Supplementary materials to

Maydeu-Olivares, A., & Shi, D. (2017). Assessing fit in structural equation models: A Monte-Carlo evaluation of RMSEA vs. SRMR confidence intervals and tests of close fit. *Structural Equation Modeling*. http://doi.org/10.1080/10705511.2017.1389611

Additional Results for the Simulations Reported in the Article

Table A.1: *Population SRMR and $SRMR_b$ (biased SRMR) across replications. Shaded results indicate relative bias <|.10|*

Kur.	Skew.	ρ	*N*	*p* = 10		*p* = 30		*p* = 60	
				pop.	SRMRb	pop.	SRMRb	pop.	SRMRb
			100	**0.021**	0.050	**0.022**	0.058	**0.023**	0.060
		0.9	200	**0.021**	0.038	**0.022**	0.044	**0.023**	0.045
			500	**0.021**	0.029	**0.022**	0.033	**0.023**	0.033
			1000	**0.021**	0.025	**0.022**	0.028	**0.023**	0.028
			100	**0.041**	0.062	**0.044**	0.071	**0.045**	0.073
		0.8	200	**0.041**	0.053	**0.044**	0.059	**0.045**	0.060
0.0	0.0		500	**0.041**	0.046	**0.044**	0.051	**0.045**	0.052
			1000	**0.041**	0.044	**0.044**	0.048	**0.045**	0.049
			100	**0.062**	0.079	**0.067**	0.088	**0.068**	0.090
		0.7	200	**0.062**	0.071	**0.067**	0.078	**0.068**	0.079
			500	**0.062**	0.066	**0.067**	0.072	**0.068**	0.073
			1000	**0.062**	0.064	**0.067**	0.069	**0.068**	0.070
			100	**0.018**	0.060	**0.019**	0.070	**0.020**	0.072
		0.9	200	**0.018**	0.044	**0.019**	0.051	**0.020**	0.053
			500	**0.018**	0.031	**0.019**	0.036	**0.020**	0.037
			1000	**0.018**	0.025	**0.019**	0.029	**0.020**	0.029
			100	**0.036**	0.068	**0.039**	0.079	**0.039**	0.081
		0.8	200	**0.036**	0.054	**0.039**	0.062	**0.039**	0.063
3.0	0.0		500	**0.036**	0.044	**0.039**	0.049	**0.039**	0.050
			1000	**0.036**	0.040	**0.039**	0.044	**0.039**	0.045
			100	**0.053**	0.079	**0.057**	0.090	**0.058**	0.092
		0.7	200	**0.053**	0.068	**0.057**	0.076	**0.058**	0.077
			500	**0.053**	0.060	**0.057**	0.066	**0.058**	0.067
			1000	**0.053**	0.057	**0.057**	0.062	**0.058**	0.063
			100	**0.020**	0.072	**0.021**	0.084	**0.022**	0.087
		0.9	200	**0.020**	0.053	**0.021**	0.061	**0.022**	0.063
			500	**0.020**	0.037	**0.021**	0.042	**0.022**	0.043
			1000	**0.020**	0.030	**0.021**	0.033	**0.022**	0.034
			100	**0.039**	0.081	**0.042**	0.093	**0.043**	0.095
		0.8	200	**0.039**	0.064	**0.042**	0.072	**0.043**	0.074
3.0	-2.0		500	**0.039**	0.050	**0.042**	0.056	**0.043**	0.057
			1000	**0.039**	0.045	**0.042**	0.049	**0.043**	0.050
			100	**0.057**	0.091	**0.062**	0.104	**0.063**	0.106
		0.7	200	**0.057**	0.076	**0.062**	0.085	**0.063**	0.087
			500	**0.057**	0.065	**0.062**	0.072	**0.063**	0.073
			1000	**0.057**	0.061	**0.062**	0.067	**0.063**	0.068

Additional Simulations: Omitting Cross-loadings

Population Model

The true model has an independent cluster structure (each indicator is loaded by a single factor) with correlated factors. However, two indicators have cross-loadings (i.e. one item is loaded on both factors). The population factor loadings were fixed to .70. The variances of the error were set to 0.51. The inter-factor correlation was fixed to .70, and the population value of the omitted cross-loadings were .40.

Fitted Model and Distributional Assumptions

The fitted model is the independent cluster CFA model where the cross-loadings are incorrectly fixed to zero. Maximum likelihood estimation was performed with robust SEs and mean corrected likelihood ratio tests statistics. Confidence intervals and *p*-values of the tests of close fit are only computed under ADF assumptions (i.e., robust to non-normality).

Table A.2. *Population RMSEA, SMSR and CRMR and sample means of the unbiased estimates across replications*

p	Kurt.	Skew.	*N*	RMSEA		SRMR		CRMR	
				pop.	ADF	pop	ADF	pop.	ADF
10	3.3	-2.0	100	0.053	0.059	0.032	0.031	0.036	0.034
			200	0.053	0.051	0.032	0.030	0.036	0.033
			500	0.053	0.052	0.032	0.032	0.036	0.035
			1000	0.053	0.053	0.032	0.032	0.036	0.036
30	3.3	-2.0	100	0.028	0.063	0.028	0.031	0.029	0.032
			200	0.028	0.038	0.028	0.028	0.029	0.029
			500	0.028	0.030	0.028	0.028	0.029	0.029
			1000	0.028	0.029	0.028	0.028	0.029	0.029

Notes: *p* = # observed variables, *pop* = population value,

Table A.3. *ADF 90% and 95% coverage rates of the population RMSEA, SRMR and CRMR: 5% empirical rejection rates for a test of close fit*

p	Kurt.	Skew.	*N*	90% CI			95% CI			5% Rejection		
				RMSEA	SRMR	CRMR	RMSEA	SRMR	CRMR	RMSEA	SRMR	CRMR
10	3.3	-2.0	100	0.90	0.94	0.94	0.94	0.99	0.99	0.11	0.01	0.01
			200	0.92	0.85	0.85	0.96	0.89	0.89	0.08	0.11	0.11
			500	0.88	0.87	0.87	0.94	0.93	0.93	0.06	0.07	0.07
			1000	0.88	0.91	0.91	0.94	0.95	0.95	0.06	0.05	0.05
30	3.3	-2.0	100	0.19	0.96	0.96	0.28	1.00	1.00	0.82	0.00	0.00
			200	0.73	0.94	0.94	0.82	0.97	0.97	0.28	0.03	0.03
			500	0.88	0.93	0.93	0.93	0.97	0.97	0.10	0.03	0.03
			1000	0.88	0.93	0.93	0.94	0.97	0.97	0.08	0.03	0.03