Example 5a: Time-Varying Predictors of Within-Person Fluctuation (complete syntax, data, and output available for R electronically)

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.

The data resemble a daily diary study of 207 persons (86 men and 121 women), each measured on 21 consecutive days (day 1 = Saturday), for a total of 4,347 observations. After examining the potential roles of "time" in the model, this example examines between-person and within-person relations between daily negative mood and glucose the next morning (lglucAM; log-transformed given positive skewness) and how these relationships are moderated by sex. It uses several custom functions to process output and add additional computations, as shown below (all in the online files).

R Syntax for Packages; Importing and Preparing Data for Analysis

```
# Install and load required packages
if (!require(pacman)) install.packages("pacman")
pacman::p_load(readxl, TeachingDemos, nlme, ggplot2)
# readxl: import .xls or .xlsx files; TeachingDemos: save output to text file
# ggplot2: figures of predicted values
# nlme: multilevel models with random effects AND residual correlation (AR1)
# (lme4/lmerTest cannot estimate AR1 residual correlation, so lme is used throughout)

# Set working directory (to import and export files to)
setwd("C:/Dropbox/26_EDF9850/Unit5/Example5a")

# Load R functions for this class from R file in folder above working directory
source("../../EDF9850_Functions.R")  # Remove ../ for same folder
source("https://www.lesahoffman.com/EDF9850/EDF9850_Functions.R") # From the web

# Import Example 5a excel data file in sheet "Diabetes5a"
Example5a = read_excel(path="Example5a_Data.xlsx", sheet="Diabetes5a")
# Convert to data frame to use for analysis
Example5a = as.data.frame(Example5a)

# Create a factor version of study day for saturated means below
Example5a$StudyDayF = factor(Example5a$StudyDay)

# Create person mean negative mood
Example5a = addUnitMeans(data=Example5a, unitVariable="PersonID",
                         meanVariables=c("lglucAM","negmood"),
                         newNames=c("PMgluc","PMnm"))
# Placeholder to remind you to center your person mean as needed
Example5a$PMnm0 = Example5a$PMnm - 0
# Create within-person negative mood using person-mean-centering
Example5a$WPnm = Example5a$negmood - Example5a$PMnm
# Create within-person lglucAM using person-mean-centering for correlations
Example5a$WPgluc = Example5a$lglucAM - Example5a$PMgluc

print("R Descriptive Statistics from Day-Level-1 Data")
univSummary(data=Example5a,vars=c("lglucAM","negmood","WPgluc","WPnm","PMgluc","PMnm"))
corrSummary(data=Example5a,vars=c("lglucAM","negmood","WPgluc","WPnm","PMgluc","PMnm"),
            p.separate=TRUE)
```

```
 Variable    N  Mean    SD Variance    Min   Max
 lglucAM  4347 4.978 0.337    0.113  3.881 6.066
 negmood  4347 0.402 0.948    0.899 -2.492 3.956
 WPgluc   4347 0.000 0.166    0.027 -0.566 0.637
 WPnm     4347 0.000 0.726    0.527 -2.770 2.601
 PMgluc   4347 4.978 0.293    0.086  4.131 5.696
 PMnm     4347 0.402 0.610    0.372 -1.093 1.982

Correlations:
 Variable lglucAM negmood WPgluc   WPnm PMgluc  PMnm
 lglucAM    1.000   0.143  0.492  0.059  0.871 0.152
 negmood    0.143   1.000  0.092  0.766  0.113 0.643
 WPgluc     0.492   0.092  1.000  0.120  0.000 0.000
 WPnm       0.059   0.766  0.120  1.000 -0.000 0.000
 PMgluc     0.871   0.113  0.000 -0.000  1.000 0.175
 PMnm       0.152   0.643  0.000  0.000  0.175 1.000
```

The descriptives show that negative mood and glucose vary substantially both between persons (PMnm SD = 0.610; PMgluc SD = 0.293) and within persons across days (WPnm SD = 0.726; WPgluc SD = 0.166). There appear to be positive correlations at both levels of analysis. We will estimate these two effects separately in the models below, beginning with an empty model for negative mood itself.

Model 0: Empty Means, Random Intercept Model for Time-Varying Negative Mood Predictor

Level 1: $NegMood_{ti} = \beta_{0i} + e_{ti}$

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

```
print("Model 0: Empty Means, Random Intercept for TV Negative Mood Predictor")
NegMood = lme(data=Example5a, method="REML",
              fixed=negmood~1, random=~1|PersonID)
lmeSummary(NegMood, ICC1=TRUE, LRT=TRUE)
```

```
Model Fit for Predicting negmood:
      AIC       BIC    logLik -2*logLik
10323.935 10343.066 -5158.967 10317.935

Model for the Variance:
 Groups    Name      Variance Std.Dev
 PersonID  Intercept    0.347   0.589
 Residual               0.554   0.744
Number of obs: 4347 , groups: PersonID , 207

Fixed Effects:
 Term         Est    SE       DF t.value p.value
 Intercept  0.402 0.042 4140.000   9.453   <.001

ICC1 intraclass correlation:
    Adjusted ICC: 0.386
  Unadjusted ICC: 0.386
```

$$ICC_1 = \frac{0.347}{0.347 + 0.554} = .\mathbf{386}$$

```
LRT for random effect(s) (full model vs. no random effects):
 Random Effect Dropped       Npar    LL  -2LL   AIC   BIC      LRT DF p.value
 <none>                         2 -5941 11881 11885 11898
(Intercept) across PersonID     3 -5159 10318 10324 10343 1563.156  1   <.001
```

Because negative mood varies at both levels, its effect on glucose may differ at each level, which we will examine by including WPnm (negmood minus the person mean) and PMnm0 (the person mean) as separate predictors. Neither needs further centering because 0 is meaningful for each: WPnm = 0 is the person's own mean, and PMnm0 = 0 is a person mean negative mood of 0 (the scale's zero point).

Model 1a: Empty Means, Random Intercept for Person, Independent Residuals

Level 1: $Glucose_{ti} = \beta_{0i} + e_{ti}$

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

```
print("Model 1a: Empty Means, Random Intercept Predicting TV AM Glucose Outcome")
Model1a = lme(data=Example5a, method="REML",
              fixed=lglucAM~1, random=~1|PersonID)
lmeSummary(Model1a, ICC1=TRUE, LRT=TRUE, randCI=TRUE)
```

```
Model Fit for Predicting lglucAM:
      AIC       BIC    logLik -2*logLik
-2219.239 -2200.108  1112.620 -2225.239

Model for the Variance:
 Groups    Name      Variance Std.Dev
 PersonID  Intercept    0.085   0.291
 Residual               0.029   0.170
Number of obs: 4347 , groups: PersonID , 207

Fixed Effects:
 Term         Est    SE       DF t.value p.value
 Intercept  4.978 0.020 4140.000 243.896   <.001

ICC1 intraclass correlation:
    Adjusted ICC: 0.747
  Unadjusted ICC: 0.747
```

$$ICC_1 = \frac{0.085}{0.085 + 0.029} = .747$$

```
LRT for random effect(s):
 Random Effect Dropped  Npar    LL  -2LL   AIC   BIC      LRT DF p.value p.mix
 <none>                    3 -5159 10318 10324 10343
 Intercept | PersonID      2 -5941 11881 11885 11898 1563.156  1   <.001 <.001

Random Effect 95% CIs (Fixed Effect +/- 1.96*SQRT(random effect variance)):
 Term      FixedEffect Variance    SD Lower Upper
 Intercept       4.978    0.085 0.291 4.407 5.549
```

Model 1b: Add AR(1) Residual Correlation Across Days

Level 1: $Glucose_{ti} = \beta_{0i} + e_{ti}$

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

Residuals: $Cov(e_{ti}, e_{t-k,i}) = \sigma_e^2 \rho^k$

```
print("Model 1b: Add AR1 Residual Correlation Across Days")
Model1b = lme(data=Example5a, method="REML",
              fixed=lglucAM~1, random=~1|PersonID,
              correlation=corAR1(form=~StudyDay|PersonID))
lmeSummary(Model1b, ICC1=TRUE, LRT=TRUE)   # ICC1 ignores the AR1 correlation
```

```
Model Fit for Predicting lglucAM:
      AIC       BIC    logLik -2*logLik
-3123.530 -3098.021  1565.765 -3131.530

Model for the Variance:
 Groups    Name      Variance Std.Dev  Corr
 PersonID  Intercept    0.082   0.286
 Residual               0.032   0.178
 Residual  AR1 Phi                    0.480
Number of obs: 4347 , groups: PersonID , 207

Fixed Effects:
 Term         Est    SE       DF t.value p.value
 Intercept  4.978 0.020 4140.000 244.224   <.001

ICC1 intraclass correlation:
    Adjusted ICC: 0.722
  Unadjusted ICC: 0.722
```

The ICC1 created by the random intercept is only part of the correlation across occasions now…

The estimated correlation among the residuals (after controlling for person mean differences via the random intercept) from adjacent days is ρ = .480. The AR(1) structure implies the correlation declines exponentially as days get farther apart: ρ^1 = .480 for 1 day apart, ρ^2 = .230 for 2 days apart, ρ^3 = .111 for 3 days 3, ρ^4 = .053 for days 4 apart, and so on, which is a more realistic pattern for daily data.

```
LRT for each random effect and residual correlation, tested separately (full model vs.
that piece dropped):
 Random Effect Dropped       Npar   LL  -2LL   AIC   BIC     LRT DF p.value p.mix
 <none>                         4 1566 -3132 -3124 -3098
 Intercept | PersonID           3 1290 -2579 -2573 -2554 552.427  1   <.001 <.001
 Residual correlation (AR1)     3 1113 -2225 -2219 -2200 906.290  1   <.001
```

The AR(1) correlation is significantly needed. The *p*-value to use is the p.value column rather than p.mix, as p.mix is the boundary-corrected *p*-value for testing whether a variance is zero, but the AR(1) correlation is not a variance, so plain χ^2 with DF = 1 is the correct reference distribution.

```
# Model-implied marginal correlation matrix (first week of the 21 days)
V = getVarCov(Model1b, type="marginal", individuals=1)
      1     2     3     4     5     6     7
1 0.114 0.097 0.089 0.086 0.084 0.083 0.082
2 0.097 0.114 0.097 0.089 0.086 0.084 0.083
3 0.089 0.097 0.114 0.097 0.089 0.086 0.084
4 0.086 0.089 0.097 0.114 0.097 0.089 0.086
5 0.084 0.086 0.089 0.097 0.114 0.097 0.089
6 0.083 0.084 0.086 0.089 0.097 0.114 0.097
7 0.082 0.083 0.084 0.086 0.089 0.097 0.114

round(cov2cor(V[[1]])[1:7, 1:7], 3)
      1     2     3     4     5     6     7
1 1.000 0.856 0.786 0.753 0.737 0.729 0.726
2 0.856 1.000 0.856 0.786 0.753 0.737 0.729
3 0.786 0.856 1.000 0.856 0.786 0.753 0.737
4 0.753 0.786 0.856 1.000 0.856 0.786 0.753
5 0.737 0.753 0.786 0.856 1.000 0.856 0.786
6 0.729 0.737 0.753 0.786 0.856 1.000 0.856
7 0.726 0.729 0.737 0.753 0.786 0.856 1.000
```

This is the V marginal model-implied covariance matrix, and below is its correlation version.

What would these matrices look like with only a random intercept variance?

Model 1c: Add Day in Study as a Factor (24 parameters)

Level 1: $Glucose_{ti} = \beta_{0i} + \beta_{1i}(Day2_{ti}) + \beta_{2i}(Day3_{ti}) + \cdots + \beta_{20i}(Day21_{ti}) + e_{ti}$

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

$\beta_{1i} = \gamma_{1,0},\ \beta_{2i} = \gamma_{2,0},\ \cdots,\ \beta_{20i} = \gamma_{20,0}$

Residuals: $Cov(e_{ti}, e_{t-k,i}) = \sigma_e^2 \rho^k$

Day2 to Day21 are 0/1 binary codes for study days 2 through 21, so study day 1 is the reference day.

```
print("Model 1c: Test Saturated Means for Day in Study as a Factor")
Model1c = lme(data=Example5a, method="REML",
              fixed=lglucAM~1+StudyDayF, random=~1|PersonID,
              correlation=corAR1(form=~StudyDay|PersonID))
lmeSummary(Model1c, predMeans=TRUE)  # predMeans = model mean for each factor level
```

```
Model Fit for Predicting lglucAM:
      AIC       BIC    logLik -2*logLik
-2959.940 -2807.003  1503.970 -3007.940

Model for the Variance:
 Groups    Name      Variance Std.Dev  Corr
 PersonID  Intercept    0.082   0.286
 Residual               0.032   0.178
 Residual  AR1 Phi                    0.481
Number of obs: 4347 , groups: PersonID , 207

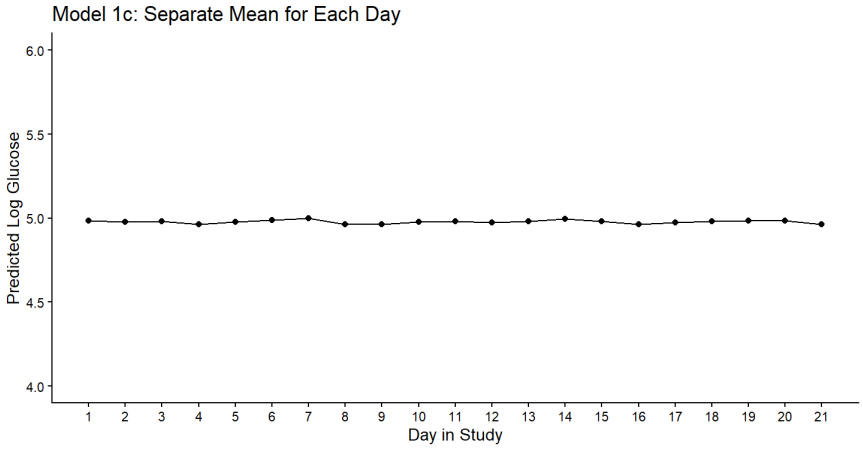
Overall F-test for All Fixed Slopes:
 Model   NumDF    DenDF F.value p.value
 Model1c    20 2135.160   0.930   0.548

Fixed Effects:
 Term                   Est    SE       DF t.value p.value
 Intercept            4.984 0.023  356.988 212.725   <.001
 StudyDayF (ref = 1)
 StudyDayF2          -0.007 0.013 3553.743  -0.584   0.559
 StudyDayF3          -0.003 0.015 4093.263  -0.199   0.842
 StudyDayF4          -0.020 0.016 3512.913  -1.235   0.217
 StudyDayF5          -0.005 0.017 2931.161  -0.284   0.776
 StudyDayF6           0.004 0.017 2571.112   0.222   0.824
 StudyDayF7           0.014 0.017 2367.311   0.830   0.406
 StudyDayF8          -0.020 0.017 2254.172  -1.155   0.248
 StudyDayF9          -0.021 0.017 2191.863  -1.197   0.232
 StudyDayF10         -0.008 0.017 2157.811  -0.452   0.651
 StudyDayF11         -0.004 0.017 2139.365  -0.232   0.817
 StudyDayF12         -0.010 0.017 2129.461  -0.567   0.571
 StudyDayF13         -0.002 0.017 2124.190  -0.114   0.909
 StudyDayF14          0.010 0.017 2121.407   0.569   0.569
 StudyDayF15         -0.004 0.017 2119.949  -0.242   0.809
 StudyDayF16         -0.019 0.017 2119.189  -1.098   0.272
 StudyDayF17         -0.010 0.017 2118.795  -0.553   0.580
 StudyDayF18         -0.002 0.017 2118.593  -0.135   0.892
 StudyDayF19         -0.001 0.017 2118.489  -0.057   0.955
 StudyDayF20         -0.001 0.017 2118.435  -0.040   0.968
 StudyDayF21         -0.020 0.017 2118.408  -1.124   0.261
```

Each fixed slope is the mean difference for that day relative to the first day of the study; such differences could indicate initial reactivity to the measurement process.

```
Model-Predicted Means for StudyDayF:
 Level  Mean    SE      DF
 1     4.984 0.023 356.988
 2     4.977 0.023 356.988
 3     4.981 0.023 356.988
 4     4.964 0.023 356.988
 5     4.979 0.023 356.988
 6     4.988 0.023 356.988
 7     4.998 0.023 356.988
 8     4.964 0.023 356.988
 9     4.963 0.023 356.988
 10    4.976 0.023 356.988
 11    4.980 0.023 356.988
 12    4.974 0.023 356.988
 13    4.982 0.023 356.988
 14    4.994 0.023 356.988
 15    4.980 0.023 356.988
 16    4.965 0.023 356.988
 17    4.974 0.023 356.988
 18    4.982 0.023 356.988
 19    4.983 0.023 356.988
 20    4.983 0.023 356.988
 21    4.964 0.023 356.988
```

These model-implied means can differ from observed data means due to missing data—use the model-estimated means whenever possible!



The overall F-test for the 20 day effects, $F(20, 2135) = 0.930$, $p = .548$, indicates no evidence that mean glucose differs across the 21 study days (as indicated by the model-predicted means above as well).

Model 1d: Replace Day in Study with Day of Week as a Factor (10 parameters)

Level 1: $$\boldsymbol{Glucose_{ti} = \beta_{0i} + \beta_{1i}(Sun_{ti}) + \beta_{2i}(Mon_{ti}) + \beta_{3i}(Tue_{ti}) + \beta_{4i}(Wed_{ti}) + \beta_{5i}(Thu_{ti}) + \beta_{6i}(Fri_{ti}) + e_{ti}}$$

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

$$\boldsymbol{\beta_{1i} = \gamma_{10},\ \beta_{2i} = \gamma_{20},\ \cdots,\ \beta_{6i} = \gamma_{60}}$$

Residuals: $$\boldsymbol{Cov(e_{ti}, e_{t-k,i}) = \sigma_e^2 \rho^k}$$

Sun to Fri are 0/1 binary codes for the days of the week, so Saturday is the reference day. Because day 1 of the study was a Saturday, each day of the week occurs three times per person (every seven days).

```
print("Model 1d: Test Saturated Means for Day of Week as a Factor")
Model11d = lme(data=Example5a, method="REML",
               fixed=lglucAM~1+DayName, random=~1|PersonID,
               correlation=corAR1(form=~StudyDay|PersonID))
lmeSummary(Model11d)
# Add pairwise differences among days of the week (Tukey-adjusted for 21 comparisons)
emmSat(Model11d, pairwise~DayName)
```

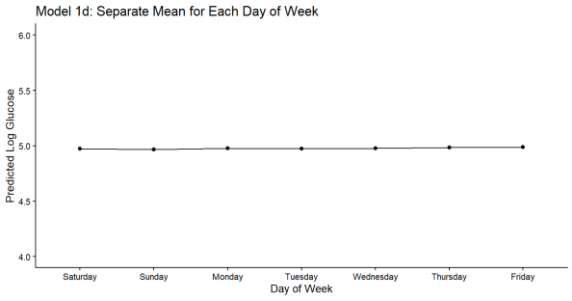
```
Model Fit for Predicting lglucAM:
      AIC       BIC    logLik -2*logLik
-3069.165 -3005.409  1544.582 -3089.165

Model for the Variance:
 Groups    Name      Variance Std.Dev  Corr
 PersonID  Intercept    0.082   0.286
 Residual               0.032   0.178
 Residual  AR1 Phi                    0.481
Number of obs: 4347 , groups: PersonID , 207
```

```
Overall F-test for All Fixed Slopes:
 Model   NumDF    DenDF F.value p.value
 Model1d     6 3116.585   1.126   0.344

Fixed Effects:
 Term                        Est    SE       DF t.value p.value
 Intercept                 4.972 0.021  235.944 235.733   <.001
 DayName (ref = Saturday)
 DayNameSunday            -0.006 0.007 3413.692  -0.796   0.426
 DayNameMonday             0.004 0.009 4118.959   0.482   0.630
 DayNameTuesday            0.003 0.009 4034.304   0.292   0.770
 DayNameWednesday          0.007 0.009 3965.812   0.731   0.465
 DayNameThursday           0.013 0.009 4101.565   1.450   0.147
 DayNameFriday             0.015 0.008 4006.466   1.930   0.054

emmeans:
 DayName   emmean    SE      df lower.CL upper.CL
 Saturday   4.972 0.021 235.944    4.931    5.014
 Sunday     4.966 0.021 238.148    4.925    5.008
 Monday     4.976 0.021 238.652    4.935    5.018
 Tuesday    4.975 0.021 238.744    4.933    5.016
 Wednesday  4.979 0.021 238.652    4.937    5.021
 Thursday   4.985 0.021 238.148    4.943    5.027
 Friday     4.987 0.021 235.944    4.946    5.029
```




```
contrasts:
 contrast             estimate    SE       df t.ratio p.value
 Saturday - Sunday       0.006 0.007 3413.692   0.796   0.985
 Saturday - Monday      -0.004 0.009 4118.959  -0.482   0.999
 Saturday - Tuesday     -0.003 0.009 4034.304  -0.292   1.000
 Saturday - Wednesday   -0.007 0.009 3965.812  -0.731   0.991
 Saturday - Thursday    -0.013 0.009 4101.565  -1.450   0.775
 Saturday - Friday      -0.015 0.008 4006.466  -1.930   0.460
 Sunday - Monday        -0.010 0.007 3438.167  -1.370   0.818
 Sunday - Tuesday       -0.008 0.009 4127.963  -0.962   0.962
 Sunday - Wednesday     -0.013 0.009 3995.922  -1.346   0.830
 Sunday - Thursday      -0.019 0.009 3927.488  -1.996   0.417
 Sunday - Friday        -0.021 0.009 4101.565  -2.337   0.227
 Monday - Tuesday        0.001 0.007 3459.349   0.206   1.000
 Monday - Wednesday     -0.003 0.009 4130.797  -0.299   1.000
 Monday - Thursday      -0.009 0.009 3995.922  -0.947   0.965
 Monday - Friday        -0.011 0.009 3965.812  -1.187   0.899
 Tuesday - Wednesday    -0.004 0.007 3459.349  -0.568   0.998
 Tuesday - Thursday     -0.010 0.009 4127.963  -1.178   0.903
 Tuesday - Friday       -0.013 0.009 4034.304  -1.359   0.823
 Wednesday - Thursday   -0.006 0.007 3438.167  -0.857   0.979
 Wednesday - Friday     -0.008 0.009 4118.959  -0.971   0.960
 Thursday - Friday      -0.002 0.007 3413.692  -0.310   1.000
P value adjustment: tukey method for comparing a family of 7 estimates
```

emmSat() with pairwise~DayName prints the model-predicted mean for each day of the week followed by all 21 pairwise differences between days with Tukey-adjusted p-values (your choice).

The overall F-test for the 6 day-of-week effects was also not significant, $F(6, 3116.59) = 1.126$, $p = .344$, so there is no evidence that mean glucose differs across days of the week. None of the 21 pairwise differences between days of the week was significant after the Tukey adjustment. So based on these preliminary analyses, we proceed with no fixed or random effects of "time" in the model (just AR1).

Model 2a: Add Within-Person and Between-Person Fixed Effects of Negative Mood

Level 1: $Glucose_{ti} = \beta_{0i} + \beta_{1i}(NM_{ti} - \overline{NM_i}) + e_{ti}$

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

$\beta_{1i} = \gamma_{10}$

Residuals: $Cov(e_{ti}, e_{t-k,i}) = \sigma_e^2 \rho^k$

```
print("Model 2a: Add WPnm and PMnm0 Fixed Effects of Negative Mood")
Model2a = lme(data=Example5a, method="REML",
              fixed=lglucAM~1+WPnm+PMnm0,
              random=~1|PersonID, correlation=corAR1(form=~StudyDay|PersonID))
lmeSummary(Model2a)
PseudoR2(baseModel=Model1b, altModel1=Model2a)
```

```
Model Fit for Predicting lglucAM:
      AIC       BIC    logLik -2*logLik
-3196.769 -3158.509  1604.384 -3208.769

Model for the Variance:
 Groups    Name      Variance Std.Dev  Corr
 PersonID  Intercept    0.080   0.282
 Residual               0.031   0.177
 Residual  AR1 Phi                    0.486
Number of obs: 4347 , groups: PersonID , 207

Overall F-test for All Fixed Slopes:
 Model   NumDF   DenDF F.value p.value
 Model2a     2 386.129  46.581   <.001

Fixed Effects:
 Term         Est    SE       DF t.value p.value
 Intercept  4.944 0.024  205.267 205.319   <.001
 WPnm       0.027 0.003 3487.102   9.313   <.001
 PMnm0      0.084 0.033  205.267   2.538   0.012
```

Interpret the Intercept (γ_{00}):

Interpret WPnm (γ_{10}):

Interpret PMnm0 (γ_{01}):

```
Pseudo-R2
 Term       Model   Variance Pseudo.R2
 Intercept  Model1b    0.082
 Intercept  Model2a    0.080     0.028
 Residual   Model1b    0.032
 Residual   Model2a    0.031     0.012
```

Which fixed slope reduced which variance?

Model 2b: Add Random Within-Person (WPnm) Effect of Negative Mood

Level 1: $Glucose_{ti} = \beta_{0i} + \beta_{1i}(NM_{ti} - \overline{NM_i}) + e_{ti}$

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

$\beta_{1i} = \gamma_{10} + U_{1i}$

Residuals: $Cov(e_{ti}, e_{t-k,i}) = \sigma_e^2 \rho^k$

```
print("Model 2b: Add Random Within-Person (WPnm) Effect of Negative Mood")
Model2b = lme(data=Example5a, method="REML",
              fixed=lglucAM~1+WPnm+PMnm0,
              random=~1+WPnm|PersonID, correlation=corAR1(form=~StudyDay|PersonID))
lmeSummary(Model2b, LRT=TRUE, digits=4) # needed more precision

Model Fit for Predicting lglucAM:
       AIC        BIC     logLik  -2*logLik
-3196.1189 -3145.1065  1606.0594 -3212.1189

Model for the Variance:
 Groups    Name       Variance Std.Dev    Corr
 PersonID  Intercept   0.0798  0.2824
           WPnm        0.0003  0.0164 -0.1874
 Residual              0.0310  0.1761
 Residual  AR1 Phi                      0.4882
Number of obs: 4347 , groups: PersonID , 207

Overall F-test for All Fixed Slopes:
 Model   NumDF    DenDF F.value p.value
 Model2b     2 193.4749 40.8822  <.0001

Fixed Effects:
 Term          Est     SE       DF  t.value p.value
 Intercept  4.9438 0.0241 204.5845 205.4476  <.0001
 WPnm       0.0273 0.0031 185.3197   8.6674  <.0001
 PMnm0      0.0842 0.0329 202.3973   2.5597  0.0112

LRT for each random effect and residual correlation, tested separately (full model vs. that
piece dropped):
Random Effect Dropped       Npar   LL  -2LL   AIC   BIC      LRT DF p.value  p.mix
 <none>                        8 1606 -3212 -3196 -3145
 WPnm | PersonID               6 1604 -3209 -3197 -3159   3.3502  2  0.1873 0.1272
 Residual correlation (AR1)    7 1140 -2280 -2266 -2221 932.3811  1  <.0001
```

The LRT comparing Model 2b to Model 2a has DF = 2 (the slope variance and its covariance with the intercept), −2ΔLL(2) = 3.349, p = .187 (the boundary-corrected p.mix = .127), so there is no evidence that the within-person effect of negative mood varies across persons. However, because one of the main research questions concerned sex differences in the effects of mood, we proceed to test both relevant interactions anyway, creating a **systematically varying WPnm slope**.

Model 3: Add Moderation of the WP and BP Effects of Negative Mood by Sex (0=M, 1=W)

Level 1: $\boldsymbol{Glucose_{ti} = \beta_{0i} + \beta_{1i}(NM_{ti} - \overline{NM}_i) + e_{ti}}$

Level 2: $\boldsymbol{\beta_{0i} = \gamma_{00} + \gamma_{01}(\overline{NM}_i - 0) + \gamma_{02}(SexMW_i) + \gamma_{03}(\overline{NM}_i - 0)(SexMW_i) + U_{0i}}$

$\boldsymbol{\beta_{1i} = \gamma_{10} + \gamma_{11}(SexMW_i)}$

Residuals: $\boldsymbol{Cov(e_{ti}, e_{t-k,i}) = \sigma_e^2 \rho^k}$

Composite equation written to show interactions (with all fixed effects first by convention):

$$\boldsymbol{Glucose_{ti} = \gamma_{00} + \gamma_{01}(\overline{NM}_i - 0) + \gamma_{02}(SexMW_i) + \gamma_{10}(NM_{ti} - \overline{NM}_i) + \gamma_{03}(\overline{NM}_i - 0)(SexMW_i) + \gamma_{11}(NM_{ti} - \overline{NM}_i)(SexMW_i) + U_{0i} + e_{ti}}$$

```
print("Model 3: Add Moderation of Both Mood Effects by Sex (0=Men, 1=Women)")
```

```
Model3 = lme(data=Example5a, method="REML",
             fixed=lglucAM~1+WPnm+PMnm0+sexMW +WPnm:sexMW +PMnm0:sexMW,
             random=~1|PersonID, correlation=corAR1(form=~StudyDay|PersonID))
lmeSummary(Model3)

Model Fit for Predicting lglucAM:
      AIC       BIC    logLik -2*logLik
-3203.822 -3146.439  1610.911 -3221.822

Model for the Variance:
 Groups    Name      Variance Std.Dev  Corr
 PersonID  Intercept    0.079   0.280
 Residual               0.031   0.176
 Residual  AR1 Phi                    0.487
Number of obs: 4347 , groups: PersonID , 207

Overall F-test for All Fixed Slopes:
 Model  NumDF   DenDF F.value p.value
 Model3     5 324.485  24.701   <.001

Fixed Effects:
 Term            Est    SE       DF t.value p.value
 Intercept     4.886 0.038  202.926 128.100   <.001
 WPnm          0.045 0.005 3505.954   9.796   <.001
 PMnm0         0.157 0.050  202.926   3.145   0.002
 sexMW         0.096 0.049  202.926   1.962   0.051
 WPnm:sexMW   -0.030 0.006 3491.648  -4.995   <.001
 PMnm0:sexMW  -0.125 0.066  202.926  -1.890   0.060
```

Interpret each fixed effect (remember that for sexMW, M = 0 and W = 1):

Intercept (γ_{00}):

WPnm (γ_{10}):

PMnm0 (γ_{01}):

sexMW (γ_{02}):

WPnm:sexMW (γ_{11}):

PMnm0:sexMW (γ_{03}):

$$\boldsymbol{Glucose_{ti} = \gamma_{00} + \gamma_{01}(\overline{NM_i} - 0) + \gamma_{02}(SexMW_i) + \gamma_{10}(NM_{ti} - \overline{NM_i}) + \gamma_{03}(\overline{NM_i} - 0)(SexMW_i) + \gamma_{11}(NM_{ti} - \overline{NM_i})(SexMW_i) + U_{0i} + e_{ti}}$$

Intercept for women: $\gamma_{00}(1) + \gamma_{02}(SexMW_i = 1)$
WPnm for women: $\gamma_{10}(1) + \gamma_{11}(SexMW_i = 1)$
PMnm0 for women: $\gamma_{01}(1) + \gamma_{03}(SexMW_i = 1)$

```
# Simple effects for women, without re-running the model with reversed sex coding
con1DTable(Model3, L=list(
"Intercept: Women"               = c("Intercept"=1, "sexMW"=1),
"Within-Person Effect: Women"    = c("WPnm"=1, "WPnm:sexMW"=1),
"Between-Person Effect: Women"   = c("PMnm0"=1, "PMnm0:sexMW"=1)))
```

```
Requested Fixed Effects:
 Name                            Est    SE       DF t.value p.value
 Intercept: Women              4.982 0.031  202.926 162.207   <.001
 Within-Person Effect: Women   0.015 0.004 3470.448   4.034   <.001
 Between-Person Effect: Women 0.032 0.044  202.926   0.730   0.466
```

```
# Joint test of all sex moderation effects (3 df)
conMDSummary(Model3, terms=c("sexMW","WPnm:sexMW","PMnm0:sexMW"))
```

```
Joint Test for:
sexMW, WPnm:sexMW, PMnm0:sexMW
 Model  NumDF   DenDF F.value p.value
 Model3     3 294.955   9.906   <.001
```

This joint test of the three sex effects (sexMW, WPnm:sexMW, PMnm0:sexMW), $F(3, 295.44) = 9.906$, $p < .001$, is conceptually equivalent to the F-test for the increase in R^2 for a set of predictors in GLMs. Here it tests whether sex matters at all (for the intercept or for either mood effect).

```
PseudoR2(baseModel=Model1b, altModel1=Model2a, altModel2=Model3)
TotalR2(altModel1=Model2a, altModel2=Model3)
```

```
Pseudo-R2 and Change in Pseudo-R2
 Term       Model   Variance Pseudo.R2 Change.R2
 Intercept  Model1b    0.082
 Intercept  Model2a    0.080     0.028
 Intercept  Model3     0.079     0.041     0.013
 Residual   Model1b    0.032
 Residual   Model2a    0.031     0.012
 Residual   Model3     0.031     0.017     0.005

Total-R2 and Change in Total-R2
 Model   Total.R2 Change.R2
 Model2a    0.027
 Model3     0.045     0.019
```

Which fixed slope reduced which variance?

Sample Results Section starts here—see the last page for a figure that could be included!

[indicates notes about what to customize or also include; note that SE and p-values are not needed if you provide tables for the model solutions; these are wordy on purpose to help illustrate how to interpret each effect]

The extent to which the next morning's log-transformed daily glucose could be predicted from daily negative mood, and whether those effects differed by sex, was examined in a series of multilevel models in which 4,347 daily observations were modeled as nested within 207 persons (86 men and 121 women), each observed on 21 consecutive days. Restricted maximum likelihood (REML) within the lme function in the nlme R package (v. 3.1-169; Pinheiro et al., 2026) was used in estimating and reporting all model parameters. The significance of fixed effects was evaluated with univariate and multivariate Wald tests using Satterthwaite denominator degrees of freedom (computed using the emmeans R package, v. 2.0.4; Lenth & Piaskowski, 2026), whereas the random effect and the AR(1) residual correlation were evaluated via likelihood ratio tests (i.e., $-2\Delta LL$ with degrees of freedom equal to the number of new parameters). Alpha was chosen as .05. Model-implied simple effects for women were obtained as linear combinations of the fixed effects of the final model. Fixed effect sizes were

evaluated via pseudo-R^2 values for the proportion reduction in each variance component relative to the model without the predictors in question, as well as with total-R^2, the squared correlation between the actual glucose outcomes and those predicted by the model fixed effects.

As derived from an empty means, random intercept model with independent residuals, log glucose had an intraclass correlation of ICC1 = .747, indicating that 74.7% of its variance was between persons, with the remaining 25.3% within persons across days. Adding an AR(1) correlation among the level-1 residuals significantly improved model fit, $-2\Delta LL(1) = 906.29$, $p < .001$, with an estimated residual correlation of $\rho = .480$ between adjacent days, declining to .230 for days two apart and .111 for days three apart. Mean glucose did not differ significantly across the 21 study days, $F(20, 2135) = 0.93$, $p = .548$, or across the days of the week, $F(6, 3116) = 1.13$, $p = .344$, so neither was retained as a predictor.

An empty means, random intercept model for the time-varying negative mood predicted yielded an ICC1 = .386, and thus the effects of mood were distinguished across the within- and between-person levels of analysis using person-mean-centering. Accordingly, we then added the within-person effect of daily negative mood (as the deviation from the person's own mean) and the between-person effect of negative mood (as the person mean, where 0 = the scale's zero point). These two fixed effects accounted for significant variance overall, $F(2, 386) = 46.58$, $p < .001$, including 2.8% of the random intercept variance (due to the person mean), 1.2% of the level-1 residual variance (due to the within-person mean daily deviation), and 2.7% of the total variance. The fixed intercept was 4.944 (SE = 0.024), which represented the expected glucose for a person with a person mean negative mood of 0 on a day when negative mood was at their own mean. The within-person slope indicated that on days when negative mood was one unit higher than the person's own mean, the next morning's glucose was expected to be significantly higher by 0.027 (SE = 0.003, $p < .001$). The between-person slope indicated that persons whose mean negative mood was one unit higher than other persons had mean glucose that was expected to be higher by 0.084 (SE = 0.033, $p = .012$). Adding a random within-person slope did not significantly improve model fit, $-2\Delta LL(1;2) = 3.35$, $p = .127$, indicating a lack of individual differences in the within-person effect of negative mood on the next morning's glucose.

Nevertheless, in order to answer our primary research question regarding sex differences, we then added sex (0 = men, 1 = women) and its interactions with the within-person and between-person effects of negative mood. The three sex effects were jointly significant, $F(3, 295) = 9.91$, $p < .001$, and the five fixed effects accounted for 4.1% of the random intercept variance (an increase of 1.3% due to the main effect of sex and its interaction with person mean negative mood), 1.7% of the level-1 residual variance (an increase of 0.5% due to the interaction of sex by daily negative mood deviation), and 4.5% of the total variance (an increase of 1.9%). The AR(1) residual correlation remained significant at $\rho = .487$. The within-person effect of negative mood was significantly smaller for women than for men by 0.030 (SE = 0.006, $p < .001$): the within-person slope was significantly positive for men (Est = 0.045, SE = 0.005, $p < .001$) and, although significantly smaller, remained significantly positive for women (Est = 0.015, SE = 0.004, $p < .001$). The between-person effect of negative mood was significantly positive for men (Est = 0.157, SE = 0.050, $p = .002$) but not for women (Est = 0.032, SE = 0.044, $p = .466$), and this sex difference of −0.125 (SE = 0.066) was only marginally significant, $p =$

.060. Finally, at both moods = 0, glucose was expected to be marginally higher for women (4.982, SE = 0.031) than for men (4.886, SE = 0.038), a difference of 0.096 (SE = 0.049, p = .051).

Lenth, R. V., & Piaskowski, J. (2026). *emmeans: Estimated marginal means, aka least-squares means* (R package version 2.0.4) [Computer software]. https://CRAN.R-project.org/package=emmeans

Pinheiro, J., Bates, D., & R Core Team. (2026). *nlme: Linear and nonlinear mixed effects models* (R package version 3.1-169) [Computer software]. https://CRAN.R-project.org/package=nlme

---

Figure to Illustrate the Sex Differences in the Within-Person and Between-Person Effects of Negative Mood using Model 3 Results—see Example 5a files online!

Predicted next morning's log glucose is based on the fixed effects of Model 3 only, for happy (person mean negative mood = −1 SD, or −0.209) and grumpy (+1 SD, or 1.013) men and women at within-person negative mood of −1 SD (lower than usual), the person's own mean (usual), and +1 SD (higher than usual; SD = 0.726). The within-person effect is the slope of each line: steeper for men (0.045) than for women (0.015). The between-person effect is the vertical distance between the happy and grumpy lines of the same sex: large for men (grumpy men are predicted 0.192 higher at usual mood) but small for women (0.039), consistent with the marginally significant sex difference in the between-person effect (p = .060).

