in Steps 2 to 4 of the algorithm (Section A1). Subsequently, the parameter estimates are updated once by means of Equations 19 to 24 and the $\log L$ value (Equation 4) is determined. The 10% most promising partitions (i.e., with the highest $\log L$) are selected as the starts for the algorithm described in Section A1.

Appendix B: Latent Gold 6.0 syntax

An example syntax for MMG-FA with three clusters and two factors for a data set with 11

variables is given and explained below (for more details, see Vermunt & Magidson, 2013):

```
options
   algorithm
      tolerance=1e-006 emtolerance=1e-006 emiterations=1000 nriterations=0
      emfa;
   startvalues
      seed=0 sets=100 tolerance=1e-004 iterations=50 PCA annealing;
   bayes
      categorical=0 variances=0 latent=0 poisson=0;
   missing includeall;
   output
      iterationdetail parameters=first standarderrors probmeans=posterior
      reorderclasses;
variables
   groupid Country;
   dependent (V1-V11) continuous;
   independent Country nominal;
   latent
      F1 continuous,
      F2 continuous,
      Cluster nominal group 4; // 1-8 to estimate models with 1 to 8 clusters
equations
// group- and cluster-specific factor (co)variances
   F1 | Country;
   F2 | Country;
   F1 <-> F2 | Country;
// logistic regression model for clusters (only intercept)
   Cluster <- 1;
// regression models for factors: group- and cluster-specific factor means
   F1 <- 1 | Country Cluster;
   F2 <- 1 | Country Cluster;
// regression models for items: cluster-specific intercepts for non-referent
// items and invariant loadings
   V1 <- (1) F1;
   V2 – V6 <- 1 | Cluster + F1;
   V7 <- (1) F2;
   V8 - V11 <- 1 | Cluster + F2;
// group-specific unique variances
   V1 - V11 | Country;
```

The LG syntax contains three sections, i.e., 'options, 'variables', and 'equations'. Firstly,

the 'options' section pertains to specifications regarding the estimation process and to output

options. The parameters in the 'algorithm' subsection indicate when the algorithm should proceed

with Newton-Raphson instead of EM iterations and when convergence is reached. To apply only EM iterations, set 'nriterations' to zero, 'emiterations' to a high number and 'emtolerance' to the same value as 'tolerance'. The option 'emfa' makes sure that the factor model parameters are estimated by means of the time-efficient EM procedure detailed in Appendix A. The 'startvalues' subsection includes the parameters pertaining to the multistart procedure used by LG. Specifically, for each set of starting values (the number of sets is specified by 'sets'), the model is re-estimated for as many iterations as specified by 'iterations' or until δ_1 or δ_2 drops below the 'tolerance' value. Subsequently, it continues with the 10% (rounded upwards) most promising sets (i.e., with the highest log L), performing another two times the specified number of iterations (i.e., $2 \times$ the value of 'iterations'). Finally, it continues with the best solution until convergence. In the example syntax above, 100 starts are requested by the user. The thus obtained multistart procedure is actually more elaborate than the one evaluated in Section 3, because the clustering and factor parameters are updated 50 times before choosing the best 10% most promising sets of starting values (as opposed to one update of the factor parameters only). 'PCA' prompts LG to use starting values for the factor loadings and unique variances that are based on a principal component analysis (PCA) of the data (Vermunt and Magidson, 2016). When group sizes are large, the algorithm may be prone to local maxima because the posterior classification probabilities quickly approach one and zero, even for a clustering that is far from the one that is actually underlying the data. This may happen especially when between-cluster intercept differences are small. To avoid this, the 'annealing' option – referring to 'deterministic annealing' – is used which implies that an auxiliary variable is used to keep the posterior classification probabilities more fuzzy for the first few iterations (Zhou & Lange, 2010). It is advised to set the options in the 'bayes' subsection to

zero when using the 'emfa' algorithm. In the 'output' and 'outfile' subsections, the user can specify the desired output.

Secondly, the 'variables' section specifies the different types of variables included in the model. Since MMG-FA operates on multilevel data, after 'groupid', the variable in the data file that indicates the group structure (i.e., the group number for each observation) should be specified, using its label in the data file (e.g, 'Country'). In the 'dependent' subsection, the dependent variables of the model (i.e., the observed variables) are specified, by means of their label in the data file and their measurement scale. Next, the 'independent' variables are listed. For MMG-FA, one has to include the grouping variable as an independent variable, since some parameters vary across groups. Finally, the 'latent' variables of the MMG-FA model are the factors (i.e., 'F1' to 'F2' in the example syntax) and the mixture model clustering (i.e., 'Cluster'). In particular, the former are specified as continuous latent variables, whereas the latter is specified as a nominal latent variable at the group level with a specified number of categories (i.e., the desired number of clusters). For estimating models with, for instance, one to eight clusters, use '1–8'.

In the 'equations' section, the model equations are listed. First, the factor variances and covariances are specified and they are allowed to differ among groups by adding '| Country'. Next, a logistic regression model for the categorical latent variable 'Cluster' is specified followed by regression equations for the factors, which contain only an intercept term and where the factor means are made group- and cluster-specific by adding '| Country Cluster' to the factors' intercept term. Then, regression models are defined for the observed variables, indicating which variables are regressed on which factors. Note that, to apply EFA, all variables should be regressed on all factors. In Latent Gold 6.0, rotation options are available to specify how the parameters should be identified in case of EFA (De Roover & Vermunt, 2019). To obtain intercepts that differ between

clusters, '| Cluster' is added to the intercept term. Note that, in the example syntax, V1 and V7 serve as referent items with intercepts of zero in all clusters (i.e., no intercept term included in their regression equations) and factor loadings of one. This model identification strategy differs from the one in Appendix A. Finally, unique variances are added, which are allowed to differ across groups. At the end of the syntax, additional restrictions may be specified or starting values for all parameters may be given, either by directly typing them in the syntax or by referring to a text file.

Appendix C: Conservation and Self-Transcendence items PVQ-21

Conservation items (male version):

- ipfrule (item 7, conformity): 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.
- ipbhprp (item 16, conformity): It is important to him always to behave properly. He wants to avoid doing anything people would say is wrong.
- ipmodst (item 9, tradition): It is important to him to be humble and modest. He tries not to draw attention to himself.
- imptrad (item 20, tradition): Tradition is important to him. He tries to follow the customs handed down by his religion or his family.
- impsafe (item 5, security): It is important to him to live in secure surroundings. He avoids anything that might endanger his safety.
- ipstrgv (item 14, security): It is important to him that the government ensures his safety against all threats. He wants the state to be strong so it can defend its citizens.

Self-transcendence items (male version):

- iphlppl (item 12, benevolence): It's very important to him to help the people around him. He wants to care for their well-being.
- iplylfr (item 18, benevolence): It is important to him to be loyal to his friends. He wants to devote himself to people close to him.
- ipeqopt (item 3, universalism): He thinks it is important that every person in the world should be treated equally. He believes everyone should have equal opportunities in life.
- ipudrst (item 8, universalism): It is important to him to listen to people who are different from him. Even when he disagrees with them, he still wants to understand them.
- impenv (item 19, universalism): He strongly believes that people should care for nature. Looking after the environment is important to him.

References to the appendices

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