(In)Congruence in Child–Mother Relationships and Depressive Symptoms in Cross-Boundary Families

SUPPLEMENTARY

This study was not preregistered.

We reported how we determined our sample size, all data exclusions, all manipulations, and all measures in the study. Here is the detailed analytical plan.

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Statistical analysis

The basis for estimating and presenting DRSA is presented in the tutorials and guidelines outlined by Schönbrodt et al. (2018) and Shanock et al. (2010). The four main analytical steps of the present research are listed below.

Preliminary analyses

Preliminary analyses were performed through SPSS 26.0. The standard deviation of absolute difference scores was standardised and compared for each independent variable (i.e., children's and mothers' ratings of closeness and conflict) to determine the percentage of congruent versus incongruent dyads. In the current sample, 34.78% of dyads were classified as congruent, while the rest (65.22%) were incongruent (where 29.89% of children reported higher closeness than their mothers and 35.33% reported lower closeness than their mothers). Regarding conflict, 41.30% demonstrated congruence, and 58.70% displayed incongruence (i.e., 29.35% of children reported higher conflict than their mothers, whereas 29.35% reported lower conflict than their mothers). The frequency distribution supported the sequent analyses.

A variance inflation factor (VIF) greater than 5 and tolerance lower than 0.2 were set as the indicator of multicollinearity among variables. Cook's distance was employed for outlier detection in multivariate regressions, with a distance larger than 1 meaning the presence of an influential case (Bollen & Jackman, 1985; Schönbrodt et al., 2018). No evidence of multicollinearity and no outliner case were detected.

Bivariate correlation analyses between all variables were conducted, given that demographic variables such as child age, child and parent sex, and family income are potential covariates (Hou et al., 2020). Small and non-significant correlations were observed between the key variables (i.e., closeness, conflict, and depressive symptoms) and demographic variables (|*r*| < .14) (see Table S1). Therefore, no covariate was added to subsequent model estimations. Out of 12 variables, eight variables contained missing data. The missingness rates were below 5%, except for age (5.88%) and income (7.49%). The missing data did not display a specific pattern, as Little's MCAR test showed that the data were missing completely at random ($\chi^2 = 29.41$, $df = 26$, $p = .29$).

Modelling DRSA

All models were estimated via the *R* package *RSA* (Schönbrodt et al., 2018) and *lavaan* (Rosseel, 2012). Based on the distinguishable nature of child–mother dyads, Ackerman et al. (2010) recommended to centre closeness and conflict scores in child–mother dyads before analysing DRSA models. Next, the saturated DRSA models for closeness (Model 0_cl) and conflict (Model 0_cf) were estimated (see Table S2), using maximum likelihood estimation with robust (MLR) for modelling and the full information maximum likelihood estimation (FIML) for missing data (Schönbrodt et al., 2018). Missing values were estimated using the full information maximum likelihood estimation (FIML), which is popular and easy to implement in RSA analysis and limits biased results when the data were missing completely at random (Humberg & Grund, 2022; Schönbrodt et al., 2018).

Specifically, the outcome variables (i.e., depressive symptoms of children and mothers) were regressed on the independent variable of children and mothers (i.e., closeness/conflict), their squared terms (child-reported closeness^2/conflict^2 and mother-reported closeness^2/conflict^2), and their interaction terms (child-reported closeness/conflict × mother-reported closeness/conflict). Equations 3.1 and 3.2 describe the dyadic polynomial regression equations,

$$Z_c = b_{0\mathrm{c}} + b_{1\mathrm{c}}X + b_{2\mathrm{c}}Y + b_{3\mathrm{c}}X^2 + b_{4\mathrm{c}}XY + b_{5\mathrm{c}}Y^2 + e_c \qquad \text{Equation 3.1}$$

$$Z_m = b_{0\mathrm{m}} + b_{1\mathrm{m}}X + b_{2\mathrm{m}}Y + b_{3\mathrm{m}}X^2 + b_{4\mathrm{m}}XY + b_{5\mathrm{m}}Y^2 + e_m \qquad \text{Equation 3.2}$$

$$e_c \sim\sim e_m$$

where Z_c and Z_m denote the outcome variable of the child (c) and mother (m), Y refers to children's' independent variables (i.e., closeness/conflict) and X corresponds to mothers' independent variables (i.e., closeness/conflict). The residual scores of children's (e_c) outcome variables are set to be correlated to mothers' (e_m), which accounts for dependence in the dyad.

Applying constraints

Following recommendations from Schönbrodt et al. (2018), the model comparison analyses were performed to obtain the nested models under the complex DRSA models by adding constraints to parameters, which helped determine whether the DRSA model was the best-fit and most parsimonious model depicting the data (see Table S2). Specifically, we ran two constrained models to test

1. whether the simple APIMs would be able to depict the data equally well (i.e., Model 1_cl for closeness and Model 1_cf for conflict), by constraining all higher terms to zero ($b_{3\mathrm{c}} = 0$; $b_{4\mathrm{c}} = 0$; $b_{5\mathrm{c}} = 0$; $b_{3\mathrm{m}} = 0$; $b_{4\mathrm{m}} = 0$; $b_{5\mathrm{m}} = 0$);
2. whether an identical surface would be adequate for illustrating both child and mother outcomes (Model 2_cl for closeness and Model 2_cf for conflict), by equating all actor and partner effects across mother and child models except for the intercepts ($b_{1\mathrm{c}} = b_{2\mathrm{m}}$; $b_{3\mathrm{c}} = b_{5\mathrm{m}}$; $b_{2\mathrm{c}} = b_{1\mathrm{m}}$; $b_{5\mathrm{c}} = b_{3\mathrm{m}}$; $b_{4\mathrm{c}} = b_{4\mathrm{m}}$).

The following three criteria were employed for model selection. First, the root-mean-square error of approximation (RMSEA < 0.08), the comparative fit index (CFI > 0.90) and the standardised root mean square residual (SRMR < 0.05) were utilised to describe the model fit (Schumacker & Lomax, 2010). Second, compared to the full DRSA model, the nested models would be preserved if the χ^2 likelihood ratio tests yielded non-significant p values. Third, comparing the constrained models, a lower value of the Akaike information criterion (AIC) with a decrease (ΔAIC) greater than seven was regarded as a superior model fit.

If the full models or the equal models are superior, we will calculate response surface parameters for children (a_{1c}, a_{2c}, a_{3c}, a_{4c}) and mothers (a_{1m}, a_{2m}, a_{3m}, a_{4m}) to interpret the relationships between the independent variables and the outcome variables via response surface plots, instead of interpreting the regression coefficients (b_0 - b_5) of the polynomial regressions. If the simpler APIM models fit the data best, we will interpret the main actor and partner effects and not plot the response surface.

Plotting and Interpreting Response Surface

The response surface is plotted in a three-dimensional coordinate system. Figure S1 was generated as an example of the response surface plot (left) and its contour plot (right) for illustration. The two predictor variables, X and Y, are located on the two axes on the floor of the coordinate cube (i.e., the X-Y plane). For each combination of X and Y—coordinate (X, Y), the respective Z value predicted by the model is reflected in the vertical axis, thus indicated by the height of the surface. Line of congruence (LOC) and line of incongruence (LOIC) are two crucial features of the response surface patterns. In Figure S1, the red line refers to LOC (line of congruence) and the blue line refers to LOIC (line of incongruence). Values of X and Y can be seen on the corresponding axes, and values of Z are indicated by gradient colours.

LOC. LOC represents all combinations where X equals Y. Statistically, LOC is described by the formula $Z = a_1X + a_2X^2$. The coefficient a_1 ($a_1 = b_1 + b_2$) describes the slope of the LOC above the point (0, 0), and the coefficient a_2 ($a_2 = b_3 + b_4 + b_5$)

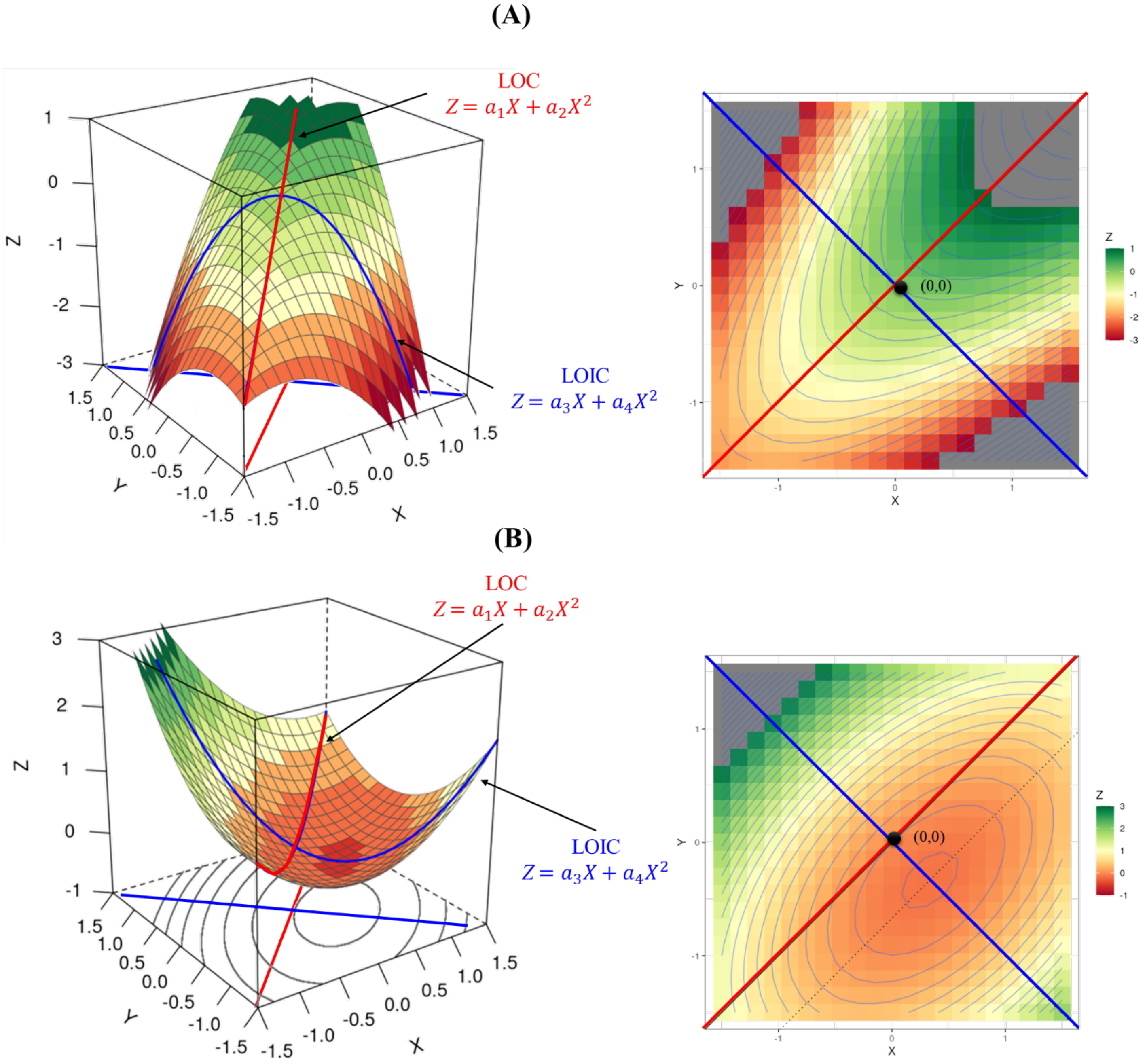
defines whether the LOC is linear ($a_2 = 0$) or curved ($a_2 \neq 0$). The two coefficients together determine how the outcome variables (Z) perform for varying congruence values of children's closeness/conflict (Y) and mothers' closeness/conflict (X). For example, in Figure S1A, a non-significant a_2 indicates that LOC is close to a straight line; in this case, if a_1 is significant and positive, it indicates that Z increases as the X and Y increase. Therefore, a significant and positive a_1 and a non-significant a_2 would confirm the convergence proposition for conflict (H4. The congruence in a high level of their ratings on conflict rather than at a low level of conflict would be associated with more depressive symptoms of both children and mothers). Similarly, a non-significant a_2 and a significant and negative a_1 indicate that Z decreases as the X and Y increase. Therefore, we expected a non-significant a_2 and a significant and negative a_1 for closeness (H1. The congruence at a high level of children's and mothers' ratings on their closeness rather than at a low level of closeness would be associated with fewer depressive symptoms of both children and mothers).

LOIC. LOIC represents all combinations where X equals -Y. Statistically, LOIC is described by the formula $Z = a_3X + a_4X^2$. Similar to LOC, the coefficients of slope ($a_3 = b_1 - b_2$) and curvature ($a_4 = b_3 - b_4 + b_5$) together determine how the incongruence of X and Y would be associated with Z. The coefficients a_3 and a_4 reveal the direction and the degree of incongruence, respectively, showing how the outcome variables vary when the incongruence value extends from one extreme (e.g., high mother-reported closeness and low child-reported closeness) to the other (e.g., high child-reported closeness and low mother-reported closeness). For example, in Figure S1B, a significant and positive a_4 indicates the LOIC is U-shaped, and the surface is a convex surface; that is, Z increases more sharply as the degree of the incongruence of X and Y increases. Therefore, a significant and positive a_4 would support the divergence proposition regarding the degree of the incongruence for closeness (H2. the greater incongruence in their ratings of closeness would be associated with more depressive symptoms of both children and mothers) and conflict (H5. The greater incongruence in their ratings of conflict would be associated with more depressive symptoms of both children and mothers).

In the case of significant positive a_4, if a_3 is significant and negative, the trough of the surface moves away from the LOC, showing that lower Z levels are observed when the direction of the incongruence is $X > Y$ rather than $Y > X$ (in Figure S1B). Therefore, we need to test two conditions in addition to a significantly positive a_4—a significantly positive a_3 for children and a significantly negative a_3 for mothers—to confirm the divergence proposition regarding the direction of the incongruence for closeness (H3. The incongruence characterised by the child-reported closeness higher than the mother-reported closeness, i.e., $Y > X$, would be associated with children's fewer depressive symptoms; The incongruence characterised by the child-reported closeness lower than the mother-reported closeness, i.e., $X > Y$, would be associated with mothers' fewer depressive symptoms).

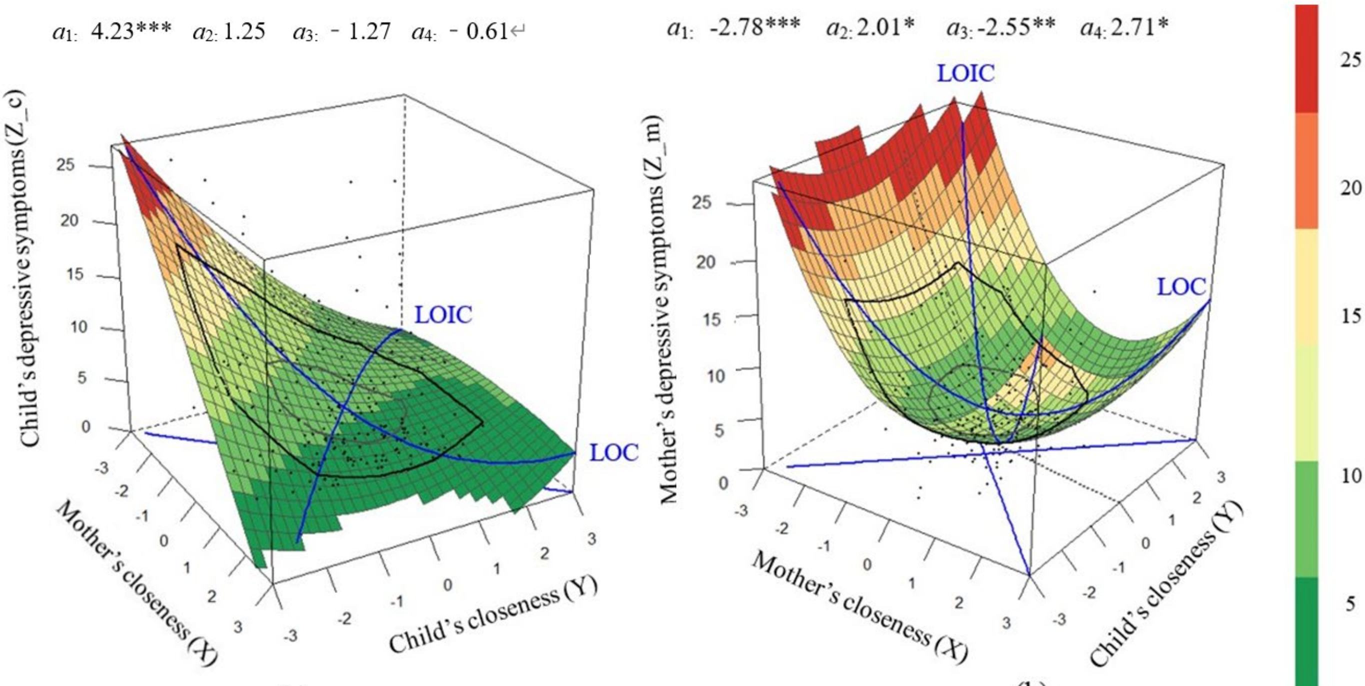
For conflict, we need to test two conditions in addition to a significantly positive a_4—a significantly negative a_3 for children and a significantly positive a_3 for mothers—to confirm the divergence proposition regarding the direction of the incongruence (H6. The incongruence characterised by the child-reported conflict higher than the mother-reported conflict, i.e., $Y > X$, would be associated with children's more depressive symptoms; The incongruence characterised by the child-reported conflict lower than the mother-reported conflict, i.e., $X > Y$, would be associated with mothers' more depressive symptoms).

Figure S1. Examples of response surfaces created by the authors



Notes. The three-dimensional response surface plot is shown on the left. The corresponding two-dimensional contour plot is shown on the right where all points that have the same response are connected to produce contour lines of constant responses. In both plots, *X* and *Y* represent the two predictors and *Z* represents the outcome variable. The red line refers to LOC (line of congruence) and the blue line refers to LOIC (line of incongruence). Values of *X* and *Y* can be seen on the corresponding axes, and values of *Z* are indicated by gradient colours. The figures were created through https://shiny.psy.lmu.de/felix/polySurface/

Figure S2 The dyadic response surface plots for the association between levels of the closeness of child–mother dyads and child's depressive symptoms (a) and mother's depressive symptoms (b) (N = 187 child–mother dyads)

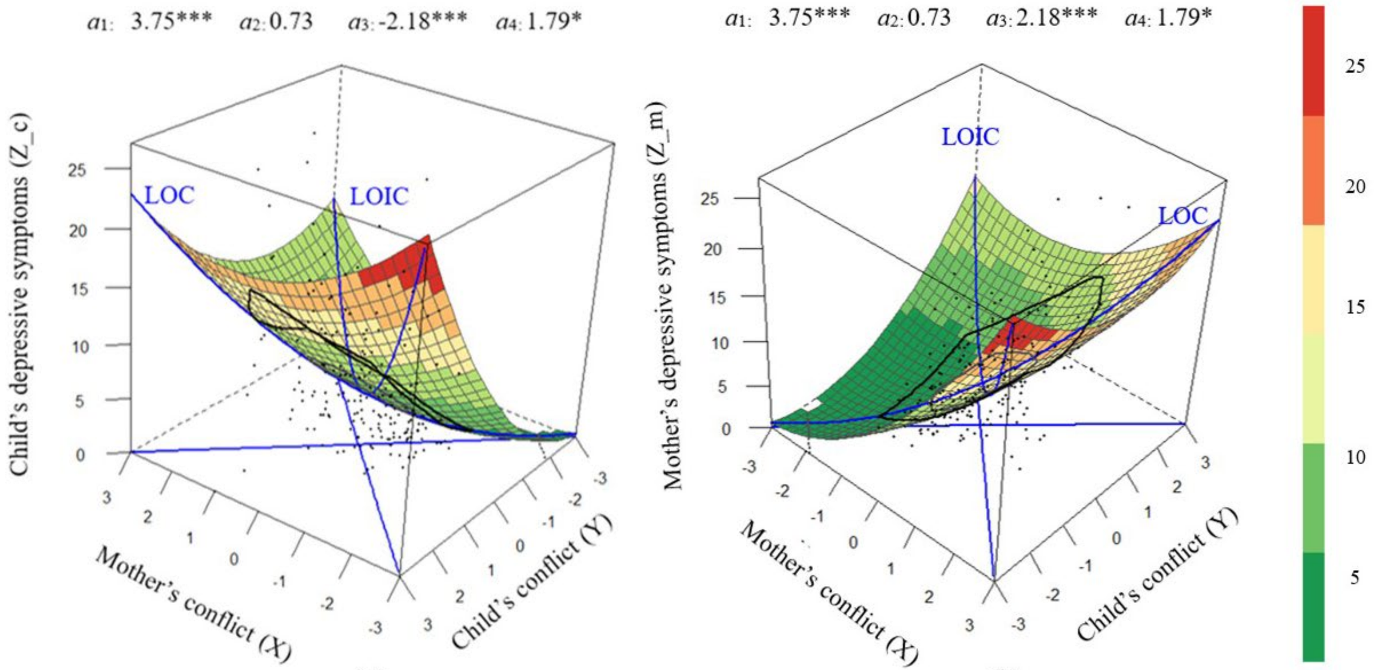


(a) (b)

Notes. LOC = the line of congruence ($X = Y$), defined by a linear slope (a_1, $a_1 = b_1 + b_2$) and a curvilinear slope (a_2, $a_2 = b_3 + b_4 + b_5$), depicts how the outcome variables behave for varying congruence values of children's closeness/conflict and mothers' closeness/conflict.

LOIC = the line of incongruence ($X = -Y$), carrying information on a linear slope (a_3, $a_3 = b_1 - b_2$) and a non-linear slope (a_4, $a_4 = b_3 - b_4 + b_5$), shows how the outcome variables vary when the incongruence value extends from one extreme (e.g., high mother-reported closeness and low child-reported closeness) to the other (e.g., high child-reported closeness and low mother-reported closeness).

Figure S3 The dyadic response surface plots for the association between levels of the conflict of child–mother dyads and child's depressive symptoms (a) and mother's depressive symptoms (b) (N = 187 child–mother dyads)



(a) (b)

Notes. LOC = the line of congruence ($X = Y$), defined by a linear slope ($a_1, a_1 = b_1 + b_2$) and a curvilinear slope ($a_2, a_2 = b_3 + b_4 + b_5$), depicts how the outcome variables behave for varying congruence values of children's closeness/conflict and mothers' closeness/conflict.

LOIC = the line of incongruence ($X = -Y$), carrying information on a linear slope (a_3, $a_3 = b_1 - b_2$) and a non-linear slope (a_4, $a_4 = b_3 - b_4 + b_5$), shows how the outcome variables vary when the incongruence value extends from one extreme (e.g., high mother-reported closeness and low child-reported closeness) to the other (e.g., high child-reported closeness and low mother-reported closeness).

Key codes for running DRSA in R

```
#======= Modelling DRSA =================
# X = mother closeness/conflict
# X.c = mother closeness/conflict (centred)
# X.c2 = mother closeness/conflict (squared terms)
# Z_m = mother’s depression symptoms
# XY = interaction terms (child- reported closeness/conflict× mother- reported closeness/conflict)
# Y = child closeness/conflict
# Y.c = child closeness/conflict (centred)
# Y.c2 = child closeness/conflict (squared terms)
# Z_c = child’s depression symptoms

# Define structure of full RSA model
dRSA.full.model <- '
Z_c ~ b1c*X.c + b2c*Y.c + b3c*X.c2 + b4c*XY + b5c*Y.c2    ## Equation 3.1
Z_m~ b1m*X.c + b2m*Y.c + b3m*X.c2 + b4m*XY + b5m*Y.c2       ## Equation 3.2
Z_c ~~ Z_m

# Derived variables: parent and child surface parameters
a1m := b1m + b2m
a2m := b3m + b4m + b5m
a3m := b1m - b2m
a4m := b3m - b4m + b5m

a1c := b1c + b2c
a2c := b3c + b4c + b5c
a3c := b1c - b2c
a4c := b3c - b4c + b5c
'
# Estimate the model including intercepts.
#Use a robust estimator and FIML handling of missing values.
s.full<- sem(dRSA.full.model, data=df, meanstructure=TRUE, fixed.x = F,
                      estimator='MLR', se='robust',missing='fiml')
summary(s.full, standardized=TRUE)

# Explained variance for both dependent variables
lavaan::inspect(s.full, 'rsquare')

#======Applying constrains=========
#---------------simple APIM model----------
# Test whether the simple APIMs would be able to depict the data equally well
# by constraining all higher terms to zero
dRSA.simple <- paste0(dRSA.full.model, '
b3m == 0
```

```
b4m == 0
b5m == 0
b4c == 0
b3c == 0
b5c == 0
')

# Estimate the model including intercepts.
s.simple<- sem(dRSA.simple, data=df, meanstructure=TRUE, fixed.x = F,
                    estimator='MLR', se='robust',missing='fiml')
summary(s.simple, standardized=TRUE)

fitMeasures(s.simple, fit.measures=c(‘rmsea’, ‘cfi’, ‘tli’, ‘SRMR’)) # Fit indexes

anova(s.full, s.simple) # Model comparison

lavaan::inspect(s.simple, 'rsquare') # Explained variance for both dependent variables


# --------------identical pattern ------------
#Test whether an identical surface would be adequate
#for illustrating both child and mother outcomes
#by equating all actor and partner effects across mother and child models except for the intercepts

dRSA.equal <- paste0(dRSA.full.model, '
b1m == b2c
b3m == b5c
b2m == b1c
b5m == b3c
b4m == b4c
' )

# Estimate the model including intercepts.
s.equal<- sem(dRSA.equal, data=df, meanstructure=TRUE, fixed.x = F,
                   estimator='MLR', se='robust',missing='fiml')
summary(s.equal, standardized=TRUE)

fitMeasures(s.equal, fit.measures=c(‘rmsea’, ‘cfi’, ‘tli’, ‘SRMR’)) # Fit indexes

anova(s.full, s.equal) # Model comparison

lavaan::inspect(s.equal, 'rsquare') # Explained variance for both dependent variables
```

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