**Appendix**

Below we outline the steps for the MCMC algorithms, in particular, how parameters can be sampled from their full conditional distributions. At iteration ,

1. For , draw the candidate values from , where is the common candidate variance of , and accept , with probability

2. Draw from the Inverse-Wishart distribution,

The sampled is then transformed into the corresponding . The provisional is accepted based on the M-H acceptance probability set by comparing the determinants of the provisional and previous values, that is,

3. For , draw the candidate values from , where is the common candidate variance of , and accept , with probability

4. For , draw the candidate values from , where is the common candidate variance of , and accept , with probability

5. For , draw the candidate values from , where is the common candidate variance of , and accept , with probability

6. Draw the components of from the multivariate normal distribution expressed above. Alternatively, elements of can be drawn from multiple univariate normal distributions, respectively, if the conditional are used, because as stated above, the dimensions of the conditional are mutually independent.

7. For and , draw the candidate values and from and , respectively, where and are the common candidate variances of and , respectively, and accept and , with probabilities

and

Multiple chains (e.g., four chains) with different initial values can be run to monitor the convergence of the algorithm. Each chain can have iterations, and the first iterations of each chain can be discarded as the burn-in. The convergence for the structural parameters (i.e., the item parameters, mean matrix, and covariance matrix) can be determined using the Gelman-Rubin (G-R; Gelman & Rubin, 1992) statistics. The G-R diagnostic statistics compare the ratio of the weighted average of the within-chain variance and between-chain variance to the within-chain variance. If this ratio is close to 1 (e.g., less than 1.1 or 1.2; Gelman et al., 2004), it indicates that the chains have reached the stationary distribution.

The estimates of interest are based on the posterior mean (i.e., expected a posteriori; EAP), and are computed as , where can be any of the following: . To fully utilize the results obtained from multiple chains with different starting values, the formula shown above is calculated and averaged across multiple chains when deriving final estimates.