

# APIM workshop 11/1/2024

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## 1 Setup

```
#load packages
library(haven)
library(tidyverse)
library(jtools)
library(lme4)
```

```
library(psych)

# Import individual-level data
acitelli_ind <- read_csv("https://raw.githubusercontent.com/RandiLGarcia/2day-dyad-workshop/re

# Recode gender variable
acitelli_ind <- acitelli_ind %>%
  mutate(gender = recode(gender,
                        "-1" = 0, #females are 0
                        "1" = 1)) #males are 1
#recoding helps to make the interpretation easier later
```

## 2 About the dataset

Today we'll use couples data from Linda Acitelli ([Acitelli, 1997](#)). Acitelli (1997) examined 148 married couples (N=296) and assessed data from both individuals within dyads in a romantic relationship. For today, we'll focus on the following variables:

1. self\_pos (ratings of positive views of the self)
2. genderE (gender, where 0=F, 1=M)
3. tension (ratings of tension in the relationship, ranging 1-4)

For more information on the variables, [View codebook](#) for the dataset

## 3 Today's research question:

Do positive views of the self predict relationship tension in romantic couples?

## 4 Step 1: Convert individual to pairwise data

The raw data you collect will just be an individual dataset, and you will need to convert it from individual to pairwise.

To make it easy on myself, I typically just use [David Kenny's handy online app](#) to convert datasets from being individual -> pairwise data

But you can try doing it through coding in R and compare if you'd like. Ethan Young has [step-by-step instructions](#) on how to do this online, but I haven't used it before. For today, we'll use [code](#) provided by Randi Garcia.

```
##Individual to Pairwise Structure

# Create dataframe for actor-variables
tempA <- acitelli_ind %>%
  mutate(genderE = gender, partnum = 1) %>%
  mutate(gender = ifelse(gender == 1, "A", "P")) %>%
  gather(variable, value, self_pos:genderE) %>%
  unite(var_gender, variable, gender) %>%
  spread(var_gender, value)

# Create dataframe for partner-variables
tempB <- acitelli_ind %>%
  mutate(genderE = gender, partnum = 2) %>%
  mutate(gender = ifelse(gender == 1, "P", "A")) %>%
  gather(variable, value, self_pos:genderE) %>%
  unite(var_gender, variable, gender) %>%
  spread(var_gender, value)

# Bind the 2 dataframes to create a pairwise dataset
acitelli_pair <- bind_rows(tempA, tempB) %>%
  arrange(cuplid)

# Preview pairwise data
head(acitelli_pair)
```

```
# A tibble: 6 x 15
  cuplid Yearsmar partnum genderE_A genderE_P other_pos_A other_pos_P
  <dbl>   <dbl>   <dbl>   <dbl>   <dbl>   <dbl>   <dbl>
1     3     8.20     1         1         0         4         4.6
2     3     8.20     2         0         1         4.6         4
3    10    10.5     1         1         0         4         3.8
4    10    10.5     2         0         1         3.8         4
5    11    -8.30     1         1         0         4.8         4.4
6    11    -8.30     2         0         1         4.4         4.8
# i 8 more variables: satisfaction_A <dbl>, satisfaction_P <dbl>,
#   self_pos_A <dbl>, self_pos_P <dbl>, simhob_A <dbl>, simhob_P <dbl>,
#   tension_A <dbl>, tension_P <dbl>
```

```
# Look at variable names
names(acitelli_pair)
```

```
[1] "cuplid"      "Yearsmar"      "partnum"      "genderE_A"
[5] "genderE_P"   "other_pos_A"   "other_pos_P"   "satisfaction_A"
[9] "satisfaction_P" "self_pos_A"    "self_pos_P"    "simhob_A"
[13] "simhob_P"    "tension_A"     "tension_P"
```

## 5 Step 2: Calculate ICC

Now that we have a research question, we'll need to examine the intraclass correlation (ICC) to examine how much of the variance is within-dyad vs. between-dyad

```
# Fit an intercept-only model for self_pos
mod_selfpos <- lmer(self_pos_A ~ 1 + (1 | cuplid), data = acitelli_pair)
# specifying random intercept based on dyad (fixed slope)
# due to the cross-sectional design
# (one measurement at one time point with a dyad)

# Fit intercept-only model for tension
mod_tension <- lmer(tension_A ~ 1 + (1 | cuplid), data = acitelli_pair)
# specifying random intercept based on dyad (fixed slope)
# due to the cross-sectional design
# (one measurement at one time point with a dyad)

# Extract variance components for self_pos
var_components_sp <- as.data.frame(VarCorr(mod_selfpos))
group_variance_sp <- var_components_sp$vcov[1] # Random intercept variance
residual_variance_sp <- var_components_sp$vcov[2] # Residual variance

# Extract variance components for tension
var_components_t <- as.data.frame(VarCorr(mod_tension))
group_variance_t <- var_components_t$vcov[1] # Random intercept variance
residual_variance_t <- var_components_t$vcov[2] # Residual variance

# Calculate ICC for self-post
```

```

icc_selfpos <- group_variance_sp / (group_variance_sp + residual_variance_sp)

# Calculate ICC for tension
icc_tension <- group_variance_t / (group_variance_t + residual_variance_t)

# View ICCs
print(icc_selfpos) #ICC 0.087

```

```
[1] 0.08677402
```

```
print(icc_tension) #ICC 0.319
```

```
[1] 0.3194196
```

## 5.1 Interpreting ICC:

A higher ICC indicates high clustering, whereas an ICC of 0 would indicate there is no group effect. In other words, no variance is explained by the dyad, and all variance is within-groups

In this case, an ICC of 0.319 indicates that about 32% of the variance in tension can be attributed between-dyads, while 68% of the variance is attributed within-dyads. This is good justification for using a dyadic approach to analyzing the data.

## 6 Step 3: Mean-center variables of interest

```

# grand-mean center all relevant predictors
library(jtools)

acitelli_pair$self_pos_A_mc <- center(acitelli_pair$self_pos_A) #actor variable
acitelli_pair$self_pos_P_mc <- center(acitelli_pair$self_pos_P) #partner variable

```

This makes interpretability of the results much easier, because 0=mean

## 7 Step 4: Analyze data using APIM (MLM)

### 7.1 Assuming distinguishable dyads

Using an interaction approach:

1. Add distinguishing variable as a covariate. Note its coding.
2. Have the distinguishing variable interact with the actor and the partner effects.
3. These interactions evaluate whether actor and partner effects are the same for the two people.

```
# Taking a distinguishable approach  
library(nlme)
```

Attaching package: 'nlme'

The following object is masked from 'package:lme4':

lmList

The following object is masked from 'package:dplyr':

collapse

```
# Fit model  
apim_tension_gender <- lme(tension_A ~  
    self_pos_A_mc + self_pos_P_mc + genderE_A +  
    self_pos_A_mc*genderE_A + self_pos_P_mc*genderE_A,  
    random = ~1|cuplid,  
    data=acitelli_pair,  
    na.action = na.omit)  
  
# View results  
summary(apim_tension_gender)
```

Linear mixed-effects model fit by REML

Data:	acitelli_pair	
AIC	BIC	logLik
615.3321	644.6911	-299.666

Random effects:

Formula: ~1 | cuplid

(Intercept) Residual

StdDev: 0.3812014 0.5536429

Fixed effects: tension\_A ~ self\_pos\_A\_mc + self\_pos\_P\_mc + genderE\_A + self\_pos\_A\_mc \*

	Value	Std.Error	DF	t-value	p-value
(Intercept)	2.5694109	0.05956778	147	43.13424	0.0000
self_pos_A_mc	-0.4531767	0.13727544	143	-3.30122	0.0012
self_pos_P_mc	0.0190840	0.14383829	143	0.13268	0.8946
genderE_A	-0.2060552	0.06938510	143	-2.96973	0.0035
self_pos_A_mc:genderE_A	0.4694065	0.20379936	143	2.30328	0.0227
self_pos_P_mc:genderE_A	-0.2156237	0.20379936	143	-1.05802	0.2918

Correlation:

	(Intr)	sl__A_	sl__P_	gndE_A	s__A_:
self_pos_A_mc	-0.279				
self_pos_P_mc	0.289	-0.157			
genderE_A	-0.582	0.163	-0.168		
self_pos_A_mc:genderE_A	0.254	-0.709	0.333	0.009	
self_pos_P_mc:genderE_A	-0.265	0.328	-0.740	0.009	-0.456

Standardized Within-Group Residuals:

Min	Q1	Med	Q3	Max
-2.02401301	-0.60870597	0.02093311	0.55814679	2.33499771

Number of Observations: 296

Number of Groups: 148

### 7.1.1 Interpretation of Effects:

- **Intercept** = 2.57—The predicted score on tension for husbands and wives who have a 0 on how positively they see themselves
- **self\_pos\_A\_mc** = -0.45—Actor Effect: The more positively you view yourself, the less tension you report in the marriage.
- **self\_pos\_P\_mc** = 0.02 (ns)—Partner Effect: The more positively your partner views themselves, the more tension you report in the marriage.
- **genderE\_A** = -0.21 (ns)—Husbands are very slightly less satisfied (about .21 points less) than wives when you control for how they both view themselves.

- **self\_pos\_A\_mc X genderE\_A** = 0.47—The actor effect is stronger for husbands.
- **self\_pos\_P\_mc X genderE\_A** = -0.22—The partner effect is stronger H -> W than W -> H.

## 7.2 Assuming indistinguishable dyads

Technically, this approach is incorrect since there IS a distinguishable variable. However, I'm including this model to illustrate the differences between distinguishable vs. indistinguishable dyads. If we had indistinguishable dyads, the model just wouldn't include the distinguishing variable (example below).

```
# Fit model
apim_tension <- lme(tension_A ~
                    self_pos_A_mc + self_pos_P_mc,
                    random = ~1|cuplid,
                    data=acitelli_pair,
                    na.action = na.omit)

# View results
summary(apim_tension)
```

Linear mixed-effects model fit by REML

Data: acitelli\_pair  
 AIC      BIC      logLik  
 616.9089 635.3097 -303.4544

Random effects:

Formula: ~1 | cuplid  
 (Intercept) Residual  
 StdDev:    0.3774594 0.5691913

Fixed effects: tension\_A ~ self\_pos\_A\_mc + self\_pos\_P\_mc

	Value	Std.Error	DF	t-value	p-value
(Intercept)	2.4307432	0.04535632	147	53.59216	0.0000
self_pos_A_mc	-0.1594193	0.09550489	146	-1.66923	0.0972
self_pos_P_mc	-0.1615932	0.09550489	146	-1.69199	0.0928

Correlation:

	(Intr)	sl__A_
self_pos_A_mc	0.000	



self\_pos\_P\_mc 0.000 0.228

Standardized Within-Group Residuals:

Min	Q1	Med	Q3	Max
-2.128123814	-0.573151542	0.009543195	0.564449682	2.352289365

Number of Observations: 296

Number of Groups: 148

### 7.2.1 Interpretation of effects:

NOTE: NOT accounting for gender, the distinguishing variable:

- **Intercept** = 2.43—The predicted score on tension for participants who have a 0 on how positively they see themselves
- **self\_pos\_A\_mc** = -0.16 (ns)—Actor Effect: no effect of how you view yourself and the tension you report in the relationship
- **self\_pos\_P\_mc** = -16 (ns)—Partner Effect: How your partner views themselves is NOT predictive of the tension you report in the relationship