

**Example 4a: Examining BP and WP Effects of Within-Person Fluctuation in Univariate MLM**  
*(complete data, syntax, and output available electronically for STATA, R, and SAS for all models and for two models in Mplus; SPSS is also available from my 2018 OSU Workshop [on this page](#))*

These data were simulated loosely based on real data reported in the citation below:

Skaff, M., Mullan J., Fisher, L., Almeida, D., **Hoffman, L.**, Masharani, U., & Mohr, D. (2009). [Daily negative mood affects fasting glucose in Type 2 Diabetes](#). *Health Psychology*, 28(3), 265-272. PMC2810194.

This daily diary study followed persons with Type II diabetes for 21 consecutive days to examine within-person relationships between mood and morning glucose (an index of how well-controlled the diabetes is). Here we will use univariate multilevel models to examine between-person and within-person relationships between daily negative mood and glucose the next morning (which was log-transformed given skewness) and how these relationships are moderated by sex. All models were estimated using REML, which means the variance components and fixed effect standard errors will differ in Mplus (which uses ML instead). No time effects were detected in the original data, and so “time” is not included as a predictor in these models. Likewise, no residual covariance was detected in the original data. However, I’ve included SAS and STATA code to explicitly specify the R matrix as diagonal (constant residual variance, no residual covariance) as a reminder that R matrices should be evaluated explicitly (although it can’t be done in R LMER, it can using R LME).

**STATA Data Import and Manipulation:**

```
// Import Example4a long data and create centered predictors for analysis
clear // clear memory in case a dataset is already open
import excel "AdvLong_Example4a.xlsx", firstrow case(preserve) clear

// Sort by ID, make a person mean for mood by averaging across rows for same ID
sort ID
egen PMnegmood = mean(negmood), by(ID)
// Center level-2 person mean of negative mood (uncentered because mean=0, SD=1)
gen PMnm0 = PMnegmood - 0
label variable PMnm0 "PMnm0: Person Mean Negative Mood (0=0)"
// Make level-1 predictor to use with PERSON-MEAN-CENTERING
gen WPnm = negmood - PMnegmood
label variable WPnm "WPnm: Within-Person Negative Mood (0=PM)"
// Make level-1 predictor to use with GRAND-MEAN-CENTERING
gen TVnm0 = negmood - 0
label variable TVnm0 "TVnm0: Time-Varying Negative Mood (0=0)"

// Binary gender already exists
label variable sexMW "sexMW: Participant Sex (0=M, 1=W)"
```

**R Data Import and Manipulation (after loading packages readxl, expss, lme4, lmerTest, performance, prediction, and TeachingDemos):**

```
# Import Example4a stacked data from excel in sheet "Data"
Example4a = read_excel(paste0(filesave,filename), sheet="Example4a")
# Convert to data frame to use in analysis
Example4a = as.data.frame(Example4a)

# Make a person mean for mood by averaging across rows for same ID
# Uses function from above to add person means (to same data here)
Example4a = addUnitMeans(data=Example4a, unitVariable="ID",
  meanVariables=c("negmood"), newNames=c("PMnegmood"))

# Center level-2 person mean of negative mood (uncentered because mean=0, SD=1)
Example4a$PMnm0 = Example4a$PMnegmood-0
# Make level-1 predictor to use with PERSON-MEAN-CENTERING (0=PM)
Example4a$WPnm = Example4a$negmood-Example4a$PMnegmood
# Make level-1 predictor to use with GRAND-MEAN-CENTERING (0=0)
Example4a$TVnm0 = Example4a$negmood-0

# Binary gender already exists as sexMW
```

## PART 1: VARIANCE PARTITIONING

### Model 1a. Empty Model for LN Morning Glucose (Daily Outcome)

$$\begin{aligned} \text{Level 1: Glucose}_{ti} &= \beta_{0i} + e_{ti} \\ \text{Level 2: } \beta_{0i} &= \gamma_{00} + U_{0i} \end{aligned}$$

```
display "STATA Model 1a: Empty Model for Daily Glucose Outcome"
mixed lglucAM , || ID: , ///
      reml residuals(independent,t(day)) dfmethod(satterthwaite) dftable(pvalue) nolog
display "-2LL = " e(11)*-2 // Print -2LL for model
estat icc // Intraclass correlation
```

```
print("R Model 1a: Empty Model for Daily Glucose Outcome")
Empty = lmer(data=Example4a, REML=TRUE, formula=lglucAM~1+(1|ID))
print("Show results using Satterthwaite DDF including -2LL as deviance")
llikAIC(Empty, chkREML=FALSE); summary(Empty, ddf="Satterthwaite")
```

```
$AICtab
      AIC      BIC    logLik  deviance  df.resid
-1929.27687 -1910.29152  967.63844 -1935.27687  4137.00000 → deviance = -2LL
```

```
Random effects:
  Groups   Name      Variance Std.Dev.
  ID       (Intercept) 0.066873 0.25860
  Residual                    0.030285 0.17403
```

```
print("Show intraclass correlation and its LRT");
icc(Empty); ranova(Empty)
```

ICC for the glucose outcome:  $ICC = \frac{.067}{.067 + .030} = .688$   
 This LRT tells us that the random intercept variance is significantly greater than 0, and thus so is the ICC.

```
# Intraclass Correlation Coefficient
  Adjusted ICC: 0.688
  Unadjusted ICC: 0.688
```

```
      npar    logLik      AIC      LRT Df Pr(>Chisq)
<none>    3    967.638 -1929.28
(1 | ID)   2 -1045.731 2095.46 4026.74  1 < 2.22e-16
```

### Model 1b. Empty Model for Negative Mood (Daily Predictor)

$$\begin{aligned} \text{Level 1: Mood}_{ti} &= \beta_{0i} + e_{ti} \\ \text{Level 2: } \beta_{0i} &= \gamma_{00} + U_{0i} \end{aligned}$$

```
display "STATA Model 1b: Empty Model for Daily Negative Mood Predictor"
mixed negmood , || ID: , ///
      reml residuals(independent,t(day)) dfmethod(satterthwaite) dftable(pvalue) nolog
display "-2LL = " e(11)*-2 // Print -2LL for model
estat icc // Intraclass correlation
```

```
print("R Model 1b: Empty Model for Daily Negative Mood Predictor")
EmptyMood = lmer(data=Example4a, REML=TRUE, formula=negmood~1+(1|ID))
print("Show results using Satterthwaite DDF including -2LL as deviance")
llikAIC(EmptyMood, chkREML=FALSE); summary(EmptyMood, ddf="Satterthwaite")
```

```
Random effects:
  Groups   Name      Variance Std.Dev.
  ID       (Intercept) 0.33726  0.58074
  Residual                    0.52582  0.72514
```

```
print("Show intraclass correlation and its LRT");
icc(EmptyMood); ranova(EmptyMood)
```

ICC for the mood predictor:  $ICC = \frac{.337}{.337 + .526} = .391$   
 This LRT tells us that the random intercept variance is significantly greater than 0, and thus so is the ICC.

```
  Adjusted ICC: 0.391
  Unadjusted ICC: 0.391
```

```
      npar    logLik      AIC      LRT Df Pr(>Chisq)
<none>    3 -4817.45  9640.9
(1 | ID)   2 -5568.71 11141.4 1502.53  1 < 2.22e-16
```

## PART 2: PERSON-MEAN-CENTERING OF NEGATIVE MOOD TO PREDICT GLUCOSE

### Model 2a. Fixed Effects of Negative Mood using Person-Mean-Centering (PMC)

$$\text{Level 1: Glucose}_{i_i} = \beta_{0i} + \beta_{1i} (\text{Mood}_{i_i} - \overline{\text{Mood}_i}) + e_{i_i}$$

$$\text{Level 2: Intercept: } \beta_{0i} = \gamma_{00} + \gamma_{01} (\overline{\text{Mood}_i} - 0) + U_{0i}$$

$$\text{Within-Person Mood: } \beta_{1i} = \gamma_{10}$$

```
display "STATA Model 2a: Fixed Effects of Negative Mood using Person-MC"
mixed lglucAM c.WPnm c.PMnm0, || ID: , ///
    reml residuals(independent,t(day)) dfmethod(satterthwaite) dftable(pvalue) nolog
display "-2LL = " e(11)*-2 // Print -2LL for model
estimates store FixWP // Save LL for LRT
test (c.WPnm=0)(c.PMnm0=0), small // F-test of 2 Mood Slopes
lincom c.WPnm*1, small // L1 Within-Person Mood Effect
lincom c.PMnm0*1, small // L2 Between-Person Mood Effect
lincom c.WPnm*-1 + c.PMnm0*1, small // L2 Contextual Mood Effect
predict predmoodP // Save fixed-effect predicted outcomes
corr lglucAM predmoodP // Get total r to make R2
display r(rho)^2 // Print total R2 relative to empty model

print("R Model 2a: Fixed Effects of Negative Mood using Person-MC")
FixWP = lmer(data=Example4a, REML=TRUE, formula=lglucAM~1+WPnm+PMnm0+(1|ID))
print("Show results using Satterthwaite DDF including -2LL as deviance")
llikAIC(FixWP, chkREML=FALSE); summary(FixWP, ddf="Satterthwaite")
```

```
$AICtab
      AIC      BIC      logLik      deviance      df.resid
-1925.17391 -1893.53165  967.58695 -1935.17391  4135.00000
```

```
Random effects:
Groups   Name      Variance Std.Dev.
ID       (Intercept)  0.065207 0.25536
Residual                0.030229 0.17387
```

```
Fixed effects:
              Estimate      Std. Error      df      t value      Pr(>|t|)
(Intercept)  4.9308575    0.0185753  204.9999489  265.4519 < 2.2e-16
WPnm         0.0110122    0.0038232 3932.0000166   2.8803  0.003994
PMnm0        0.0740295    0.0298473  204.9999523   2.4803  0.013934
```

Interpret each effect of negative mood:

```
print("F-Test for 2 Mood Slopes")
contestMD(FixWP, ddf="Satterthwaite", L=rbind(c(0,1,0),c(0,0,1)))
      Sum Sq   Mean Sq NumDF   DenDF   F value   Pr(>F)
1  0.43675061  0.2183753     2 388.05847  7.2240231 0.00083107583

print("L1 Within-Person Mood Effect"); contest1D(FixWP, L=c(0, 1,0))
print("L2 Between-Person Mood Effect"); contest1D(FixWP, L=c(0, 0,1))
print("L2 Contextual Mood Effect");    contest1D(FixWP, L=c(0,-1,1))
```

Estimates (from SAS output)

Label	Estimate	Standard Error	DF	t Value	Pr >  t
L1 Within-Person Mood Effect	0.01101	0.003823	3932	2.88	0.0040
L2 Between-Person Mood Effect	0.07403	0.02985	205	2.48	0.0139
L2 Contextual Mood Effect	0.06302	0.03009	212	2.09	0.0374

```
# Save predicted outcomes to compute total-R2
Example4a$PredMoodP = predict(FixWP, re.form=NA)
rFixWP = cor.test(Example4a$PredMoodP, Example4a$lglucAM, method="pearson")
print("Total R2"); rFixWP$estimate^2
0.021103143
```

<i>Proportions of variance from empty model:</i>		0.31170	0.68830		
<b>Pseudo-R2 for Each Model</b>		<b>Residual Variance</b>	<b>Random Intercept Variance</b>		
				<b>Residual Variance Pseudo-R2</b>	<b>Random Intercept Pseudo-R2</b>
1a. Empty		0.03029	0.06687		
2a. Add WPnm, PMnm0		0.03023	0.06521		
<b>Total Mood R2 relative to 1a. Empty</b>				<b>0.002</b>	<b>0.025</b>

Which pile of variance did each new fixed effect explain?

### Model 2b. Random Effect of WP Negative Mood under PMC

$$\text{Level 1: Glucose}_{i_i} = \beta_{0i} + \beta_{1i} (\text{Mood}_{i_i} - \overline{\text{Mood}}_i) + e_{i_i}$$

$$\text{Level 2: Intercept: } \beta_{0i} = \gamma_{00} + \gamma_{01} (\overline{\text{Mood}}_i - 0) + U_{0i}$$

$$\text{Within-Person Mood: } \beta_{1i} = \gamma_{10} + U_{1i}$$

```
display "STATA Model 2b: Random Effect of WP Negative Mood using Person-MC"
mixed lglucAM c.WPnm c.PMnm0, || ID: WPnm, covariance(un) ///
    reml residuals(independent,t(day)) dfmethod(satterthwaite) dftable(pvalue) nolog
display "-2LL = " e(11)*-2 // Print -2LL for model
estat recovariance, relevel(ID) correlation // GCORR matrix
estimates store RandWP // Save LL for LRT
lrtest RandWP FixWP // LRT against fixed WPnm model

print("R Model 2b: Random Effect of WP Negative Mood using Person-MC")
RandWP = lmer(data=Example4a, REML=TRUE, formula=lglucAM~1+WPnm+PMnm0+(1+WPnm|ID))
print("Show results using Satterthwaite DDF including -2LL as deviance");
llikAIC(RandWP, chkREML=FALSE); summary(RandWP, ddf="Satterthwaite")
```

```
$AICtab
      AIC      BIC      logLik      deviance      df.resid
-1924.40332 -1880.10417  969.20166 -1938.40332  4133.00000
```

```
Random effects:
Groups      Name      Variance      Std.Dev.      Corr
ID          (Intercept)  0.06522214  0.255386
           WPnm      0.00053553  0.023142  -0.035
Residual                    0.02994736  0.173053
```

```
Fixed effects:
      Estimate      Std. Error      df      t value      Pr(>|t|)
(Intercept)  4.9308732    0.0185754  204.9996984  265.4522 < 2.2e-16
WPnm         0.0110816  0.0041575  201.4184259   2.6655  0.008312
PMnm0        0.0739314  0.0298448  204.9933709   2.4772  0.014051
```

Note the change in DDF and SE for the now-random WPnm effect.

```
print("LRT against fixed effect model"); ranova(RandWP)

      npar      logLik      AIC      LRT      Df      Pr(>Chisq)
<none>          7  969.202 -1924.40
WPnm in (1 + WPnm | ID)  5  967.587 -1925.17  3.22941  2      0.19895
```

Is this a better model than the fixed effects person-MC model (2a)? What does this result mean?

**Model 2c. Adding Moderation by Sex (0=M, 1=W) for Each Mood Effect under PMC**

$$\text{Level 1: Glucose}_{i_i} = \beta_{0i} + \beta_{1i} (\text{Mood}_{i_i} - \overline{\text{Mood}_i}) + e_{i_i}$$

$$\text{Level 2: Intercept: } \beta_{0i} = \gamma_{00} + \gamma_{01} (\overline{\text{Mood}_i} - 0) + \gamma_{02} (\text{Woman}_i) + \gamma_{03} (\overline{\text{Mood}_i} - 0) (\text{Woman}_i) + U_{0i}$$

$$\text{Within-Person Mood: } \beta_{1i} = \gamma_{10} + \gamma_{12} (\text{Woman}_i)$$

```

display "STATA Model 2c: Fixed Effects of Sex (0=M, 1=W) by Person-MC Negative Mood"
mixed lglucAM c.WPnm c.PMnm0 c.sexMW c.WPnm#c.sexMW c.PMnm0#c.sexMW, || ID: , ///
    reml residuals(independent,t(day)) dfmethod(satterthwaite) dftable(pvalue) nolog
display "-2LL = " e(11)*-2 // Print -2LL for model
test (c.sexMW=0) (c.WPnm#c.sexMW=0) (c.PMnm0#c.sexMW=0), small // F-test of 3 Sex Slopes
lincom _cons*1 + c.sexMW*0, small // Intercept: Men (at mood=0)
lincom _cons*1 + c.sexMW*1, small // Intercept: Women (at mood=0)
lincom c.sexMW*1, small // Intercept: Women Diff (at mood=0)
lincom c.WPnm*1 + c.WPnm#c.sexMW*0, small // L1 Within-Person Mood Effect: Men
lincom c.WPnm*1 + c.WPnm#c.sexMW*1, small // L1 Within-Person Mood Effect: Women
lincom c.WPnm#c.sexMW*1, small // L1 Within-Person Mood Effect: Women diff
lincom c.PMnm0*1 + c.PMnm0#c.sexMW*0, small // L2 Between-Person Mood Effect: Men
lincom c.PMnm0*1 + c.PMnm0#c.sexMW*1, small // L2 Between-Person Mood Effect: Women
lincom c.PMnm0#c.sexMW*1, small // L2 Between-Person Mood Effect: Women Diff
lincom c.WPnm*-1 + c.WPnm#c.sexMW*0 + c.PMnm0*1 + c.PMnm0#c.sexMW*0, small // L2 Context Effect: Men
lincom c.WPnm*-1 + c.WPnm#c.sexMW*-1 + c.PMnm0*1 + c.PMnm0#c.sexMW*1, small // L2 Context Effect: Women
lincom c.WPnm#c.sexMW*-1 + c.PMnm0#c.sexMW*1, small // L2 Context: Women Diff
margins, at(c.WPnm=(-1 0 1) c.PMnm0=(-1 1) c.sexMW=(0 1)) vsquish // Create predicted values
marginsplot, noci xdimension(WPnm) name(predicted_meansP, replace) // Plot predicted values, no CI
graph export "STATA Sex Moderation Plot WPnm.png", replace
predict predsexP // Save fixed-effect predicted outcomes
corr lglucAM predsexP // Get total r to make R2
display r(rho)^2 // Print total R2 relative to empty model

```

```

print("R Model 2c: Fixed Effects of Sex (0=M, 1=W) by Person-MC Negative Mood")
SexWP = lmer(data=Example4a, REML=TRUE,
    formula=lglucAM~1+WPnm+PMnm0+sexMW +WPnm:sexMW +PMnm0:sexMW +(1|ID))
print("Show results using Satterthwaite DDF including -2LL as deviance")
llikAIC(SexWP, chkREML=FALSE); summary(SexWP, ddf="Satterthwaite")

```

```

$AICtab
      AIC      BIC    logLik  deviance  df.resid
-1932.81398 -1882.18637  974.40699 -1948.81398  4132.00000

```

```

Random effects:
 Groups Name Variance Std.Dev.
 ID      (Intercept) 0.062562 0.25012
 Residual              0.030085 0.17345

```

```

Fixed effects:
      Estimate Std. Error   df t value Pr(>|t|)
(Intercept)  4.9557502  0.0277060 202.9999856 178.8693 < 2.2e-16
WPnm         0.0313154  0.0059415 3931.0000067  5.2706 0.0000001433
PMnm0        0.1775457  0.0465523 202.9999815  3.8139 0.0001815
sexMW        -0.0377633  0.0368045 202.9999834 -1.0261 0.3060883
WPnm:sexMW   -0.0345345  0.0077489 3931.0000068 -4.4567 0.0000085550
PMnm0:sexMW  -0.1650701  0.0599648 202.9999813 -2.7528 0.0064447

```

Interpret the new effects of sexMW:

```

print("F-Test for 3 Sex Slopes")
contestMD(SexWP, ddf="Satterthwaite",
    L=rbind(c(0,0,0,1,0,0),c(0,0,0,0,1,0),c(0,0,0,0,0,1)))
      Sum Sq Mean Sq NumDF DenDF F value Pr(>F)
1 0.91306215 0.30435405 3 295.98025 10.116565 0.0000023044749

```

```

print("Intercept: Men (at mood=0)");          contest1D(SexWP, L=c(1, 0,0,0, 0,0))
print("Intercept: Women (at mood=0)");        contest1D(SexWP, L=c(1, 0,0,1, 0,0))
print("Intercept: Women Diff (at mood=0)");   contest1D(SexWP, L=c(0, 0,0,1, 0,0))

print("L1 Within-Person Mood Effect: Men");   contest1D(SexWP, L=c(0, 1,0,0, 0,0))
print("L1 Within-Person Mood Effect: Women"); contest1D(SexWP, L=c(0, 1,0,0, 1,0))
print("L1 Within-Person Mood Effect: Women Diff"); contest1D(SexWP, L=c(0, 0,0,0, 1,0))

print("L2 Between-Person Mood Effect: Men");  contest1D(SexWP, L=c(0, 0,1,0, 0,0))
print("L2 Between-Person Mood Effect: Women"); contest1D(SexWP, L=c(0, 0,1,0, 0,1))
print("L2 Between-Person Mood Effect: Women Diff"); contest1D(SexWP, L=c(0, 0,0,0, 0,1))

print("L2 Contextual Mood Effect: Men");      contest1D(SexWP, L=c(0,-1,1,0, 0,0))
print("L2 Contextual Mood Effect: Women");    contest1D(SexWP, L=c(0,-1,1,0,-1,1))
print("L2 Contextual Mood Effect: Women Diff"); contest1D(SexWP, L=c(0, 0,0,0,-1,1))

```

Estimates (from SAS output)					
Label	Estimate	Standard Error	DF	t Value	Pr >  t
Intercept: Men (at mood=0)	4.9558	0.02771	203	178.87	<.0001
Intercept: Women (at mood=0)	4.9180	0.02423	203	203.00	<.0001
Intercept: Women Diff (at mood=0)	-0.03776	0.03680	203	-1.03	0.3061
L1 Within-Person Effect: Men	0.03132	0.005941	3931	5.27	<.0001
L1 Within-Person Effect: Women	-0.00322	0.004974	3931	-0.65	0.5176
L1 Within-Person Effect: Women Diff	-0.03453	0.007749	3931	-4.46	<.0001
L2 Between-Person Effect: Men	0.1775	0.04655	203	3.81	0.0002
L2 Between-Person Effect: Women	0.01248	0.03780	203	0.33	0.7416
L2 Between-Person Effect: Women Diff	-0.1651	0.05996	203	-2.75	0.0064
L2 Contextual Effect: Men	0.1462	0.04693	210	3.12	0.0021
L2 Contextual Effect: Women	0.01570	0.03812	210	0.41	0.6809
L2 Contextual Effect: Women Diff	-0.1305	0.06046	210	-2.16	0.0320

Which of these estimated effects were already given to us in the model?

Which of these estimated effects were NOT already given to us in the model?

```

# Save predicted outcomes to compute total-R2
Example4a$PredSexP = predict(SexWP, re.form=NA)
rSexWP = cor.test(Example4a$PredSexP, Example4a$lglucAM, method="pearson")
print("Total R2"); rSexWP$estimate^2
0.056115636

print("Change in Total R2"); rSexWP$estimate^2-rFixWP$estimate^2
0.035012493

```

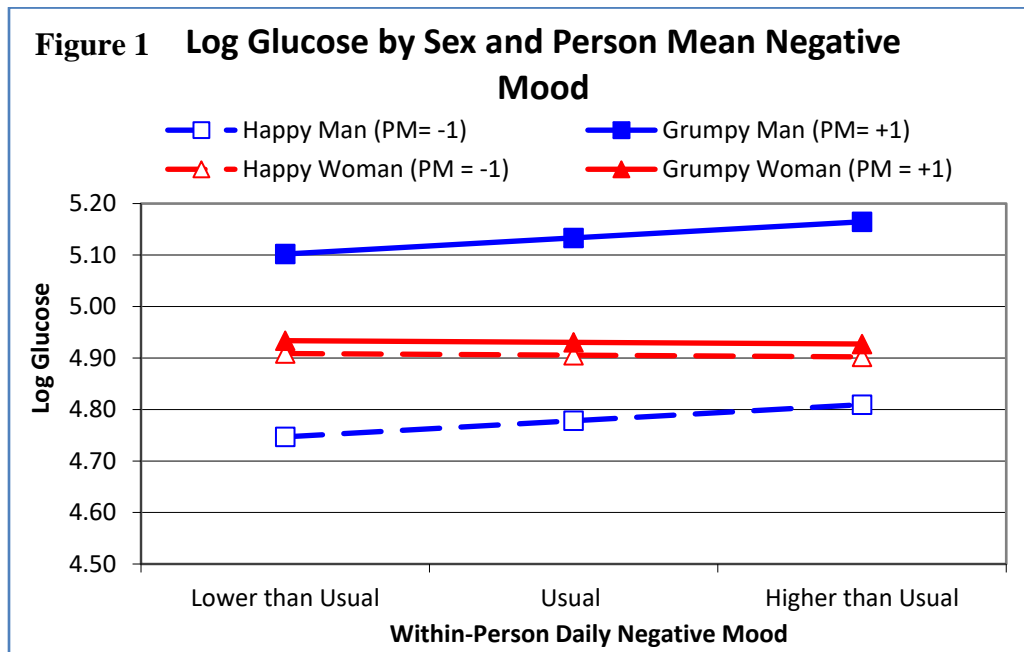
Pseudo-R2 for Each Model	Residual Variance	Random Intercept Variance	Residual Variance Pseudo-R2	Random Intercept Pseudo-R2
2a. Add WPnm, PMnm0	0.03023	0.06521		
2c. Add sex, sex*WPnm, sex*PMnm0	0.03008	0.06256		
<b>Total sex R2 relative to 2a. Mood</b>			<b>0.005</b>	<b>0.041</b>
<b>Total R2 relative to 1a. Empty</b>			<b>0.007</b>	<b>0.064</b>

Which pile of variance did each new fixed effect explain?

```

print("Predicted Outcomes for Men")
PredMenP = summary(prediction(model=SexWP, type="response",
  at=list(WPnm=seq(-1,1,by=1), PMnm0=seq(-1,1,by=2), sexMW=0))); PredMenP
print("Predicted Outcomes for Women")
PredWomenP = summary(prediction(model=SexWP, type="response",
  at=list(WPnm=seq(-1,1,by=1), PMnm0=seq(-1,1,by=2), sexMW=1))); PredWomenP

```



### Model 2c. in Mplus M-SEM using ML Estimation Instead of REML (and no Denominator DF):

```

TITLE: Model 2c: Fixed Effects of Sex (0=M,1=W) by Person-MC Negative Mood
DATA: FILE = AdvLong_Example4a.csv; ! Data 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 = ID lGlucAM TVnm0 WPnm PMnm0 sexMW;
! List of ALL variables used in model (DEFINED variables at end)
  USEVARIABLES = lGlucAM WPnm PMnm0 sexMW PMnmsex;
! Missing data codes (here, -999)
  MISSING = 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

ANALYSIS:   TYPE = TWOLEVEL RANDOM;      ! 2-level model with random slopes
                ESTIMATOR = ML;             ! Can also use MLR for non-normality

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); ! L2 BP fixed effect of mood->Y
lGlucAM ON sexMW (fsex); ! L2 BP 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: ! Linear combinations of fixed effectS
! Need to name each new created linear combination
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; ! L1 WP Effect: Men
WPwom = fWPmood + fWPmsex; ! L1 WP Effect: Women
WPdif = fWPmsex; ! L1 WP Effect: Difference
BPmen = fBPmood; ! L2 BP Effect: Men
BPwom = fBPmood + fBPmsex; ! L2 BP Effect: Women
BPDif = fBPmsex; ! L2 BP Effect Women Diff
Contmen = fBPmood - fWPmood; ! L2 Contextual Effect: Men
Contwom = fBPmood - fWPmood + fBPmsex - fWPmsex; ! L2 Contextual Effect: Women
Contdif = fBPmsex - fWPmsex; ! L2 Contextual Effect: Women Diff

Number of Free Parameters 8
Loglikelihood
      H0 Value 993.344 → Using ML, so not same as REML in STATA and R

Information Criteria
      Akaike (AIC) -1970.689
      Bayesian (BIC) -1920.061
      Sample-Size Adjusted BIC -1945.482
      (n* = (n + 2) / 24)

Estimate S.E. Est./S.E. Two-Tailed P-Value
Within Level
Residual Variances
      LGLUCAM 0.030 0.001 44.267 0.000
Between Level
      WPMOOD ON
      SEXMW -0.035 0.008 -4.393 0.000
      LGLUCAM ON
      PMNM0 0.178 0.046 3.851 0.000
      SEXMW -0.038 0.036 -1.036 0.300
      PMNMSEX -0.165 0.059 -2.780 0.005
Intercepts
      LGLUCAM 4.956 0.027 180.623 0.000
      WPMOOD 0.031 0.006 5.192 0.000
Residual Variances
      LGLUCAM 0.061 0.006 9.930 0.000
      WPMOOD 0.000 0.000 999.000 999.000
New/Additional Parameters
      INTMEN 4.956 0.027 180.623 0.000
      INTWOM 4.918 0.024 204.986 0.000
      INTDIF -0.038 0.036 -1.036 0.300
      WPMEN 0.031 0.006 5.192 0.000
      WPWOM -0.003 0.005 -0.642 0.521
      WPDIF -0.035 0.008 -4.393 0.000
      BPMEN 0.178 0.046 3.851 0.000
      BPWOM 0.012 0.037 0.333 0.739
      BPDIF -0.165 0.059 -2.780 0.005
      CONTMEN 0.146 0.046 3.144 0.002
      CONTWOM 0.016 0.038 0.416 0.677
      CONTDIF -0.130 0.060 -2.178 0.029

```



### PART 3: GRAND-MEAN-CENTERING OF NEGATIVE MOOD TO PREDICT GLUCOSE

#### Model 3. Predicting Glucose from Time-Varying Negative Mood only (GMC):

Level 1:  $Glucose_{it} = \beta_{0i} + \beta_{1i} (Mood_{it} - 0) + e_{it}$

Level 2: Intercept:  $\beta_{0i} = \gamma_{00} + U_{0i}$

Time-Varying Mood:  $\beta_{1i} = \gamma_{10}$

```
display "STATA Smushed Model 3: Fixed Effect of TV Negative Mood only using Grand-MC"
mixed lglucAM c.TVnm0, || ID: , ///
      reml residuals(independent,t(day)) dfmethod(satterthwaite) dftable(pvalue) nolog
display "-2LL = " e(11)*-2      // Print -2LL for model
```

```
print("R Smushed Model 3: Fixed Effect of Negative Mood only using Grand-MC")
Smush = lmer(data=Example4a, REML=TRUE, formula=lglucAM~1+TVnm0+(1|ID))
print("Show results using Satterthwaite DDF including -2LL as deviance")
llikAIC(Smush, chkREML=FALSE); summary(Smush, ddf="Satterthwaite")
```

```
$AICtab
      AIC          BIC      logLik   deviance   df.resid
-1927.98402 -1902.67021   967.99201 -1935.98402  4136.00000
```

```
Random effects:
  Groups   Name      Variance Std.Dev.
  ID       (Intercept) 0.066286 0.25746
  Residual                   0.030229 0.17387
```

```
Fixed effects:
              Estimate   Std. Error   df   t value   Pr(>|t|)
(Intercept)   4.9407639    0.0181078 206.3190593 272.8524 < 2.2e-16
TVnm0         0.0120135    0.0037928 4039.8545313  3.1675  0.001549
```

Btw, the L1 within slope was 0.01101 instead.

What does the level-1 effect of TVnm0 represent in this model?

<i>Proportions of variance from empty model:</i>		0.31170	0.68830			
<b>Pseudo-R2 for Each Model</b>		<b>Residual Variance</b>	<b>Random Intercept Variance</b>		<b>Residual Variance Pseudo-R2</b>	<b>Random Intercept Pseudo-R2</b>
1a. Empty		0.03029	0.06687			
3 . With Tvmood only		0.03023	0.06629			
<b>Total Mood R2 relative to 1a. Empty</b>					<b>0.002</b>	<b>0.009</b>

How do these pseudo-R<sup>2</sup> values tell us that the level-1 effect of TVnm0 is smushed?

#### Model 3a. Fixed Effects of Negative Mood using Grand-Mean-Centering (GMC)

Level 1:  $Glucose_{it} = \beta_{0i} + \beta_{1i} (Mood_{it} - 0) + e_{it}$

Level 2: Intercept:  $\beta_{0i} = \gamma_{00} + \gamma_{01} (\overline{Mood_i} - 0) + U_{0i}$

Time-Varying Mood:  $\beta_{1i} = \gamma_{10}$

```
display "STATA Model 3a: Fixed Effects of Negative Mood using GMC"
mixed lglucAM c.TVnm0 c.PMnm0, || ID: , ///
      reml residuals(independent,t(day)) dfmethod(satterthwaite) dftable(pvalue) nolog
display "-2LL = " e(11)*-2      // Print -2LL for model
estimates store FixTV          // Save LL for LRT
test (c.TVnm0=0) (c.PMnm0=0), small // F-test of 2 Mood Slopes
lincom c.TVnm0*1, small        // L1 Within-Person Mood Effect
lincom c.TVnm0*1 + c.PMnm0*1, small // L2 Between-Person Mood Effect
lincom c.PMnm0*1, small        // L2 Contextual Mood Effect
```

```

predict predmoodG      // Save fixed-effect predicted outcomes
corr lglucAM predmoodG // Get total r to make R2
  display r(rho)^2     // Print total R2 relative to empty model

print("R Model 3a: Fixed Effects of Negative Mood using Person-MC")
FixTV = lmer(data=Example4a, REML=TRUE, formula=lglucAM~1+TVnm0+PMnm0+(1|ID))
print("Show results using Satterthwaite DDF including -2LL as deviance");
llikAIC(FixTV, chkREML=FALSE); summary(FixTV, ddf="Satterthwaite")

```

```

$AICtab
      AIC      BIC      logLik      deviance      df.resid
-1925.17391 -1893.53165  967.58695 -1935.17391  4135.00000

```

```

Random effects:
 Groups      Name      Variance Std.Dev.
 ID          (Intercept) 0.065207 0.25536
 Residual                    0.030229 0.17387
Number of obs: 4140, groups: ID, 207

```

```

Fixed effects:
      Estimate      Std. Error      df      t value      Pr(>|t|)
(Intercept)  4.9308575    0.0185753  204.9999555  265.4519 < 2.2e-16
TVnm0        0.0110122    0.0038232 3932.0000166   2.8803  0.003994
PMnm0        0.0630173    0.0300912  211.7793107   2.0942  0.037431

```

Interpret each effect of negative mood:

```

print("F-Test for 2 Mood Slopes")
contestMD(FixTV, ddf="Satterthwaite", L=rbind(c(0,1,0),c(0,0,1)))

```

```

      Sum Sq      Mean Sq NumDF      DenDF      F value      Pr(>F)
1  0.43675061  0.2183753      2  401.26713  7.2240231  0.00082757674

```

```

print("L1 Within-Person Mood Effect"); contest1D(FixTV, L=c(0,1,0))
print("L2 Between-Person Mood Effect"); contest1D(FixTV, L=c(0,1,1))
print("L2 Contextual Mood Effect");      contest1D(FixTV, L=c(0,0,1))

```

Estimates (from SAS output)					
Label	Estimate	Standard Error	DF	t Value	Pr >  t
L1 Within-Person Mood Effect	0.01101	0.003823	3932	2.88	0.0040
L2 Between-Person Mood Effect	0.07403	0.02985	205	2.48	0.0139
L2 Contextual Mood Effect	0.06302	0.03009	212	2.09	0.0374

```

# Save predicted outcomes to compute total-R2
Example4a$PredMoodG = predict(FixTV, re.form=NA)
rFixTV = cor.test(Example4a$PredMoodG, Example4a$lglucAM, method="pearson")
print("Total R2"); rFixTV$estimate^2
0.021103143

```

Pseudo-R2 for Each Model	Residual Variance	Random Intercept Variance	Residual Variance Pseudo-R2	Random Intercept Pseudo-R2
1a. Empty	0.03029	0.06687		
3 . With Tv mood only	0.03023	0.06629		
<b>Total Mood R2 relative to 1a. Empty</b>			<b>0.002</b>	<b>0.009</b>
3a. With tvnm0+PMnm0	0.03023	0.06521		
<b>R2 relative to 3 TV mood only</b>			<b>0.000</b>	<b>0.016</b>
<b>Total Mood R2 relative to 1a. empty</b>			<b>0.002</b>	<b>0.025</b>

How much variance did the new level-2 effect of PMnm0 account for?

### Model 3b. Random Effect of TV Negative Mood under GMC

Level 1:  $\text{Glucose}_{i_i} = \beta_{0i} + \beta_{1i} (\text{Mood}_{i_i} - 0) + e_{i_i}$

Level 2: Intercept:  $\beta_{0i} = \gamma_{00} + \gamma_{01} (\overline{\text{Mood}}_i - 0) + U_{0i}$

Time-Varying Mood:  $\beta_{1i} = \gamma_{10} + U_{1i}$

```
display "STATA Model 3b: Random Effect of WP Negative Mood using Grand-MC"
display "FOR COMPARISON WITH MODEL 2B ONLY BECAUSE RANDOM SLOPE IS SMUSHED"
mixed lglucAM c.TVnm0 c.PMnm0, || ID: TVnm0, covariance(un) ///
    reml residuals(independent,t(day)) dfmethod(satterthwaite) dftable(pvalue) nolog
display "-2LL = " e(11)*-2 // Print -2LL for model
estat recovariance, relevel(ID) correlation // GCORR matrix
estimates store RandTV // Save LL for LRT
lrtest RandTV FixTV // LRT against fixed TVnm0 model

print("R Model 3b: Random Effect of TV Negative Mood using Grand-MC")
print("FOR COMPARISON WITH MODEL 2B ONLY BECAUSE RANDOM SLOPE IS SMUSHED")
RandTV = lmer(data=Example4a, REML=TRUE, formula=lglucAM~1+TVnm0+PMnm0+(1+TVnm0|ID))
print("Show results using Satterthwaite DDF including -2LL as deviance");
llikAIC(RandTV, chkREML=FALSE); summary(RandTV, ddf="Satterthwaite")
```

SAICtab

	AIC	BIC	logLik	deviance	df.resid
	-1925.1878	-1880.8886	969.5939	<b>-1939.1878</b>	4133.0000

Random effects:

Groups	Name	Variance	Std.Dev.	Corr
ID	(Intercept)	0.06485266	0.254662	
	TVnm0	<b>0.00059328</b>	<b>0.024357</b>	<b>-0.052</b>
Residual		0.02992278	0.172982	

Comparing with Random WPnm slope instead (Model 2b):				
Groups	Name	Variance	Std.Dev.	Corr
ID	(Intercept)	0.06522214	0.255386	
	<b>WPnm</b>	<b>0.00053553</b>	<b>0.023142</b>	<b>-0.035</b>
Residual		0.02994736	0.173053	

Fixed effects:

	Estimate	Std. Error	df	t value	Pr(> t )
(Intercept)	4.9309030	0.0185589	203.7379516	265.6892	< 2.2e-16
TVnm0	0.0110582	0.0041917	204.5574788	2.6381	0.008978
PMnm0	0.0636551	0.0300621	212.6333409	2.1175	0.035383

```
print("LRT against fixed effect model"); ranova(RandTV)
npar logLik AIC LRT Df Pr(>Chisq)
<none> 7 969.594 -1925.19
TVnm0 in (1 + TVnm0 | ID) 5 967.587 -1925.17 4.0139 2 0.1344
```

Note that the Person-MC and Grand-MC models no longer yield equivalent results if the level-1 effect is random because the Grand-MC random slope is smushed—it assumes equal quadratic heterogeneity of variance at both levels of mood.

### Model 3c. Adding Moderation Effects by Sex (0=M, 1=W) for Each Mood Effect under GMC

Level 1:  $\text{Glucose}_{i_i} = \beta_{0i} + \beta_{1i} (\text{Mood}_{i_i} - 0) + e_{i_i}$

Level 2: Intercept:  $\beta_{0i} = \gamma_{00} + \gamma_{01} (\overline{\text{Mood}}_i - 0) + \gamma_{02} (\text{Woman}_i) + \gamma_{03} (\overline{\text{Mood}}_i - 0)(\text{Woman}_i) + U_{0i}$

Time-Varying Mood:  $\beta_{1i} = \gamma_{10} + \gamma_{12} (\text{Woman}_i)$

```
display "STATA Model 3c: Fixed Effects of Sex (0=M, 1=W) by Grand-MC Negative Mood"
mixed lglucAM c.TVnm0 c.PMnm0 c.sexMW c.TVnm0#c.sexMW c.PMnm0#c.sexMW, || ID: , ///
    reml residuals(independent,t(day)) dfmethod(satterthwaite) dftable(pvalue) nolog
display "-2LL = " e(11)*-2 // Print -2LL for model
test (c.sexMW=0) (c.TVnm0#c.sexMW=0) (c.PMnm0#c.sexMW=0), small // F-test of 3 Sex Slopes
lincom _cons*1 + c.sexMW*0, small // Intercept: Men (at mood=0)
lincom _cons*1 + c.sexMW*1, small // Intercept: Women (at mood=0)
lincom c.sexMW*1, small // Intercept: Women Diff (at mood=0)
lincom c.TVnm0*1 + c.TVnm0#c.sexMW*0, small // L1 Within-Person Mood Effect: Men
lincom c.TVnm0*1 + c.TVnm0#c.sexMW*1, small // L1 Within-Person Mood Effect: Women
lincom c.TVnm0#c.sexMW*1, small // L1 Within-Person Mood Effect: Women Diff
```

```

lincom c.TVnm0*1 + c.TVnm0#c.sexMW*0 + c.PMnm0*1 + c.PMnm0#c.sexMW*0, small // L2 Between Effect: Men
lincom c.TVnm0*1 + c.TVnm0#c.sexMW*1 + c.PMnm0*1 + c.PMnm0#c.sexMW*1, small // L2 Between Effect: Women
lincom c.TVnm0#c.sexMW*1 + 1*c.PMnm0#c.sexMW, small // L2 Between: Women Diff
lincom c.PMnm0*1 + c.PMnm0#c.sexMW*0, small // L2 Contextual Mood Effect: Men
lincom c.PMnm0*1 + c.PMnm0#c.sexMW*1, small // L2 Contextual Mood Effect: Women
lincom c.PMnm0#c.sexMW*1, small // L2 Contextual Mood Effect: Women Diff
margins, at(c.TVnm0=(-2(1)2) c.PMnm0=(-1 1) c.sexMW=(0 1)) vsquish // Create predicted values
marginsplot, noci xdimension(TVnm0) name(predicted_meansG, replace) // Plot predicted values, no CI
graph export "STATA Sex Moderation Plot TVnm.png", replace
predict predsexG // Save fixed-effect predicted outcomes
corr lglucAM predsexG // Get total r to make R2
display r(rho)^2 // Print total R2 relative to empty model

```

```

print("R Model 3c: Fixed Effects of Sex (0=M, 1=W) by Grand-MC Negative Mood")
SexTV = lmer(data=Example4a, REML=TRUE,
            formula=lglucAM~1+TVnm0+PMnm0+sexMW +TVnm0:sexMW +PMnm0:sexMW +(1|ID))
print("Show results using Satterthwaite DDF including -2LL as deviance");
llikAIC(SexTV, chkREML=FALSE); summary(SexTV, ddf="Satterthwaite")

```

	AIC	BIC	logLik	deviance	df.resid
	-1932.81398	-1882.18637	974.40699	<b>-1948.81398</b>	4132.00000

Random effects:

Groups	Name	Variance	Std.Dev.
ID	(Intercept)	0.062562	0.25012
Residual		0.030085	0.17345

Fixed effects:

	Estimate	Std. Error	df	t value	Pr(> t )
(Intercept)	4.9557502	0.0277060	202.9999860	178.8693	< 2.2e-16
TVnm0	0.0313154	0.0059415	3931.0000070	5.2706	0.0000001433
PMnm0	0.1462303	0.0469299	209.6645343	3.1159	0.00209
sexMW	-0.0377633	0.0368045	202.9999839	-1.0261	0.30609
TVnm0:sexMW	-0.0345345	0.0077489	3931.0000069	-4.4567	0.0000085550
PMnm0:sexMW	-0.1305356	0.0604634	209.8332723	-2.1589	0.03199

Interpret the new effects of sexMW:

```

print("F-Test for 3 Sex Slopes")
contestMD(SexTV, ddf="Satterthwaite",
          L=rbind(c(0,0,0,1,0,0),c(0,0,0,0,1,0),c(0,0,0,0,0,1)))

```

	Sum Sq	Mean Sq	NumDF	DenDF	F value	Pr(>F)
	1 0.91306215	0.30435405	3	301.47588	<b>10.116565</b>	<b>0.000002277761</b>

```

print("Intercept: Men (at mood=0)"); contest1D(SexTV, L=c(1,0,0,0,0,0))
print("Intercept: Women (at mood=0)"); contest1D(SexTV, L=c(1,0,0,1,0,0))
print("Intercept: Women Diff (at mood=0)"); contest1D(SexTV, L=c(0,0,0,1,0,0))
print("L1 Within-Person Mood Effect: Men"); contest1D(SexTV, L=c(0,1,0,0,0,0))
print("L1 Within-Person Mood Effect: Women"); contest1D(SexTV, L=c(0,1,0,0,1,0))
print("L1 Within-Person Mood Effect: Women Diff"); contest1D(SexTV, L=c(0,0,0,0,1,0))
print("L2 Between-Person Mood Effect: Men"); contest1D(SexTV, L=c(0,1,1,0,0,0))
print("L2 Between-Person Mood Effect: Women"); contest1D(SexTV, L=c(0,1,1,0,1,1))
print("L2 Between-Person Mood Effect: Women Diff"); contest1D(SexTV, L=c(0,0,0,0,1,1))
print("L2 Contextual Mood Effect: Men"); contest1D(SexTV, L=c(0,0,1,0,0,0))
print("L2 Contextual Mood Effect: Women"); contest1D(SexTV, L=c(0,0,1,0,0,1))
print("L2 Contextual Mood Effect: Women Diff"); contest1D(SexTV, L=c(0,0,0,0,0,1))

```

Estimates (from SAS output)

Label	Estimate	Standard Error	DF	t Value	Pr >  t
Intercept: Men (at mood=0)	4.9558	0.02771	203	178.87	<.0001
Intercept: Women (at mood=0)	4.9180	0.02423	203	203.00	<.0001
Intercept: Women Diff (at mood=0)	-0.03776	0.03680	203	-1.03	0.3061
L1 Within-Person Effect: Men	0.03132	0.005941	3931	5.27	<.0001
L1 Within-Person Effect: Women	-0.00322	0.004974	3931	-0.65	0.5176
L1 Within-Person Effect: Women Diff	-0.03453	0.007749	3931	-4.46	<.0001

Estimates (from SAS output)					
Label	Estimate	Standard Error	DF	t Value	Pr >  t
L2 Between-Person Effect: Men	0.1775	0.04655	203	3.81	0.0002
L2 Between-Person Effect: Women	0.01248	0.03780	203	0.33	0.7416
L2 Between-Person Effect: Women Diff	-0.1651	0.05996	203	-2.75	0.0064
L2 Contextual Effect: Men	0.1462	0.04693	210	3.12	0.0021
L2 Contextual Effect: Women	0.01570	0.03812	210	0.41	0.6809
L2 Contextual Effect: Women Diff	-0.1305	0.06046	210	-2.16	0.0320

Which of these estimated effects were already given to us in the model?

Which of these estimated effects were NOT already given to us in the model?

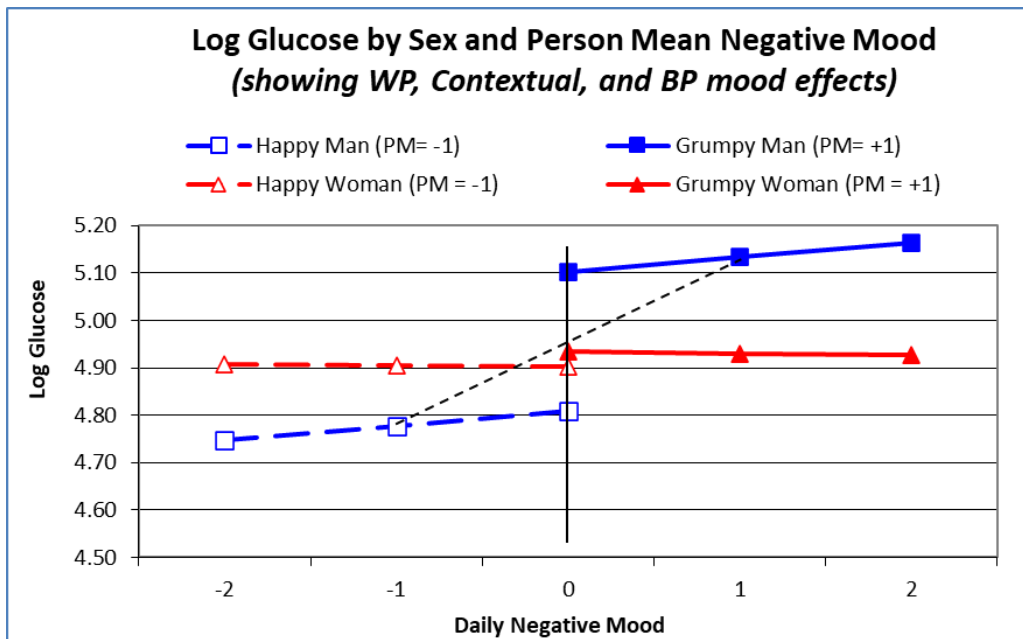
```
# Save predicted outcomes to compute total-R2
Example4a$PredSexG = predict(SexTV, re.form=NA)
rSexTV = cor.test(Example4a$PredSexG, Example4a$lglucAM, method="pearson")
print("Total R2"); rSexTV$estimate^2
0.056115636

print("Change in Total R2"); rSexTV$estimate^2-rFixTV$estimate^2
0.035012493
```

Pseudo-R2 for Each Model	Residual Variance	Random Intercept Variance	Residual Variance Pseudo-R2	Random Intercept Pseudo-R2	Total R2
3c. With sex, sex*TVnm0, sex*PMnm0	0.03008	0.06256			
<b>Total Sex R2 relative to 3a. mood</b>			<b>0.005</b>	<b>0.041</b>	<b>0.030</b>
<b>Total Sex R2 relative to 1a. empty</b>			<b>0.007</b>	<b>0.064</b>	<b>0.047</b>

Which pile of variance did each new fixed effect explain?

```
print("Predicted Outcomes for Men")
PredMenG = summary(prediction(model=SexTV, type="response",
at=list(TVnm0=seq(-2,2,by=1), PMnm0=seq(-1,1,by=2), sexMW=0))); PredMenG
print("Predicted Outcomes for Women")
PredWomenG = summary(prediction(model=SexTV, type="response",
at=list(TVnm0=seq(-2,2,by=1), PMnm0=seq(-1,1,by=2), sexMW=1))); PredWomenG
```



The solid vertical black line conveys the level-2 contextual effect, whereas the dashed black line conveys the level-2 between-person effect for men (it was ~0 in women).

**Model 3c. in Mplus M-SEM using ML Estimation Instead of REML (and no Denominator DF):**

```

TITLE: Model 3c: Fixed Effects of Sex (0=M,1=W) by Grand-MC Negative Mood
DATA: FILE = AdvLong_Example4a.csv; ! Data 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 = ID lGlucAM TVnm0 WPnm PMnm0 sexMW;
! List of ALL variables used in model (DEFINED variables at end)
  USEVARIABLES = lGlucAM WPnm PMnm0 sexMW PMnmsex;
! Missing data codes (here, -999)
  MISSING = 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;

DEFINE:      PMnmsex = PMnm0*sexMW;    ! Create observed level-2 interaction

ANALYSIS:   TYPE = TWOLEVEL RANDOM;    ! 2-level model with random slopes
                ESTIMATOR = ML;          ! Can also use MLR for non-normality

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); ! L2 Contextual fixed effect of mood->Y
  lGlucAM ON sexMW (fsex);    ! L2 BP fixed effect of women->Y
  lGlucAM ON PMnmsex (fBPmsex); ! 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: ! Linear combinations of fixed effects
! Need to name each new created linear combination
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;             ! L1 WP Effect: Men
WPwom = fWPmood + fWPmsex;    ! L1 WP Effect: Women
WPdif = fWPmsex;             ! L1 WP Effect: Difference
BPmen = fWPmood + fconmood;   ! L2 BP Effect: Men
BPwom = fWPmood + fconmood + fWPmsex + fconsex; ! L2 BP Effect: Women
BPDif = fWPmsex + fconsex;    ! L3 BP Effect: Women Diff
Contmen = fconmood;          ! L2 Contextual Effect: Men
Contwom = fconmood + fconsex; ! L2 Contextual Effect: Women
Contdif = fconsex;          ! L2 Contextual Effect: Women Diff

Number of Free Parameters      8
Loglikelihood
  H0 Value                    993.370 → Using ML, so not same as REML in STATA and R

Information Criteria
  Akaike (AIC)                 -1970.740
  Bayesian (BIC)               -1920.112
  Sample-Size Adjusted BIC     -1945.533
    (n* = (n + 2) / 24)

```

MODEL RESULTS		Estimate	S.E.	Est./S.E.	Two-Tailed P-Value
Within Level					
Residual Variances					
LGLUCAM		0.030	0.001	44.267	0.000
Between Level					
WPMOOD	ON				
SEXMW		-0.035	0.008	-4.393	0.000
LGLUCAM	ON				
PMNMO		0.147	0.046	3.151	0.002
SEXMW		-0.038	0.036	-1.034	0.301
PMNMSEX		-0.131	0.060	-2.182	0.029
Intercepts					
LGLUCAM		4.956	0.027	180.646	0.000
WPMOOD		0.031	0.006	5.191	0.000
Residual Variances					
LGLUCAM		0.061	0.006	9.924	0.000
WPMOOD		0.000	0.000	999.000	999.000
New/Additional Parameters					
INTMEN		4.956	0.027	180.646	0.000
INTWOM		4.918	0.024	205.016	0.000
INTDIF		-0.038	0.036	-1.034	0.301
WPMEN		0.031	0.006	5.191	0.000
WPWOM		-0.003	0.005	-0.643	0.520
WPDIF		-0.035	0.008	-4.393	0.000
BPMEN		0.178	0.046	3.856	0.000
BPWOM		0.013	0.037	0.336	0.736
BPDIF		-0.165	0.059	-2.782	0.005
CONTMEN		0.147	0.046	3.151	0.002
CONTWOM		0.016	0.038	0.420	0.675
CONTDIF		-0.131	0.060	-2.182	0.029

**Sample Results Section for Example 4a using REML Estimation (note that the order of the models is different than what is in this handout, so I have added model numbers in parentheses to help with the translation):**

The effects of negative mood and sex on next day's morning glucose level were examined in 207 persons with type-2 diabetes over a 20-day period. Glucose was natural log transformed (after adding 1 to each score) to improve normality. Intraclass correlations as calculated from an empty means, random intercept only model were .69 for glucose (1a) and .39 for negative mood (1b), such that 69% and 39% of the variance in each variable was due to between-person mean differences, respectively. Preliminary analyses suggested that a model for the variance for glucose with only a random intercept over time had acceptable fit, and thus all conditional (predictor) models were examined using that structure as a baseline.

The time-varying (level-1) predictor for negative mood (left uncentered, given that 0 represented average level of the measure) was first entered into the model (3). It had a significant positive slope, such that higher daily levels of negative mood were related to higher daily levels of glucose. However, the inclusion of a single parameter for the slope of negative mood presumes that its between-person and within-person effects would be equivalent. This convergence hypothesis was tested explicitly by including person mean negative mood (also left uncentered, given that 0 represented average level of the original measure) as a level-2 predictor (3a). The level-2 contextual effect of person mean negative mood was significant, indicating that after controlling for absolute level of daily negative mood, persons with higher mean negative mood had higher mean glucose. Given that the significance of the level-2 contextual effect also indicates that the between-person and within-person effects of negative mood were not equivalent, the model was re-specified to facilitate interpretation of these separate effects using person-mean-centering. Specifically, a new level-1 predictor variable was created by subtracting each person's mean from daily negative mood, while the level-2 predictor remained the person mean. In this specification using person-mean-centering, the slope of the level-2 person mean of negative mood represents the level-2 between-person effect directly and the slope of the level-1 within-person deviation of negative mood represents the level-1 within-person effect directly. Both the between- and within-person effects of negative mood were significantly positive. A random level-1 within-person slope of negative mood was tested, and was not found to be significant in either,  $-2\Delta LL (\sim 2) < 5.14, p > .05$ , indicating no significant individual differences (at level 2) in the within-person effect of negative mood (at level 1).

Three moderation effects of binary sex (coded 0 = men, 1 = women) were then entered into the person-mean-centered mood model, including a main effect of sex and interactions with the between- and within-person effects of negative mood (2c). The main effect of

sex was non-significant, indicating no sex differences in mean glucose among persons with average levels of mean negative mood on average days (i.e., when average persons were at their mean). Given that both interactions were significant, however, results for both men and women will be presented as derived from linear combinations of the model fixed effects.

Parameters are given in Table 1. As shown, the intercept of 4.95 represents the expected morning LN glucose for a man with an average level of mean negative mood on an average day (i.e., both mean and person-mean-centered negative mood at 0). Men showed significant between- and within-person effects of negative mood, such that for every unit higher in mean negative mood, mean glucose was expected to be 0.178 higher (i.e., the level-2 between-person effect), and for every unit higher in negative mood on a given day relative to his own mean, glucose that next morning was expected to be 0.031 higher as well (i.e., the level-1 within-person effect). Thus, in men, being higher overall in negative mood and higher than usual in negative mood were each related to higher levels of glucose, and these effects were significantly different in magnitude (level-2 contextual effect = 0.146, SE = 0.047,  $p = .002$ ). Said differently, the level-2 contextual effect also indicates a significant incremental positive contribution of person mean negative mood on mean glucose over time after controlling for daily negative mood.

As shown in Figure 1, however, these patterns were not found in women, as indicated by the significant interactions of mood with sex at each level. Specifically, the between-person and within-person slopes of negative mood in women were 0.012 (SE = 0.038) and  $-0.003$  (SE = 0.005), respectively. Neither effect was significant nor did they differ significantly in magnitude (level-2 contextual effect = 0.016, SE = 0.038). Both effects of negative mood were significantly smaller (less positive) in women than in men (interaction terms of sex with between-person and within-person negative mood of  $-0.165$  and  $-0.035$ , respectively). Finally, the level-2 contextual effect of negative mood, or the difference between the between-person and within-person effects of negative mood, was significantly smaller for women for men ( $-0.131$ , SE = 0.060,  $p = .032$ ).

(Table 1 would have all parameter estimates from final model; see my textbook chapter 8 for examples)