Day 1: Actor-Partner Interdependence Model

Back to schedule

Read in the individual data (or a pairwise dataset)

```r
library(tidyr)
library(dplyr)
library(nlme)

acitelli_ind <- read.csv(file.choose(), header=TRUE)
```

Convert individual data to pairwise. If you imported a pairwise set, skip this chunk. I also create a gender variable that's a **factor** and has labels `hus` and `wife`. This vairable will be useful later.

```r
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)

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)

acitelli_pair <- bind_rows(tempA, tempB) %>%
  arrange(cuplid) %>%
  mutate(gender_A = ifelse(genderE_A == 1, "hus", "wife"), gender_A = as.factor(gender_A)) #String, fac

rm(tempA, tempB)
```

Indistinguishable Dyads

```r
apim_in <- gls(satisfaction_A ~ other_pos_A + other_pos_P,
               data = acitelli_pair,
               correlation = corCompSymm(form=~1|cuplid),
               na.action = na.omit)

summary(apim_in)

## Generalized least squares fit by REML
##   Model: satisfaction_A ~ other_pos_A + other_pos_P
##   Data: acitelli_pair
##        AIC      BIC    logLik
##   306.7183 325.1191 -148.3591
##
```

```
## Correlation Structure: Compound symmetry
##  Formula: ~1 | cuplid
##  Parameter estimate(s):
##       Rho
## 0.4693414
##
## Coefficients:
##                  Value Std.Error  t-value p-value
## (Intercept) 0.6697541 0.3224381 2.077155  0.0387
## other_pos_A 0.4004231 0.0473141 8.463075  0.0000
## other_pos_P 0.2879705 0.0473141 6.086351  0.0000
##
##  Correlation:
##             (Intr) oth__A
## other_pos_A -0.793
## other_pos_P -0.793  0.267
##
## Standardized residuals:
##        Min         Q1        Med        Q3        Max
## -4.7764701 -0.4655155  0.1302733  0.6414975  1.7720088
##
## Residual standard error: 0.4173659
## Degrees of freedom: 296 total; 293 residual
```

```
names(apim_in)
```

```
##  [1] "modelStruct"  "dims"        "contrasts"    "coefficients"
##  [5] "varBeta"      "sigma"       "apVar"        "logLik"
##  [9] "numIter"      "groups"      "call"         "method"
## [13] "fitted"       "residuals"   "parAssign"    "na.action"
```

Pseudo-R^2

How much variance in the response variable does the actor and partner effects explain together? First we run the empty model so that we can get the total variance in the response—which we need to calculate the pseudo-R^2.

```
apim_in_empty <- gls(satisfaction_A ~ 1,
                data = acitelli_pair,
                correlation = corCompSymm(form=~1|cuplid),
                na.action = na.omit)
```

```
summary(apim_in_empty)
```

```
## Generalized least squares fit by REML
##   Model: satisfaction_A ~ 1
##   Data: acitelli_pair
##        AIC      BIC    logLik
##   364.4574 375.5183 -179.2287
##
## Correlation Structure: Compound symmetry
##  Formula: ~1 | cuplid
##  Parameter estimate(s):
##      Rho
## 0.61847
```

```
## 
## Coefficients:
##              Value  Std.Error   t-value  p-value
## (Intercept) 3.60473 0.03674615 98.09815        0
## 
## Standardized residuals:
##        Min         Q1        Med         Q3        Max
## -4.9061352 -0.5461333  0.4600210  0.7954058  0.7954058
## 
## Residual standard error: 0.4969417
## Degrees of freedom: 296 total; 295 residual
```

```
#This will perform a likilihood ratio test for the set of all fixed effects in the model.
anova(apim_in, apim_in_empty)
```

```
##               Model df      AIC      BIC    logLik   Test  L.Ratio p-value
## apim_in           1  5 306.7183 325.1191 -148.3591
## apim_in_empty     2  3 364.4574 375.5183 -179.2287 1 vs 2 61.73909  <.0001
```

```
#to have R calculate the pseudo-R2.
pesudo_r2 <- 1-(apim_in$sigma^2/apim_in_empty$sigma^2)
pesudo_r2
```

```
## [1] 0.29462
```

Rho: ICC = .618470
Residual SE^2 empty model = .246951
Residual SE^2 standard model = .174194
Pseudo-R^2 = 1 - (.174194 / .246951) = .295

Called the "pseudo R2"—29.5% of the variance in satisfaction is explained by other positivity of the actor and the partner. Set it to zero if it's negative.

Interpretation of Model Estimates

Fixed Effects

Intercept: Predicted level of satisfaction for those scoring zero on the actor and partner variables. Because these variables are not centered, it is not all that meaningful.

other_pos_A or the Actor Variable: If you see your partner positively, are you satisfied in the relationship? Yes!

other_pos_P or the Partner effect: If your partner sees you positively, are you satisfied in the relationship? (Or: If you see your partner positively, is your partner satisfied in the relationship?) Yes!

Random Effects

Residual SE^2 is the error or unexplained variance.
The partial ICC, or Rho, is .469.

Distingushable Dyads

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.

4. Add a `weights =` argument to allow for different error variances for the two members.

```
apim_di_int <- gls(satisfaction_A ~ other_pos_A + other_pos_P + genderE_A
                   + other_pos_A*genderE_A + other_pos_P*genderE_A,
                   data = acitelli_pair,
                   correlation = corCompSymm(form=~1|cuplid),
                   weights = varIdent(form=~1|genderE_A),
                   na.action = na.omit)

summary(apim_di_int)
```

```
## Generalized least squares fit by REML
##   Model: satisfaction_A ~ other_pos_A + other_pos_P + genderE_A + other_pos_A *       genderE_A + oth
##   Data: acitelli_pair
##        AIC      BIC    logLik
##   322.3805 355.4094 -152.1902
##
## Correlation Structure: Compound symmetry
##  Formula: ~1 | cuplid
##  Parameter estimate(s):
##       Rho
## 0.4751092
## Variance function:
##  Structure: Different standard deviations per stratum
##  Formula: ~1 | genderE_A
##  Parameter estimates:
##        1         -1
## 1.000000 1.203894
##
## Coefficients:
##                          Value Std.Error    t-value p-value
## (Intercept)          0.6508537 0.3250050   2.002596  0.0462
## other_pos_A          0.4010433 0.0472656   8.484896  0.0000
## other_pos_P          0.2915640 0.0482245   6.045967  0.0000
## genderE_A            0.0396052 0.1958905   0.202180  0.8399
## other_pos_A:genderE_A  0.0233433 0.0528291   0.441865  0.6589
## other_pos_P:genderE_A -0.0299142 0.0536888 -0.557177  0.5778
##
##  Correlation:
##                       (Intr) oth__A oth__P gndE_A o__A:E
## other_pos_A           -0.786
## other_pos_P           -0.797  0.263
## genderE_A             -0.207  0.101  0.226
## other_pos_A:genderE_A -0.006 -0.088  0.089 -0.411
```

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```
## other_pos_P:genderE_A   0.182 -0.003 -0.278 -0.444 -0.631
##
## Standardized residuals:
##         Min          Q1         Med          Q3         Max
## -4.6821686 -0.4599787   0.1298148   0.6321989   1.9431082
##
## Residual standard error: 0.3783372
## Degrees of freedom: 296 total; 290 residual
```

Interpretation of Effects

Intercept = .650854—The predicted score for husbands and wives who have a 0 on how positively they see the spouse (We should have centered!)

genderE__A = .039605—Husband are very slightly more satisfied (about .08 points more) than wives when you control for how they both view their spouse. (Recall wives are -1 on Gender_A and Husbands are +1; the difference between husbands and wives is then twice the difference of the effect of Gender_A.)

other__pos__A = .401043—Actor Effect: The more positively you view your spouse, the more satisfied you are in the marriage.

other__pos__P = .291564—Partner Effect: The more positively your partner views you, the more satisfied you are in the marriage.

genderE__A X other__pos__A = .023343—The actor effect is stronger for husbands.

genderE__A X other__pos__P = -.029914—The partner effect is stronger H -> W than W -> H.

Actor Effect for Husbands = .401043 + .023343 = 0.424386
Actor Effect for Wives = .401043 - .023343 = 0.37770
Partner Effect for W -> H = .291564 + (-.029914) = 0.261650
Partner Effect for H -> W = .291564 - (-.029914) = 0.321478

.207460, error variance for Wives
.143139, error variance for Husbands

Two-Intercept Approach

This involves a trick by which one equation becomes two. We create two dummy variables: H_{ij} which equals 1 for husbands and 0 for wives and W_{ij} which equals 1 for wives and zero for husband. We then estimate the following equation:

$$Y_{ij} = b_H H_{ij} + a_H H_{ij} A_{ij} + p_H H_{ij} P_{ij} + H_{ij} e_{ij} + b_W W_{ij} + a_W W_{ij} A_{ij} + p_W W_{ij} P_{ij} + W_{ij} e_{ij}$$

Note that the equation has no ordinary intercept, but rather, in some sense, two intercepts, b_H and b_W. Note that when $H_{ij} = 1$ and $W_{ij} = 0$, the above becomes

$$Y_{ij} = b_H + a_H A_{ij} + p_H P_{ij} + e_{ij}$$

and when $H_{ij} = 0$ and $W_{ij} = 1$, the above becomes

$$Y_{ij} = b_W + a_W A_{ij} + p_W P_{ij} + e_{ij}$$

Thus, one equals becomes two and we have actor and partner for both members.

To implement this in R, we do the following:

1. Add distinguishing variable as a factor, using `gender_A` created above.

2. Have no intercept in the fixed model by adding `-1` to the formula.
3. Have the distinguishing variable (`gender_A`) interact with actor and partner effect, but no actor and partner main effects. We need to use `:` for this instead of `*`. Separate actor and partner effects will be estimated for each member.

4. Keep the `weights =` argument to allow for different error variances for the two members.

```
apim_di_two <- gls(satisfaction_A ~ gender_A + other_pos_A:gender_A + other_pos_P:gender_A - 1,
                   data = acitelli_pair,
                   correlation = corCompSymm(form=~1|cuplid),
                   weights = varIdent(form=~1|genderE_A),
                   na.action = na.omit)

summary(apim_di_two)
```

```
## Generalized least squares fit by REML
##   Model: satisfaction_A ~ gender_A + other_pos_A:gender_A + other_pos_P:gender_A -       1
##   Data: acitelli_pair
##        AIC      BIC    logLik
##   318.2216 351.2505 -150.1108
##
## Correlation Structure: Compound symmetry
##  Formula: ~1 | cuplid
##  Parameter estimate(s):
##       Rho
## 0.4751092
## Variance function:
##  Structure: Different standard deviations per stratum
##  Formula: ~1 | genderE_A
##  Parameter estimates:
##        1        -1
## 1.000000 1.203894
##
## Coefficients:
##                               Value Std.Error  t-value p-value
## gender_Ahus               0.6904589 0.3429034 2.013567  0.0450
## gender_Awife              0.6112485 0.4128195 1.480668  0.1398
## gender_Ahus:other_pos_A   0.4243866 0.0677157 6.267184  0.0000
## gender_Awife:other_pos_A  0.3777000 0.0739222 5.109428  0.0000
## gender_Ahus:other_pos_P   0.2616498 0.0614025 4.261221  0.0000
## gender_Awife:other_pos_P  0.3214782 0.0815225 3.943427  0.0001
##
##   Correlation:
##                           gndr_Ah gndr_Aw gndr_Ah:__A gndr_Aw:__A
## gender_Awife               0.475
## gender_Ahus:other_pos_A   -0.667  -0.317
## gender_Awife:other_pos_A  -0.267  -0.562  -0.111
## gender_Ahus:other_pos_P   -0.562  -0.267  -0.234          0.475
## gender_Awife:other_pos_P  -0.317  -0.667   0.475         -0.234
##                           gndr_Ah:__P
## gender_Awife
## gender_Ahus:other_pos_A
## gender_Awife:other_pos_A
## gender_Ahus:other_pos_P
## gender_Awife:other_pos_P  -0.111
```

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```
##
## Standardized residuals:
##         Min         Q1         Med         Q3         Max
## -4.6821686 -0.4599787  0.1298148  0.6321989  1.9431082
##
## Residual standard error: 0.3783372
## Degrees of freedom: 296 total; 290 residual
```

We could also get pseudo R^2 for husbands and wives separately.

```
apim_di_empty <- gls(satisfaction_A ~ gender_A - 1,
                     data = acitelli_pair,
                     correlation = corCompSymm(form=~1|cuplid),
                     weights = varIdent(form=~1|genderE_A),
                     na.action = na.omit)

summary(apim_di_empty)
```

```
## Generalized least squares fit by REML
##   Model: satisfaction_A ~ gender_A - 1
##   Data: acitelli_pair
##        AIC       BIC    logLik
##   368.1852 386.6031 -179.0926
##
## Correlation Structure: Compound symmetry
##  Formula: ~1 | cuplid
##  Parameter estimate(s):
##        Rho
## 0.6234498
## Variance function:
##   Structure: Different standard deviations per stratum
##  Formula: ~1 | genderE_A
##  Parameter estimates:
##         1        -1
## 1.00000 1.14777
##
## Coefficients:
##                 Value  Std.Error  t-value p-value
## gender_Ahus  3.618243 0.03795870 95.32053       0
## gender_Awife 3.591216 0.04356787 82.42808       0
##
##  Correlation:
##              gndr_Ah
## gender_Awife 0.623
##
## Standardized residuals:
##         Min         Q1         Med         Q3         Max
## -5.3088847 -0.4865476  0.4568023  0.7712523  0.8266936
##
## Residual standard error: 0.4617875
## Degrees of freedom: 296 total; 294 residual
```

Error variance for Wives: .280928 - Pseudo R^2 is 1 - .207460 /.280928 = .2615
Error variance for Husbands: .213248 - Pseudo R^2 is 1 - .143139/.213248 = .3288

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