Example 2: Time-Varying Predictors 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., Almeida, D., **Hoffman, L.**, Masharani, U., Mohr, D., & Fisher, L. (2009). Daily negative mood affects fasting glucose in Type 2 Diabetes. *Health Psychology, 28*(3), 265–272. PMC2810194.

This daily diary study followed 207 persons with Type II diabetes for 20 consecutive days to examine within-person relationships between mood and morning glucose (an index of how well-controlled their 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 Example2 long data and create centered predictors for analysis
clear // clear memory in case a dataset is already open
import excel "AdvLong_Example2.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)"

// Create new variable to hold number of missing cases
// Then drop cases with incomplete predictors
egen nummiss = rowmiss(lglucAM negmood PMnegmood)
drop if nummiss>0
```

R Data Import and Manipulation (after loading packages *readxl*, *lme4*, *lmerTest*, *performance*, *prediction*, and *TeachingDemos*, as well as several custom functions):

```
# Import Example2 stacked data from excel in sheet "Data"
Example2 = read_excel(paste0(filesave,filename), sheet="Example2")
# Convert to data frame to use in analysis
Example2 = as.data.frame(Example2)

# Sort by person and occasion (needed for correct V matrix)
Example2 = Example2[order(Example2$ID, Example2$day), ]

# 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)
Example2 = addUnitMeans(data=Example2, unitVariable="ID",
        meanVariables=c("negmood"), newNames=c("PMnegmood")
```

```
# Center level-2 person mean of negative mood (uncentered because mean=0, SD=1)
Example2$PMnm0 = Example2$PMnegmood-0
# Make level-1 predictor to use with PERSON-MEAN-CENTERING (0=PM)
Example2$WPnm = Example2$negmood-Example2$PMnegmood
# Make level-1 predictor to use with GRAND-MEAN-CENTERING (0=0)
Example2$TVnm0 = Example2$negmood-0
# Binary gender already exists as sexMW


# Filter to only cases complete on all variables to be used below
Example2 = Example2[complete.cases(Example2[ , c("lglucAM","negmood","PMnegmood")]), ]
```

PART 1: VARIANCE PARTITIONING

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

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

```
display "STATA Model 1a: Empty Model for Daily Glucose Outcome"
mixed lglucAM  , || ID: , ///
     reml residuals(independent,t(day)) dfmethod(satterthwaite) dftable(pvalue) nolog
matrix Empty = r(table)      // Save results for computations below
```

```
-----------------------------------------------------------------
     lglucAM |    Coef.   Std. Err.         DF      t    P>|t|
-------------+---------------------------------------------------
       _cons |  4.942683   .0181761      206.0   271.93   0.000
-----------------------------------------------------------------
------------------------------------------------------------------------
  Random-effects Parameters  |   Estimate  Std. Err.    [95% Conf. Interval]
-----------------------------+------------------------------------------------
ID: Identity                 |
                 var(_cons)  |   .0668727   .0067384      .054888    .0814742
-----------------------------+------------------------------------------------
              var(Residual)  |   .0302851   .0006829     .0289757    .0316537
------------------------------------------------------------------------
LR test vs. linear model: chibar2(01) = 4026.74      Prob >= chibar2 = 0.0000
```

```
display "-2LL = " e(ll)*-2    // Print -2LL for model
-2LL = -1935.2769
```

ICC1 for 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.

```
estat icc                    // Intraclass correlation
--------------------------------------------------------------------
                        Level |     ICC   Std. Err.    [95% Conf. Interval]
------------------------------+-------------------------------------------
                         ID  |  .6882893   .0221776     .6432582    .7300219
--------------------------------------------------------------------
```

```
matrix list Empty  // Show saved results (variances are saved as log of SD)

Empty[9,3]
          lglucAM:    lns1_1_1:     lnsig_e:
           _cons        _cons        _cons
     b    4.942683   -1.3524825   -1.7485494
    se    .01817613    .05038266    .01127517
     t    271.93267   -26.844202   -155.0797
pvalue    2.82e-265    9.86e-159             0
    ll    4.9068479   -1.4512307   -1.7706483
    ul    4.978518    -1.2537342   -1.7264504
    df        206            .            .
  crit    1.9715467    1.959964     1.959964
 eform         0            0            0
```

```
display "STATA Intercept Reliability = ICC2" // IntVar / (IntVar + ResVar/L1n)
display exp(Empty[1,2])^2/(exp(Empty[1,2])^2+(exp(Empty[1,3])^2/20))
.97785752
```

```
print("R Model 1a: Empty Model for Daily Glucose Outcome")
Empty = lmer(data=Example2, REML=TRUE, formula=lglucAM~1+(1|ID))
print("Show results with -2LL using Satterthwaite DDF")
llikAIC(Empty, chkREML=FALSE); summary(Empty, ddf="Satterthwaite")

print("Show ICC1 and its LRT"); icc(Empty); ranova(Empty)

print("Print variances as data frame for use below"); data.frame(VarCorr(Empty))
# ICC2 using custom function
IntRel(L1n=20, IntVar=data.frame(VarCorr(Empty))[1,4],
               ResVar=data.frame(VarCorr(Empty))[2,4])
```

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

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

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

display "STATA Intercept Reliability = ICC2" // IntVar / (IntVar + ResVar/L1n)
display exp(EmptyMood[1,2])^2/(exp(EmptyMood[1,2])^2+(exp(EmptyMood[1,3])^2/20))

print("R Model 1b: Empty Model for Daily Negative Mood Predictor")
EmptyMood = lmer(data=Example2, REML=TRUE, formula=negmood~1+(1|ID))
print("Show results with -2LL using Satterthwaite DDF")
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
```

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

```
Fixed effects:
            Estimate Std. Error         df t value  Pr(>|t|)
(Intercept) 0.159740   0.041908 205.999998  3.8117 0.0001823
```

```
print("Show ICC1 and its LRT"); icc(EmptyMood); ranova(EmptyMood)

    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

print("Print variances as data frame for use below"); data.frame(VarCorr(EmptyMood))

      grp         var1 var2       vcov       sdcor
1      ID (Intercept) <NA> 0.33725979 0.58074072
2 Residual        <NA> <NA> 0.52582404 0.72513726

# ICC2 using custom function
IntRel(L1n=20, IntVar=data.frame(VarCorr(EmptyMood))[1,4],
               ResVar=data.frame(VarCorr(EmptyMood))[2,4])
[1] 0.92768222
```

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

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

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

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

 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
matrix FixWP = r(table)            // Save results for computations below
display "-2LL = " e(ll)*-2         // Print -2LL for model
estimates store FixWP              // Save LL for LRT

// Label slopes of interest (only contextual is new)
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

// Build total-R2
predict predmoodP                  // Save fixed-effect predicted outcome
quietly corr lglucAM predmoodP     // Get total r to make R2
global R2Mood = r(rho)^2           // Save total-R2 for comparison
display "Total-R2 = " $R2Mood      // Print total-R2 relative to empty model

// Build pseudo-R2
matrix list FixWP  // Show saved results (variances are saved as log of SD)
display "Pseudo-R2 for Intercept = " 1-(exp(FixWP[1,4])^2/exp(Empty[1,2])^2)
display "Pseudo-R2 for Residual = "  1-(exp(FixWP[1,5])^2/exp(Empty[1,3])^2)

print("R Model 2a: Fixed Effects of Negative Mood using Person-MC")
FixWP = lmer(data=Example2, REML=TRUE, formula=lglucAM~1+WPnm+PMnm0+(1|ID))
print("Show results with -2LL using Satterthwaite DDF")
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    → deviance = –2LL

Random effects:
 Groups    Name        Variance Std.Dev.
 ID        (Intercept) 0.065207 0.25536   var(U_0i)
 Residual              0.030229 0.17387   var(e_ti)

Fixed effects:
               Estimate    Std. Error            df   t value   Pr(>|t|)
(Intercept)   4.9308575    0.0185753   204.9999489  265.4519   < 2.2e-16   gamma00
WPnm          0.0110122    0.0038232  3932.0000166    2.8803   0.003994    gamma10
PMnm0         0.0740295    0.0298473   204.9999523    2.4803   0.013934    gamma01
```

Interpret slope for WPnm:

Interpret slope for PMnm0:


```
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
```

```
# Label slopes of interest (only contextual is new)
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

```
# Total R2 for mood model relative to empty model using custom function
TotalR2(data=Example2, dvName="lglucAM", model1=FixWP, name1="Mood")

Total R2 for Mood
[1] 0.021103742

# Pseudo-R2 for mood model relative to empty model using custom function
PseudoR2(data=Example2, baseModel=Empty, model1=FixWP, name1="Mood")

Pseudo-R2 for Mood
        term        base     model1 pseudoR2.model1
1 (Intercept) 0.066872680 0.065206900          0.0249
2    Residual 0.030285122 0.030229043          0.0019
```

Which pile of variance did each new fixed slope explain?

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

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

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

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
matrix RandWP = r(table)          // Save results for computations below

                                        F(2,   198.38)    =        6.62
Log restricted-likelihood =  969.20177  Prob > F          =     0.0016
-----------------------------------------------------------------
    lglucAM |    Coef.   Std. Err.        DF       t    P>|t|
------------+----------------------------------------------------
       WPnm |   .0110816    .0041575      192.2    2.67   0.008   gamma10
      PMnm0 |   .0739328    .0298446      205.0    2.48   0.014   gamma01
       _cons |   4.930873    .0185752      205.0  265.45   0.000   gamma00
-----------------------------------------------------------------
```

Note the change in DDF and SE for the now-random

```
-----------------------------------------------------------------
  Random-effects Parameters |   Estimate   Std. Err.    [95% Conf. Interval]
----------------------------+------------------------------------------------
ID: Unstructured            |
              var(WPnm) |    .0005356    .0003385      .0001552    .0018486   var(U_1i)
             var(_cons) |     .065221    .0065901      .0535032     .079505   var(U_0i)
         cov(WPnm,_cons) |   -.0002092    .0010801     -.0023261    .0019077   covar(U_1i,U_0i)
----------------------------+------------------------------------------------
           var(Residual) |    .0299474    .0006918      .0286217    .0313344   var(e_ti)
-----------------------------------------------------------------
LR test vs. linear model: chi2(3) = 3957.56              Prob > chi2 = 0.0000
```

```
display "-2LL = " e(ll)*-2            // Print -2LL for model
-2LL = -1938.4035


estat recovariance, relevel(ID) correlation  // GCORR matrix

             |        WPnm       _cons
-------------+----------------------
       WPnm  |          1
      _cons  | -.0353916              1
```

> Same conclusion even if we used the more correct χ^2 distribution with a mixture of df = 2 or 1 (1 for when the random slope variance would have been negative)

```
estimates store RandWP               // Save LL for LRT
lrtest RandWP FixWP                  // LRT against fixed WPnm model

Likelihood-ratio test                              LR chi2(2)   =      3.23
(Assumption: FixWP nested in RandWP)               Prob > chi2  =    0.1989
```

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

```
matrix list RandWP  // Show saved results (variances are saved as log of SD)

RandWP[9,7]
           lglucAM:    lglucAM:    lglucAM:    lns1_1_1:   lns1_1_2:   atr1_1_1_2:   lnsig_e:
             WPnm       PMnm0       _cons       _cons       _cons       _cons        _cons
     b     .01108155  .07393275   4.9308729  -3.7660627  -1.3649873  -.03540638   -1.7541571
    se     .0041575   .02984462   .01857522   .31602235   .05052098   .18343019    .01154978
     t    2.6654385   2.4772557   265.45438  -11.917077  -27.018227  -.19302375   -151.87796
pvalue     .00834303  .01404849   4.45e-262   9.643e-33   9.03e-161   .84694037            0
    ll     .00288137   .015091     4.89425   -4.3854551  -1.4640066  -.39492295   -1.7767942
    ul     .01928174  .13277451   4.9674959  -3.1466703  -1.265968    .32411018   -1.7315199
    df    192.18533   204.99916   205.00467         .           .           .            .
  crit    1.9723844   1.9716035   1.9716032    1.959964    1.959964    1.959964     1.959964
 eform            0           0           0           0           0           0            0

display "Random Effect 95% CI for WPnm"
display "Lower = " RandWP[1,1] - 1.96*exp(RandWP[1,4])
display "Upper = " RandWP[1,1] + 1.96*exp(RandWP[1,4])
Lower = -.03427874
Upper =  .05644184


display "Random Slope Reliability"  // SlpVar/(SlpVar + ResVar/(L1n*PredVar))
quietly summarize WPnm, detail
global WPnmVar = r(Var)             // Save variance of WPnm predictor
display exp(RandWP[1,4])^2/(exp(RandWP[1,4])^2+(exp(RandWP[1,7])^2/(20*$WPnmVar)))
.15162411


print("R Model 2b: Random Effect of WP Negative Mood using Person-MC")
RandWP = lmer(data=Example2, REML=TRUE, formula=lglucAM~1+WPnm+PMnm0+(1+WPnm|ID))
print("Show results with -2LL using Satterthwaite DDF")
llikAIC(RandWP, chkREML=FALSE); summary(RandWP, ddf="Satterthwaite")
print("LRT against fixed effect model"); ranova(RandWP)

print("Print variances as data frame for use below"); data.frame(VarCorr(RandWP))

        grp          var1 var2          vcov           sdcor
1        ID  (Intercept) <NA>   0.06522205102   0.255386082
2        ID         WPnm <NA>   0.00053553376   0.023141602
3        ID  (Intercept) WPnm  -0.00020911257  -0.035382578
4  Residual        <NA> <NA>   0.02994736250   0.173053063


# Random slope 95% CI using custom function
RandCI(FixEst=fixef(RandWP)[2], RandVar=data.frame(VarCorr(RandWP))[2,4], pred="WPnm")


# Random slope reliability using custom function
SlpRel(pred="WPnm", PredVar=var(Example2$WPnm), L1n=20,
       SlpVar=data.frame(VarCorr(RandWP))[2,4], ResVar=data.frame(VarCorr(RandWP))[4,4])
```

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

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

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

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

```
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
matrix SexWP = r(table)          // Save results for computations below
display "-2LL = " e(ll)*-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

// Label slopes of interest (only those for women and contextual are new)
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 Contextual Mood Effect: Men
lincom c.WPnm*-1 + c.WPnm#c.sexMW*-1 + c.PMnm0*1 + c.PMnm0#c.sexMW*1, small  // L2 Contextual Mood Effect: Women
lincom c.WPnm#c.sexMW*-1 + c.PMnm0#c.sexMW*1, small             // L2 Contextual Mood Effect: 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

// Build total-R2
predict predsexP                   // Save fixed-effect predicted outcome
quietly corr lglucAM predsexP      // Get total r to make R2
global R2Sex = r(rho)^2            // Save total-R2 for comparison
display "Total-R2 = " $R2Sex       // Print total-R2 relative to empty model
display "Change in Total-R2 = "  $R2Sex - $R2Mood

// Build pseudo-R2
matrix list SexWP  // Show saved results (variances are saved as log of SD)
```

```
SexWP[9,8]
           lglucAM:     lglucAM:     lglucAM:     lglucAM:     lglucAM:     lglucAM:     lns1_1_1:     lnsig_e:
                                                   c.WPnm#      c.PMnm0#
                                                   c.sexMW      c.sexMW
              WPnm         PMnm0        sexMW      c.sexMW      c.sexMW       _cons        _cons        _cons
    b     .03131541    .17754458    -.037764    -.03453456    -.1650661    4.9557503   -1.3858008   -1.7518689
   se      .0059415     .0465523   .03680453     .00774889    .05996492     .027706    .05082317    .01127804
    t     5.2706278    3.8138733  -1.0260696     -4.456709   -2.7527111   178.86922   -27.267105   -155.33457
pvalue    1.433e-07      .00018148    .30607989    8.555e-06    .00644607    2.61e-225    1.04e-163            0
   ll      .01966671    .08575653  -.11033218    -.04972679   -.28330006    4.9011218   -1.4854124   -1.7739734
   ul      .04296411    .26933264   .03480417    -.01934233   -.04683214    5.0103787   -1.2861892   -1.7297643
   df          3931          203         203          3931          203          203            .            .
 crit     1.9605676    1.9717188   1.9717188    1.9605676    1.9717188    1.9717188    1.959964     1.959964
eform            0            0           0            0            0            0            0            0
```

```
display "Pseudo-R2 for Intercept = " 1-(exp(SexWP[1,7])^2/exp(Empty[1,2])^2)
display "Pseudo-R2 for Residual = "  1-(exp(SexWP[1,8])^2/exp(Empty[1,3])^2)

display "Change in Pseudo-R2 for Intercept = " ///
(1-(exp(SexWP[1,7])^2/exp(Empty[1,2])^2)) - (1-(exp(FixWP[1,4])^2/exp(Empty[1,2])^2))

display "Change in Pseudo-R2 for Residual = " ///
(1-(exp(SexWP[1,8])^2/exp(Empty[1,3])^2)) - (1-(exp(FixWP[1,5])^2/exp(Empty[1,3])^2))
```

```
print("R Model 2c: Fixed Effects of Sex (0=M, 1=W) by Person-MC Negative Mood")
SexWP = lmer(data=Example2, REML=TRUE,
            formula=lglucAM~1+WPnm+PMnm0+sexMW +WPnm:sexMW +PMnm0:sexMW +(1|ID))
print("Show results with -2LL using Satterthwaite DDF")
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   var(U_0i)
 Residual             0.030085 0.17345   var(e_ti)
```

```
Fixed effects:
              Estimate    Std. Error          df   t value      Pr(>|t|)
(Intercept)   4.9557502    0.0277060  202.9999856  178.8693    < 2.2e-16   gamma00
WPnm          0.0313154    0.0059415 3931.0000067    5.2706  0.0000001433   gamma10
PMnm0         0.1775457    0.0465523  202.9999815    3.8139     0.0001815   gamma01
sexMW        -0.0377633    0.0368045  202.9999834   -1.0261     0.3060883   gamma02
WPnm:sexMW   -0.0345345    0.0077489 3931.0000068   -4.4567  0.0000085550   gamma12
PMnm0:sexMW  -0.1650701    0.0599648  202.9999813   -2.7528     0.0064447   gamma03
```

Interpret main effect of sexMW:

Interpret interaction of WPnm*sexMW:

Interpret interaction of PMnm0*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
```

```
# Label slopes of interest (only those for women and contextual are new)

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

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?

```
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

at(WPnm) at(PMnm0) at(sexMW) Prediction SE   z  p lower upper
      -1       -1        0       4.747 NA NA NA    NA    NA
       0       -1        0       4.778 NA NA NA    NA    NA
       1       -1        0       4.810 NA NA NA    NA    NA
      -1        1        0       5.102 NA NA NA    NA    NA
       0        1        0       5.133 NA NA NA    NA    NA
       1        1        0       5.165 NA NA NA    NA    NA

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

at(WPnm) at(PMnm0) at(sexMW) Prediction SE   z  p lower upper
      -1       -1        1       4.909 NA NA NA    NA    NA
       0       -1        1       4.906 NA NA NA    NA    NA
       1       -1        1       4.902 NA NA NA    NA    NA
      -1        1        1       4.934 NA NA NA    NA    NA
       0        1        1       4.930 NA NA NA    NA    NA
       1        1        1       4.927 NA NA NA    NA    NA
```
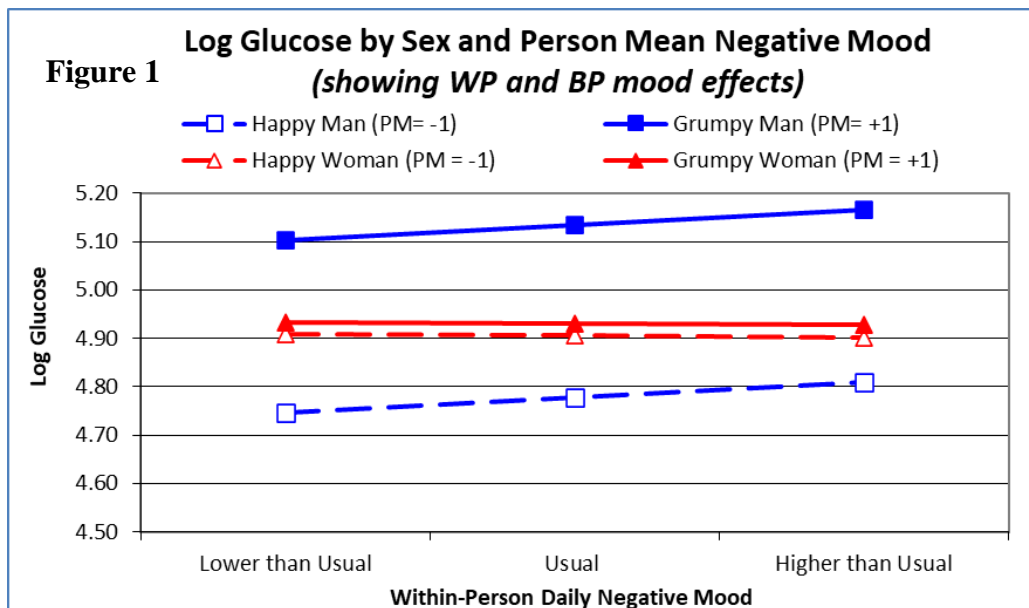

Figure 1

Log Glucose by Sex and Person Mean Negative Mood
(showing WP and BP mood effects)

```
# Total R2 for sex model relative to mood model using custom function
TotalR2(data=Example2, dvName="lglucAM", model1=FixWP, name1="Mood", model2=SexWP, name2="Sex")
```

```
Total-R2 and Change in Total-R2 for Mood vs Sex
    totalR2.1   totalR2.2    changeR2
1 0.021103742 0.056115312 0.035011571
```

```
# Pseudo-R2 for sex model relative to mood model using custom function
PseudoR2(data=Example2, baseModel=Empty, model1=FixWP, name1="Mood", model2=SexWP, name2="Sex")
```

```
Pseudo-R2 and Change in Pseudo-R2 for Mood vs Sex
          term       base      model1      model2 pseudoR2.model1 pseudoR2.model2 pseudoR2.change
1 (Intercept) 0.066872680 0.065206900 0.062561733          0.0249          0.0645          0.0396
2    Residual 0.030285122 0.030229043 0.030084723          0.0019          0.0066          0.0048
```

Which pile of variance did each new fixed effect explain?

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_Example2_Data.csv;  ! Data in same folder as input
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)


                                               Two-Tailed
                     Estimate     S.E.   Est./S.E.   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: $\text{Glucose}_{ti} = \beta_{0i} + \beta_{1i}(\text{Mood}_{ti} - 0) + e_{ti}$

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
matrix Smush = r(table)        // Save results for computations below
display "-2LL = " e(ll)*-2     // Print -2LL for model
```

```
// Build pseudo-R2
display "Pseudo-R2 for Intercept = " 1-(exp(Smush[1,3])^2/exp(Empty[1,2])^2)
display "Pseudo-R2 for Residual = "  1-(exp(Smush[1,4])^2/exp(Empty[1,3])^2)


print("R Smushed Model 3: Fixed Effect of Negative Mood only using Grand-MC")
Smush = lmer(data=Example2, 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
```

> Btw, the L1 within slope was 0.01101 instead.

```
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
```

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


```
# Pseudo-R2 for smushed model relative to empty model using custom function
PseudoR2(data=Example2, baseModel=Empty, model1=Smush, name1="Smushed Mood")
```

```
Pseudo-R2 for Smushed Mood
         term         base      model1 pseudoR2.model1
1 (Intercept) 0.066872680 0.066286499          0.0088
2    Residual 0.030285122 0.030229448          0.0018
```

How do these pseudo-R^2 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: $\text{Glucose}_{ti} = \beta_{0i} + \beta_{1i}\left(\text{Mood}_{ti} - 0\right) + e_{ti}$

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

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
matrix FixTV = r(table)                  // Save results for computations below
```

```
                                             F(2,    401.27)    =       7.22
Log restricted-likelihood =   967.58705      Prob > F           =     0.0008
-------------------------------------------------------------------
     lglucAM |     Coef.   Std. Err.           DF       t    P>|t|
-------------+-----------------------------------------------------
       TVnm0 |   .0110121   .0038232        3932.0    2.88   0.004
       PMnm0 |   .0630188   .0300913         211.8    2.09   0.037
       _cons |   4.930857   .0185753         205.0  265.45   0.000
-------------------------------------------------------------------
```

Interpret the slope of TVnm0:

Interpret the slope of PMnm0:

```
------------------------------------------------------------------------------
  Random-effects Parameters  |   Estimate   Std. Err.     [95% Conf. Interval]
-----------------------------+------------------------------------------------
ID: Identity                 |
                  var(_cons) |   .0652069    .0065901      .0534894    .0794912
-----------------------------+------------------------------------------------
               var(Residual) |    .030229    .0006818      .0289219    .0315952
------------------------------------------------------------------------------
LR test vs. linear model: chibar2(01) = 3954.33       Prob >= chibar2 = 0.0000
```

```
display "-2LL = " e(ll)*-2          // Print -2LL for model
-2LL = -1935.1741

estimates store FixTV               // Save LL for LRT

// Label slopes of interest (only between is new)
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
```

Estimates (from SAS output)					
		Standard			
Label	Estimate	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

```
// Build total-R2
predict predmoodG                   // Save fixed-effect predicted outcome
quietly corr lglucAM predmoodG      // Get total r to make R2
global R2Mood = r(rho)^2            // Save total-R2 for comparison
display "Total-R2 = " $R2Mood       // Print total-R2 relative to empty model


Total-R2 = .02110373


// Build pseudo-R2
display "Pseudo-R2 for Intercept = " 1-(exp(FixTV[1,4])^2/exp(Empty[1,2])^2)
display "Pseudo-R2 for Residual  = " 1-(exp(FixTV[1,5])^2/exp(Empty[1,3])^2)


Pseudo-R2 for Intercept = .02490961
Pseudo-R2 for Residual  = .00185172


display "Change in Pseudo-R2 for Intercept = " ///
1-(exp(FixTV[1,4])^2/exp(Empty[1,2])^2) - (1-(exp(Smush[1,3])^2/exp(Empty[1,2])^2))


Change in Pseudo-R2 for Intercept = .01614424


display "Change in Pseudo-R2 for Residual = " ///
1-(exp(FixTV[1,5])^2/exp(Empty[1,3])^2) - (1-(exp(Smush[1,4])^2/exp(Empty[1,3])^2))


Change in Pseudo-R2 for Residual = .00001338
```

How much variance did the new level-2 effect of PMnm0 account for, and which kind?

```
print("R Model 3a: Fixed Effects of Negative Mood using Grand-MC")
FixTV = lmer(data=Example2, REML=TRUE, formula=lglucAM~1+TVnm0+PMnm0+(1|ID))
print("Show results with -2LL using Satterthwaite DDF")
llikAIC(FixTV, chkREML=FALSE); summary(FixTV, ddf="Satterthwaite")

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

# Label slopes of interest (only between is new, though)
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))


# Total R2 for mood model relative to smushed model using custom function
TotalR2(data=Example2, dvName="lglucAM", model1=Smush, name1="Smushed", model2=FixTV, name2="Mood")
# Pseudo-R2 for mood model relative to smushed model using custom function
PseudoR2(data=Example2, baseModel=Empty, model1=Smush, name1="Smushed", model2=FixTV, name2="Mood")
```

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

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

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(ll)*-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=Example2, REML=TRUE, formula=lglucAM~1+TVnm0+PMnm0+(1+TVnm0|ID))
print("Show results with -2LL using Satterthwaite DDF")
llikAIC(RandTV, chkREML=FALSE); summary(RandTV, ddf="Satterthwaite")
```

```
$AICtab
       AIC        BIC     logLik   deviance   df.resid
-1925.1878 -1880.8886   969.5939  -1939.1878  4133.0000
```

Random effects:				
Groups	Name	Variance	Std.Dev.	Corr
ID	(Intercept)	0.06485266	0.254662	
	TVnm0	**0.00059328**	**0.024357**	**-0.052**
Residual		0.02992278	0.172982	

Comparing with Random WPnm slope instead (Model 2b):

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)	4.9309030	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 for both mood predictors.

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

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

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

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

```
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
matrix SexTV = r(table)        // Save results for computations below
```

			F(5, 333.85)	**=**	**9.02**
Log restricted-likelihood = 974.40694			Prob > F	=	0.0000

lglucAM	Coef.	Std. Err.	DF	t	P>|t|
TVnm0	.0313154	.0059415	3931.0	5.27	0.000
PMnm0	.1462292	.0469299	209.7	3.12	0.002
sexMW	-.037764	.0368045	203.0	-1.03	0.306
c.TVnm0#c.sexMW	-.0345346	.0077489	3931.0	-4.46	0.000
c.PMnm0#c.sexMW	-.1305315	.0604635	209.8	-2.16	0.032
_cons	4.95575	.027706	203.0	178.87	0.000

Interpret main effect of sexMW:

Interpret interaction of TVnm0*sexMW:

Interpret interaction of PMnm0*sexMW:

Random-effects Parameters	Estimate	Std. Err.	[95% Conf. Interval]	
ID: Identity				
var(_cons)	.0625617	.0063592	.051261	.0763537
var(Residual)	.0300847	.0006786	.0287837	.0314446

LR test vs. linear model: chibar2(01) = 3837.96   Prob >= chibar2 = 0.0000

```
display "-2LL = " e(ll)*-2    // Print -2LL for model
-2LL = -1948.8139

test (c.sexMW=0)(c.TVnm0#c.sexMW=0)(c.PMnm0#c.sexMW=0), small  // F-test of 3 Sex Slopes

     F( 3,301.48) =   10.12
         Prob > F =    0.0000

// Label slopes of interest (only those for women and between are new)
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 BP Mood Effect: Men
lincom c.TVnm0*1 + c.TVnm0#c.sexMW*1 + c.PMnm0*1 + c.PMnm0#c.sexMW*1, small    // L2 BP Mood Effect: Women
lincom c.TVnm0#c.sexMW*1 + 1*c.PMnm0#c.sexMW, small                            // L2 BP Mood Effect: 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
```

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?

```
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 pred values, no CI
graph export "STATA Sex Moderation Plot TVnm.png", replace
```
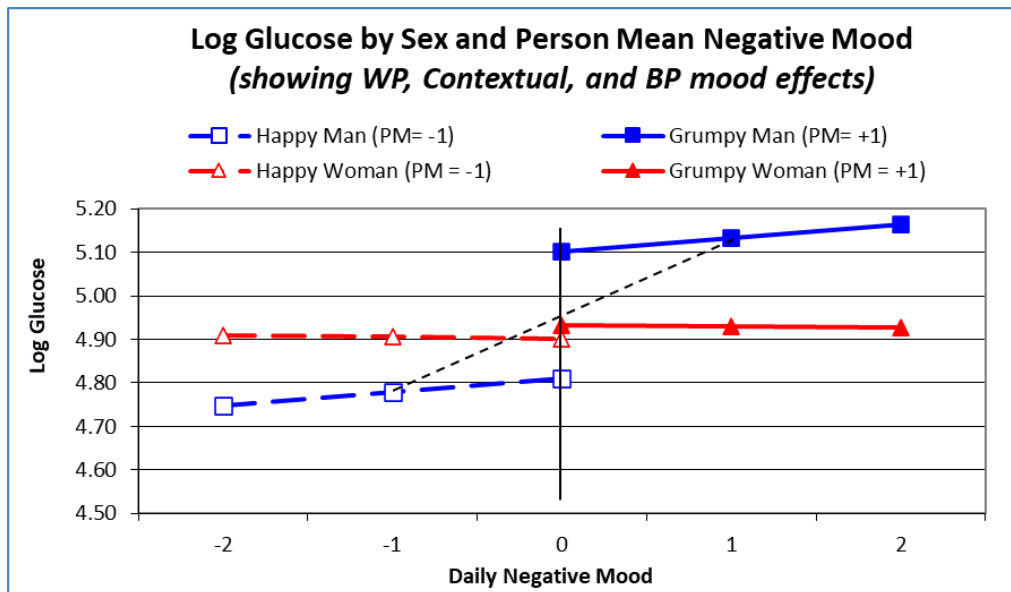

The solid vertical black line conveys the level-2 contextual effect, whereas the dashed black line conveys the level-2 between-person effect for men (it was ~0 in women).

```
// Build total-R2
predict predsexG                    // Save fixed-effect predicted outcome
quietly corr lglucAM predsexG       // Get total r to make R2
global R2Sex = r(rho)^2             // Save total-R2 for comparison
display "Total-R2 = " $R2Sex        // Print total-R2 relative to empty model
display "Change in Total-R2 = "  $R2Sex - $R2Mood

Total-R2 = .05611533
Change in Total-R2 = .03501159


// Build pseudo-R2
//matrix list SexTV  // Show saved results (variances are saved as log of SD)
display "Pseudo-R2 for Intercept = " 1-(exp(SexTV[1,7])^2/exp(Empty[1,2])^2)
display "Pseudo-R2 for Residual = "  1-(exp(SexTV[1,8])^2/exp(Empty[1,3])^2)
```

```
Pseudo-R2 for Intercept = .06446497
Pseudo-R2 for Residual = .00661708

display "Change in Pseudo-R2 for Intercept = " ///
(1-(exp(SexTV[1,7])^2/exp(Empty[1,2])^2)) - (1-(exp(FixTV[1,4])^2/exp(Empty[1,2])^2))

Change in Pseudo-R2 for Intercept = .03955536

display "Change in Pseudo-R2 for Residual = " ///
(1-(exp(SexTV[1,8])^2/exp(Empty[1,3])^2)) - (1-(exp(FixTV[1,5])^2/exp(Empty[1,3])^2))

Change in Pseudo-R2 for Residual = .00476536
```

Which pile of variance did each new fixed effect explain?

```
print("R Model 3c: Fixed Effects of Sex (0=M, 1=W) by Grand-MC Negative Mood")
SexTV = lmer(data=Example2, REML=TRUE,
            formula=lglucAM~1+TVnm0+PMnm0+sexMW +TVnm0:sexMW +PMnm0:sexMW +(1|ID))
print("Show results with -2LL using Satterthwaite DDF")
llikAIC(SexTV, chkREML=FALSE); summary(SexTV, ddf="Satterthwaite")

print("F-Test fof 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)))

# Label slopes of interest (only those for women and between are new)
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))

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

# Total R2 for sex model relative to mood model using custom function
TotalR2(data=Example2, dvName="lglucAM", model1=FixTV, name1="Mood", model2=SexTV, name2="Sex")
# Pseudo-R2 for sex model relative to mood model using custom function
PseudoR2(data=Example2, baseModel=Empty, model1=FixTV, name1="Mood", model2=SexTV, name2="Sex")
```

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_Example2_Data.csv;  ! Data in same folder as input
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

                                          Two-Tailed
               Estimate    S.E.   Est./S.E.  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          0.147    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 2 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 level-1 residual normality (i.e., reduce positive skewness). 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 variance (and no fixed effects of 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 significantly 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 variance in the level-1 within-person slope of negative mood across level-2 persons was tested, and it was nonsignificant, $-2\Delta LL$ (~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 4.956 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 in predicting 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)

Here is a summary of all variance explained across models:

Proportions of variance from empty model:	0.31170	0.68830						
Pseudo-R2 for Each Model	Residual Variance	Random Intercept Variance	Residual Variance Pseudo-R2	Random Intercept Pseudo-R2	Total R2 ish		Change in Residual Pseudo-R2	Change in Intercept Pseudo-R2
1a. Empty	0.03029	0.06687						
2a. Add WPnm, PMnm0	0.03023	0.06521						
2c. Add sex, sex*WPnm, sex*PMnm0	0.03008	0.06256						
Pseudo-R2 for 2a relative to 1a			0.002	0.025	0.018			
Pseudo-R2 for 2c relative to 1			0.007	0.064	0.047		0.005	0.040
3 . With Tvmood only	0.03023	0.06629						
3a. With tvnm0+PMnm0	0.03023	0.06521						
3c. With sex, sex*TVnm0, sex*PMnm0	0.03008	0.06256						
Pseudo-R2 for 3 relative to 1a			0.002	0.009	0.007			
Pseudo-R2 for 3a relative to 1a			0.002	0.025	0.018		0.000	0.016
Pseudo-R2 for 3c relative to 1			0.007	0.064	0.047		0.005	0.040