

Supplemental Models for Example 2 in Mplus

<pre>TITLE: Model 2c: Fixed Effects of Sex (0=M,1=W) by PMC Negative Mood; DATA: FILE = Example2.csv; ! Can just list file if in same folder; VARIABLE: ! List of ALL variables in stacked data file, in order; ! Mplus does NOT know what they used to be called, though; NAMES ARE ID lGlucAM TVnm0 WPnm PMnm0 sexmW; ! List of ALL variables used in model (DEFINED variables at end); USEVARIABLES ARE lGlucAM WPnm PMnm0 sexMW PMnmsex; ! Missing data codes (here, -999); MISSING ARE ALL (-999); ! Identify level-2 ID; CLUSTER = ID; ! Predictor variables with variation ONLY at level 1; WITHIN = WPnm; ! Predictor variables with variation ONLY at level 2; BETWEEN = PMnm0 sexMW PMnmsex; DEFINE: PMnmsex = PMnm0*sexMW; ! Create observed level-2 interaction; ! 2-level model with random slopes via ML (or MLR for non-normality); ANALYSIS: TYPE IS TWOLEVEL RANDOM; ESTIMATOR IS ML; MODEL: ! Level-1, Within-Person (WP) Model; %WITHIN% lGlucAM; ! L1 R: residual variance in Y; WPmood lGlucAM ON WPnm; ! Placeholder for L1 WP mood->Y; ! Level-2, Person-Level Model; %BETWEEN% [lGlucAM] (fint); ! Fixed intercept for Y; lGlucAM; ! L2 random intercept variance in Y; [WPmood] (fWPmood); ! L1 WP fixed effect (label) of mood->Y; WPmood@0; ! L2 G: No random mood slope variance->Y; WPmood ON sexMW (fWPmsex); ! Cross-level fixed effect of WP*women->Y; lGlucAM ON PMnm0 (fBPmood); ! BP fixed effect of mood->Y; lGlucAM ON sexMW (fsex); ! BP total fixed effect of women->Y; lGlucAM ON PMnmsex (fBPmsex); ! L2 interaction of BP*women->Y; ! Request all effects in same place for easier interpretation; ! Those with only one term are already given by the model output; MODEL CONSTRAINT: ! Equivalent to ESTIMATE in SAS; ! Need to name each new created fixed effect; NEW(intmen intwom intdif WPmen WPwom WPdif BPmen BPwom BPdif Contmen Contwom Contdif); intman = fint; ! Intercept: Men (Mood=0); intwom = fint + fsex; ! Intercept: Women (Mood=0); intdif = fsex; ! Intercept: Difference (Mood=0); WPmen = fWPmood; ! WP Effect: Men; WPwom = fWPmood + fWPmsex; ! WP Effect: Women; WPdif = fWPmsex; ! WP Effect: Difference; BPmen = fBPmood; ! BP Effect: Men; BPwom = fBPmood + fBPmsex; ! BP Effect: Women; BPdif = fBPmsex; ! BP Effect Difference; Contmen = fBPmood - fWPmood; ! Context Effect: Men; Contwom = fBPmood - fWPmood + fBPmsex - fWPmsex; ! Context Effect: Women; Contdif = fBPmsex - fWPmsex; ! Context Effect: Difference;</pre>	<table><tr><th colspan="5">MODEL FIT INFORMATION</th></tr><tr><td>Number of Free Parameters</td><td></td><td></td><td></td><td>8</td></tr><tr><td>Loglikelihood</td><td></td><td></td><td></td><td></td></tr><tr><td>H0 Value</td><td></td><td></td><td></td><td>994.308</td></tr><tr><td>Information Criteria</td><td></td><td></td><td></td><td></td></tr><tr><td>Akaike (AIC)</td><td></td><td></td><td></td><td>-1972.615</td></tr><tr><td>Bayesian (BIC)</td><td></td><td></td><td></td><td>-1921.988</td></tr><tr><td>Sample-Size Adjusted BIC</td><td></td><td></td><td></td><td>-1947.408</td></tr><tr><td colspan="5">(n* = (n + 2) / 24)</td></tr><tr><th colspan="5">MODEL RESULTS</th></tr><tr><td></td><td>Estimate</td><td>S.E.</td><td>Est./S.E.</td><td>Two-Tailed P-Value</td></tr><tr><td>Within Level</td><td></td><td></td><td></td><td></td></tr><tr><td>Residual Variances</td><td></td><td></td><td></td><td></td></tr><tr><td>LGLUCAM</td><td>0.030</td><td>0.001</td><td>44.267</td><td>0.000</td></tr><tr><td>Between Level</td><td></td><td></td><td></td><td></td></tr><tr><td>WPMOOD ON</td><td></td><td></td><td></td><td></td></tr><tr><td>SEXMW</td><td>-0.035</td><td>0.008</td><td>-4.383</td><td>0.000</td></tr><tr><td>LGLUCAM ON</td><td></td><td></td><td></td><td></td></tr><tr><td>PMNM0</td><td>0.200</td><td>0.048</td><td>4.119</td><td>0.000</td></tr><tr><td>SEXMW</td><td>-0.036</td><td>0.036</td><td>-0.999</td><td>0.318</td></tr><tr><td>PMNMSEX</td><td>-0.185</td><td>0.061</td><td>-3.017</td><td>0.003</td></tr><tr><td>Intercepts</td><td></td><td></td><td></td><td></td></tr><tr><td>LGLUCAM</td><td>4.954</td><td>0.027</td><td>181.203</td><td>0.000</td></tr><tr><td>WPMOOD</td><td>0.031</td><td>0.006</td><td>5.174</td><td>0.000</td></tr><tr><td>Residual Variances</td><td></td><td></td><td></td><td></td></tr><tr><td>LGLUCAM</td><td>0.061</td><td>0.006</td><td>9.928</td><td>0.000</td></tr><tr><td>WPMOOD</td><td>0.000</td><td>0.000</td><td>999.000</td><td>999.000</td></tr><tr><td colspan="5">BOLD VALUES ARE NOT GIVEN DIRECTLY BY THE MODEL</td></tr><tr><td>New/Additional Parameters</td><td></td><td></td><td></td><td></td></tr><tr><td>INTMEN</td><td>4.954</td><td>0.027</td><td>181.203</td><td>0.000</td></tr><tr><td>INTWOM</td><td>4.918</td><td>0.024</td><td>206.412</td><td>0.000</td></tr><tr><td>INTDIF</td><td>-0.036</td><td>0.036</td><td>-0.999</td><td>0.318</td></tr><tr><td>WPMEN</td><td>0.031</td><td>0.006</td><td>5.174</td><td>0.000</td></tr><tr><td>WPWOM</td><td>-0.003</td><td>0.005</td><td>-0.648</td><td>0.517</td></tr><tr><td>WPDIF</td><td>-0.035</td><td>0.008</td><td>-4.383</td><td>0.000</td></tr><tr><td>BPMEN</td><td>0.200</td><td>0.048</td><td>4.119</td><td>0.000</td></tr><tr><td>BPWOM</td><td>0.015</td><td>0.038</td><td>0.389</td><td>0.697</td></tr><tr><td>BPDIF</td><td>-0.185</td><td>0.061</td><td>-3.017</td><td>0.003</td></tr><tr><td>CONTMEN</td><td>0.168</td><td>0.049</td><td>3.447</td><td>0.001</td></tr><tr><td>CONTWOM</td><td>0.018</td><td>0.038</td><td>0.473</td><td>0.637</td></tr><tr><td>CONTDIF</td><td>-0.151</td><td>0.062</td><td>-2.434</td><td>0.015</td></tr></table>	MODEL FIT INFORMATION					Number of Free Parameters				8	Loglikelihood					H0 Value				994.308	Information Criteria					Akaike (AIC)				-1972.615	Bayesian (BIC)				-1921.988	Sample-Size Adjusted BIC				-1947.408	(n* = (n + 2) / 24)					MODEL RESULTS						Estimate	S.E.	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TITLE: Model 3c: Fixed Effects of Sex (0=M,1=W) by GMC Negative Mood;
(DATA, DEFINE, and ANALYSIS are the same)

VARIABLE:
! List of ALL variables in stacked data file, in order;
! Mplus does NOT know what they used to be called, though;
NAMES ARE ID lGlucAM TVnm0 WPnm PMnm0 sexmW;
! List of ALL variables used in model (DEFINED variables at end);
USEVARIABLES ARE lGlucAM TVnm0 PMnm0 sexMW PMnmsex;
! Missing data codes (here, -999);
MISSING ARE ALL (-999);
! Identify level-2 ID;
CLUSTER = ID;
! Predictor variables with variation ONLY at level 1;
WITHIN = TVnm0;
! Predictor variables with variation ONLY at level 2;
BETWEEN = PMnm0 sexMW PMnmsex;

MODEL:
! Level-1, Within-Person (WP) Model;
%WITHIN%
lGlucAM; ! L1 R: residual variance in Y;
WPmood | lGlucAM ON TVnm0; ! Placeholder for L1 WP mood->Y;

! Level-2, Person-Level Model;
%BETWEEN%
[lGlucAM] (fint); ! Fixed intercept for Y;
lGlucAM; ! L2 random intercept variance in Y;
[WPmood] (fWPmood); ! L1 WP fixed effect (label) of mood->Y;
WPmood@0; ! L2 G: No random mood slope variance->Y;
WPmood ON sexMW (fWPmsex); ! Cross-level fixed effect of WP*women->Y;
lGlucAM ON PMnm0 (fconmood); ! BP contextual effect of mood->Y;
lGlucAM ON sexMW (fsex); ! BP total fixed effect of women->Y;
lGlucAM ON PMnmsex (fconsex); ! L2 interaction of contextual*women->Y;

! Request all effects in same place for easier interpretation;
! Those with only one term are already given by the model output;
MODEL CONSTRAINT: ! Equivalent to ESTIMATE in SAS;

! Need to name each new created fixed effect;
NEW(intmen intwom intdif WPmen WPwom WPdif
BPmen BPwom BPdif Contmen Contwom Contdif);
intmen = fint; ! Intercept: Men (Mood=0);
intwom = fint + fsex; ! Intercept: Women (Mood=0);
intdif = fsex; ! Intercept: Difference (Mood=0);
WPmen = fWPmood; ! WP Effect: Men;
WPwom = fWPmood + fWPmsex; ! WP Effect: Women;
WPdif = fWPmsex; ! WP Effect: Difference;
BPmen = fWPmood + fconmood; ! BP Effect: Men
BPwom = fWPmood + fconmood + fWPmsex + fconsex; ! BP Effect: Women
BPdif = fWPmsex + fconsex; ! BP Effect Difference
Contmen = fconmood; ! Contextual Effect: Men
Contwom = fconmood + fconsex; ! Contextual Effect: Women
Contdif = fconsex; ! Contextual Effect: Difference

! Now the BP contextual effects are given directly instead of the BP total effects;

MODEL FIT INFORMATION - THIS MODEL IS EQUIVALENT TO 2C

Number of Free Parameters 8

Loglikelihood
H0 Value 994.308

Information Criteria
Akaike (AIC) -1972.615
Bayesian (BIC) -1921.988
Sample-Size Adjusted BIC -1947.408
(n* = (n + 2) / 24)

MODEL RESULTS

	Estimate	S.E.	Est./S.E.	Two-Tailed P-Value
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Within Level

Residual Variances	Estimate	S.E.	Est./S.E.	Two-Tailed P-Value
LGLUCAM	0.030	0.001	44.267	0.000

Between Level

WPMOOD ON	Estimate	S.E.	Est./S.E.	Two-Tailed P-Value
SEXMW	-0.035	0.008	-4.383	0.000

BOLD VALUES ARE DIFFERENT IN THIS MODEL

LGLUCAM ON	Estimate	S.E.	Est./S.E.	Two-Tailed P-Value
PMNMO	0.169	0.049	3.450	0.001
SEXMW	-0.036	0.036	-0.999	0.318
PMNMSEX	-0.150	0.062	-2.433	0.015

Intercepts

	Estimate	S.E.	Est./S.E.	Two-Tailed P-Value
LGLUCAM	4.954	0.027	181.203	0.000
WPMOOD	0.031	0.006	5.174	0.000

Residual Variances

	Estimate	S.E.	Est./S.E.	Two-Tailed P-Value
LGLUCAM	0.061	0.006	9.928	0.000
WPMOOD	0.000	0.000	999.000	999.000

BOLD VALUES ARE NOT GIVEN DIRECTLY BY THE MODEL

New/Additional Parameters

	Estimate	S.E.	Est./S.E.	Two-Tailed P-Value
INTMEN	4.954	0.027	181.203	0.000
INTWOM	4.918	0.024	206.412	0.000
INTDIF	-0.036	0.036	-0.999	0.318
WPMEN	0.031	0.006	5.174	0.000
WPWOM	-0.003	0.005	-0.648	0.517
WPDIF	-0.035	0.008	-4.383	0.000
BPMEN	0.200	0.048	4.119	0.000
BPWOM	0.015	0.038	0.389	0.697
BPDIF	-0.185	0.061	-3.017	0.003
CONTMEN	0.168	0.049	3.447	0.001
CONTWOM	0.018	0.038	0.473	0.637
CONTDIF	-0.151	0.062	-2.434	0.015