#GAPIM_I Output

Group Actor-Partner Interdependence Model Results
November 24, 2020

1. Text

CAUTION: If you do decide to use information contained here in a paper, please make sure that you acknowledge that you have used this program.   Moreover, should you decide to copy the exact text below, you would need to put quotes around that material to avoid plagiarism. Although great effort has been undertaken to ensure the accuracy of results, no complete guarantee can be about their accuracy. It is your responsibility to check the results and text for accuracy. If you do find an error, please report it to David A. Kenny.

WARNING: 1. Because group sizes vary, the chi square difference tests involving diversity, contrast, and group effects are approximate.

Summary of Group Actor-Partner Interdependence Model Results

The variable Gender is presumed to affect Group Identification in four different ways: the effect of the actor's own Gender or X, the effect of other group members' Gender or X', the effect of Actor-Others Similarity (I), and the effect of the Others' Similarity in their Gender or I'. The effect of the others equals +1 when all the others are Women and -1 when all the others are Men. The effect of the Actor-Others Similarity (I) equals +1 when all the others are the same Gender as the actor and -1 when all the others are a different Gender. The effect of the Others' Similarity equals +1 when all the others are the same Gender, zero when half of the pairs are the same, and -1 only for groups of size three when the two others have a different Gender. (Groups of four or more have lower limit of Others' Similarity that is always greater than -1.) The alpha used in all analyses is .05.

The GAPIM variable Actor is the Gender of the respondent. The GAPIM variable Others is the average Gender of the other members in the group besides the respondent. The GAPIM variable Actor-Others Similarity (I) is the average of the similarity of the actor's Gender to the other members in the group. The GAPIM variable Others' Similarity is the average similarity in Gender of all pairs of the others. Various other GAPIM variables can be constructed from these four GAPIM variables. They are Group, Contrast, Diversity, and Contrast Similarity. The Group variable is simply the mean of the group's Gender scores and potentially can range from -1 to +1. The Contrast variable is the difference between Actor and Others variables and potentially can range from -2 to +2. The Diversity variable measures how different the members are in the group and is a weighted average of Actor-Others Similarity (I) and Others' Similarity (I') variables; it equals -1 when all the group's members have the same Gender and some value above zero when the group is maximally diverse. (Note for a group of three or more, all of the members cannot be different from one another.) Remember that Diversity is the opposite of similarity. The Contrast Similarity variable is the difference between the Actor-Others Similarity (I) effect and the Others' Similarity (I') effect and can range from -2 for three-person groups to +2. The means, standard deviations, maxima, and minima of the GAPIM variables and Group Identification are presented in Table 1. Table 2 contains the GAPIM scores for groups of size 5 with various combinations of Men and Women. Table 3 contains the predicted values on Group Identification for groups with various combinations of Men and Women.

There are 2 outliers (standardized residuals greater than 3 in absolute value).   Examine the data to see what observation might be an outlier. Case 98 has a standardized residual of 3.308 whose score on Group Identification equals 6.692. Case 214 has a standardized residual of 3.064 whose score on Group Identification equals 6.923.

The effect of the actor's Gender is 0.004 (p = .958) with a 95% CI from -0.144 to 0.152. Women score 0.008 units higher on Group Identification than do Men. The effect of the Gender of the other group members is -0.189 (p = .179) with a 95% CI from -0.465 to 0.086. A member, all of whose other group members are Women, scores 0.379 units lower on Group Identification than a member, all of whose other members are Men. The effect of Actor-Others Similarity (I) is 0.248 (p = .049) with a 95% CI from 0.002 to 0.494. A person, who has the same Gender as the other group members scores 0.496 units higher on Group Identification than an actor who has a different Gender from the other members in the group. The effect of the Others' Similarity in Gender is -0.105 (p = .424) with a 95% CI from -0.363 to 0.152. If all the other members in the group have the same Gender, a person scores 0.210 units lower than a person in a group that is most diverse (Others' Similarity of -1.000). The effect of the Others' Similarity in Gender is -0.105 (p = .424) with a 95% CI from -0.363 to 0.152. If all the other members in the group have the same Gender, a person scores 0.105 units lower than a person in a group in which only half the members in the group are similar.

The multiple correlation between the four GAPIM-I fixed effects with Group Identification equals .090. The chi square test with two degrees of freedom that compares the Complete Model to the Empty Model equals 6.629 (p = .157). Because this chi square test is not statistically significant, there is no evidence that any of the terms of the Complete Model are non-zero. The chi square test with two degrees of freedom that compares the Complete Model to the Main Effects Model equals 4.405 (p = .111). Because this chi square test is not statistically significant, we do not have evidence that the interaction effects of the Complete Model are non-zero. The sample size adjusted BIC or SABIC for the Complete Model is 793.261 whereas the value for the Empty Model is 796.224. Because the index is smaller for the Complete Model, that model is a better fitting than the Empty Model.

The best fitting model is the Group with Interaction Model with a multiple correlation of .106. This model implies that there is a group effect for Gender, an effect for Actor Similarity, and an effect for Others' Similarity. The group effect equals -0.211 (p = .187) with a 95% CI from -0.523 to 0.101. Ideally, the multiple correlation of the best fitting model should be statistically significant, but that multiple correlation is not statistically significant (p = .087). Moreover, the difference between the Complete Model and the Best Fitting model should not be statistically significant. It is not significant, which indicates the Complete Model does not contain one or more meaningful terms not included in the Best Fitting Model (p = .794).

2. Tables

Table 1: Descriptive Statistics

Variable	Mean	SD	Minimum	Maximum
Group Identification	4.102	1.102	1.231	7.000
Actor (X)	0.278	0.963	-1.000	1.000
Others (X')	0.278	0.614	-1.000	1.000
Actor-Others Similarity (I)	0.227	0.634	-1.000	1.000
Others' Similarity (I')	0.227	0.618	-1.000	1.000
Group	0.278	0.570	-1.000	1.000
Contrast	0.000	1.001	-2.000	2.000
Diversity	-0.227	0.511	-1.000	0.333

Table 2: GAPIM Variable Scores for All Possible 5-Person Groups

Number	Men	Women

```
Men Women      X       X'      I       I'       X       X'     I'      I'
   0    5 -------  ------- -------  -------   1.000   1.000  1.000   1.000
   1    4 -1.000   1.000  -1.000   1.000    1.000   0.500  0.500   0.000
   2    3 -1.000   0.500  -0.500   0.000    1.000   0.000  0.000  -0.333
   3    2 -1.000   0.000   0.000  -0.333    1.000  -0.500 -0.500   0.000
   4    1 -1.000  -0.500   0.500   0.000    1.000  -1.000 -1.000   1.000
   5    0 -1.000  -1.000   1.000   1.000  -------  ------- -----   -------
```

Table 3: Complete Model Predicted Scores for Men and Women for All Possible 5-Person Groups

```
Number        Predicted Value
  Men Women              Men   Women
   0    5            -------   4.077
   1    4             3.573   4.153
   2    3             3.897   4.159
   3    2             4.150   4.094
   4    1             4.334   3.960
   5    0             4.448  -------
```

Table 4: Model Results

Model	Actor	Others	AO Similarity	O Similarity	SABIC	R
Empty	0.000	0.000	0.000	0.000	796.224	.029
Main Effects	0.049	-0.172*	0.000	0.000	795.833	.029
Actor Only	0.038	0.000	0.000	0.000	796.872	.000
Others Only	0.000	0.049	0.000	0.000	794.917	.029
Group	-0.139	-0.139	0.000	0.000	796.066	.019
Contrast	0.076	-0.076	0.000	0.000	795.760	.036
Complete	0.004	-0.189	0.248*	-0.105	793.261	.090
Person Fit	0.003	-0.235	0.243	0.000	793.012	.096
Diversity	0.039	-0.205	-0.094	-0.094	796.456	.000
Interaction Contrast	0.018	-0.138	0.180	-0.180	793.015	.102
Main Effects & Others' Similarity	0.051	0.000	-0.130	0.000	796.309	.000
Others & Others' Similarity	0.000	-0.123	0.000	-0.087	795.889	.000
Group & Diversity	-0.189	-0.189	-0.107	-0.107	796.606	.000
Full Contrast	0.045	-0.045	0.181	-0.181	792.898	.105
Group with Interaction	-0.211	-0.211	0.271*	-0.115	792.413	.106
Contrast with Interaction	0.045	-0.045	0.199	-0.162	793.755	.078

3. Computer Output

GAPIM Complete Model

Complete Model R code: gls(y~x+xprime+i+iprime, na.action=na.omit,method = "REML",
verbose=TRUE, correlation=corCompSymm(form=~1|ggnn), data=gapimdata -- Note that x is Gender,
xprime is average Gender, i is how similar the actor is to others, and iprime is how similar
others are to one another.

Generalized least squares fit by REML
  Model: mats

```
   Data: gapimdata
       AIC      BIC     logLik
  814.5262 839.3969 -400.2631

Correlation Structure: Compound symmetry
 Formula: ~1 | ggnn
 Parameter estimate(s):
       Rho
0.08906743

Coefficients:
                Value  Std.Error  t-value p-value
(Intercept)  4.119423 0.08808240 46.76784  0.0000
x            0.004021 0.07546785  0.05328  0.9575
xprime      -0.189479 0.14062800 -1.34738  0.1790
i            0.247825 0.12539724  1.97632  0.0492
iprime      -0.105200 0.13146991 -0.80018  0.4243

 Correlation:
       (Intr) x      xprime i
x      -0.130
xprime -0.238 -0.003
i      -0.131 -0.313 -0.214
iprime -0.131 -0.020 -0.408 -0.054

Standardized residuals:
        Min          Q1          Med          Q3          Max
-2.593350249 -0.649780274 -0.004250848  0.631192172  2.659469094

Residual standard error: 1.097353
Degrees of freedom: 263 total; 258 residual

GAPIM Best Fitting Model

Best Fitting Model of Group with Interaction code: gls(y~xbar+i+iprime,
na.action=na.omit,method = "ML", verbose=TRUE, correlation = corCompSymm(form=~1|ggnn),
data=gapimdata)  --  Note that xbar is the mean of X, i is actor-others similarity, and iprime
is the similarity of others..


Generalized least squares fit by REML
  Model: mats
  Data: gapimdata
       AIC      BIC     logLik
  809.0121 830.353 -398.506

Correlation Structure: Compound symmetry
 Formula: ~1 | ggnn
 Parameter estimate(s):
       Rho
0.09020058

Coefficients:
                Value  Std.Error  t-value p-value
```

```
(Intercept)   4.123610 0.08812837 46.79095   0.0000
xbar         -0.210829 0.15928863 -1.32357   0.1868
i             0.270699 0.12358394  2.19041   0.0294
iprime       -0.115385 0.12862707 -0.89705   0.3705


 Correlation:
       (Intr) xbar    i
xbar   -0.274
i      -0.130 -0.348
iprime -0.136 -0.363 -0.025

Standardized residuals:
       Min         Q1        Med         Q3        Max
-2.5898395 -0.6779170  0.0309801  0.6399798  2.6288783

Residual standard error: 1.09556
Degrees of freedom: 263 total; 259 residual
```