



Dyadic Data Analysis with R

Part I: Conceptual Foundations

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Introduction

- Turu & Pascal
- Tell us about you and your dyadic data!
 - Name, affiliation & career stage
 - Your dyadic data and RQ

Today's aims and program

Time	Focus
11:00–12:45	Introduction and types of dyadic models
12:45–14:00	<i>Lunch break</i>
14:00–15:30	Estimating cross-sectional dyadic models in R
15:30–15:45	<i>Short break</i>
15:45–16:45	Intensive longitudinal extensions
16:45–17:00	<i>Short break</i>
17:00–18:00	Exercises in R



Introduction

Relevance and today's example dataset

Why dyadic data?

“Much of what we think, do, and feel is determined not by who we are but by whom we are with.” (Kenny & Cook, 1999, p. 446)

- **Partners matter:** An outcome may depend on both *my characteristics* and *my partner's characteristics*.
- **Some constructs and processes are dyadic:** Shared contexts and interdependence processes can make partners' outcomes correlated.
- **The configuration matters:** Partners' similarity or theoretically patterned differences, such as complementarity, may predict outcomes beyond either individual score.

Introducing today's dyadic dataset!

- 36 physically inactive romantic couples
- Both partners intended to become more physically active
- Smartphone-based planning interventions and JITAIs
- Daily diaries over 55 days

Küng et al. (2026); Höhener et al. (2026)

Guiding question

Guiding question: In romantic couples, how is provided health-related social support linked to physical activity?

Measurement - predictor

Provided emotional support

Rough English translation of the original German item

“How much did you emotionally support your partner today so that they would be physically active with greater enjoyment?”

Adapted from Bolger et al. (2000)

0 = *not at all today*

5 = *very much today*

Measurement - outcome

Moderate to vigorous physical activity (MVPA)

Rough English translation of the original German item

“How many minutes did you spend engaging in moderate-to-vigorous physical activity today?”

Adapted from Amireault & Godin (2015)

- Alone: _____ minutes
- Together with your partner: _____ minutes

Total MVPA = solo MVPA + joint MVPA.

Person-level data for cross-sectional examples

For the cross-sectional examples, we use a prepared person-level version of the daily diary data.

```
1 pilot_aggregated <- readRDS("dyadic-person-means.rds")
```

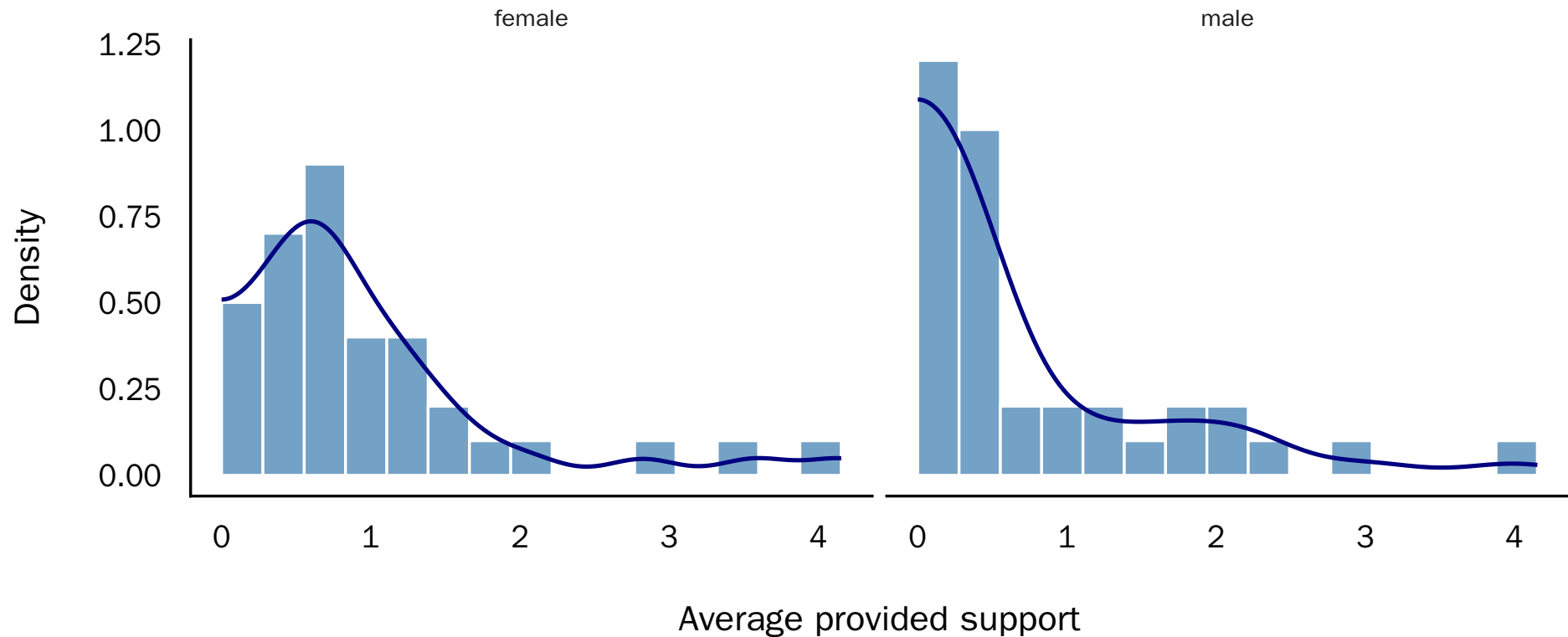
Each row is one partner. Measures are averages across available diary days:

- `provided_support`: average daily support provided
- `received_support`: average daily support received
- `total_mvpa`: average daily total MVPA (minutes)

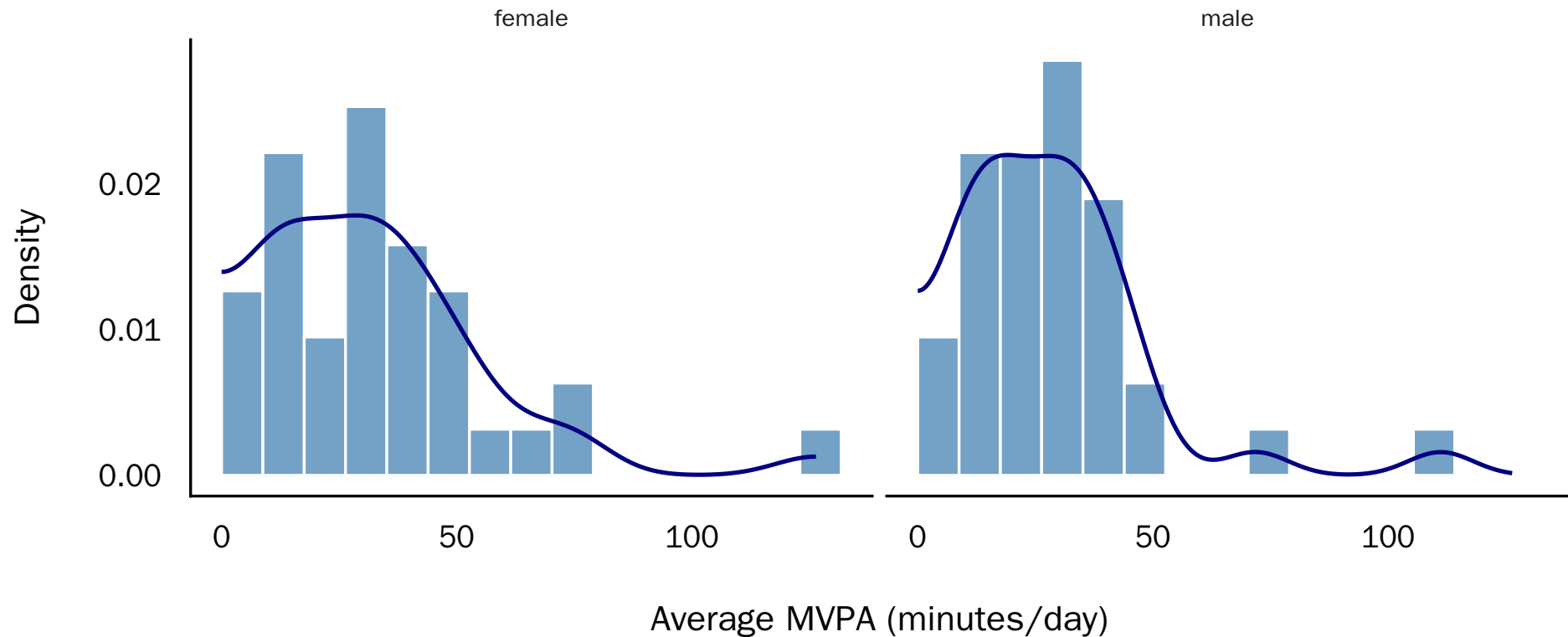
Plotting provided support by partner role

```
support_distribution_plot <- ggplot(  
  pilot_aggregated,  
  aes(provided_support, y = after_stat(density))  
) +  
  geom_histogram(  
    bins = 15, boundary = 0,  
    fill = "steelblue", color = "white", alpha = 0.75  
  ) +  
  geom_density(  
    bounds = c(0, Inf), color = "navy", linewidth = 1.1  
  ) +  
  facet_wrap(~gender, nrow = 1) +  
  labs(x = "Average provided support", y = "Density") +  
  see::theme_modern(base_size = 16)
```

Provided support by partner role

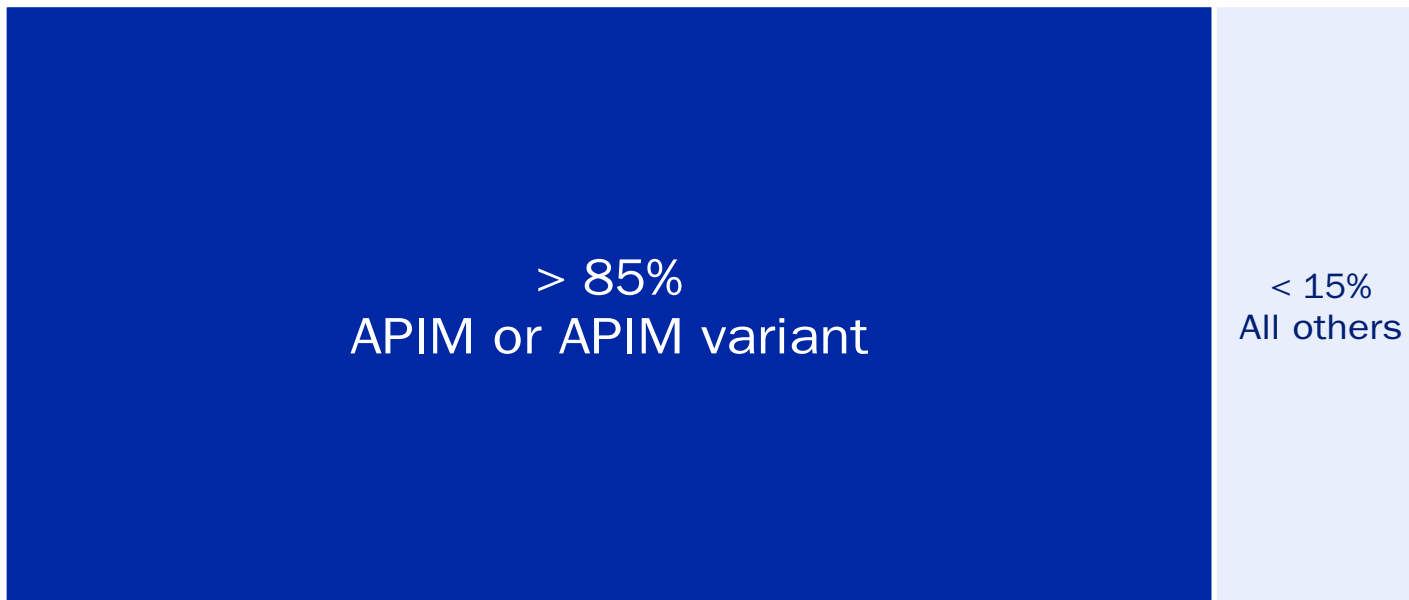


MVPA by partner role



Different types of dyadic models

One model dominates dyadic research



Preliminary results from an ongoing systematic review (APIM use coded for $n = 998$ eligible articles)
(Sakaluk et al., 2025, p. 6).

Many models to choose from

Various dyadic models can be used, each answering different questions!

- **Actor-partner interdependence model (APIM)**: actor and partner associations between interdependent individuals
- **Dyad-individual model (DIM)** and **dyadic score model (DSM)**: associations involving dyad levels and within-dyad differences
- **Common fate model (CFM)**: latent dyad-level constructs reflected in both partners' reports

Other approaches include the **mutual-influence model**, for reciprocal influence between partners ([Iida et al., 2018, p. 62](#)), and the **Truth and Bias model**, for separating directional bias, direct accuracy, and assumed-similarity bias in judgments of a partner ([Kenny & Acitelli, 2001](#); [West & Kenny, 2011](#)).

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Various dyadic models can be used, each answering different questions!

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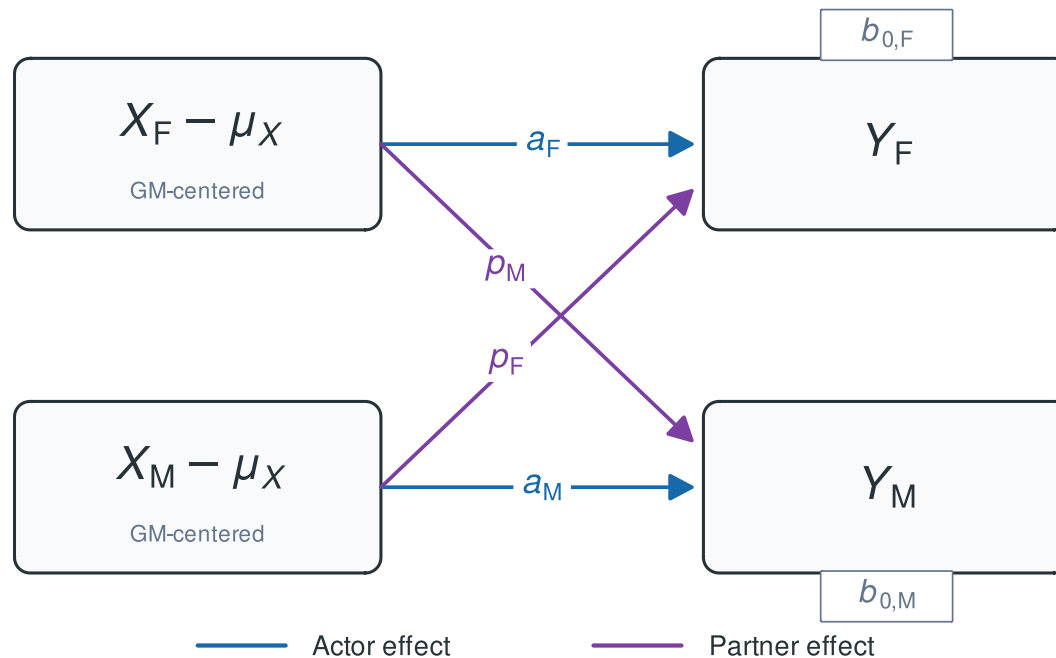
Actor-partner interdependence models

Distinguishable & exchangeable APIM

RQ1 · Actor and partner associations

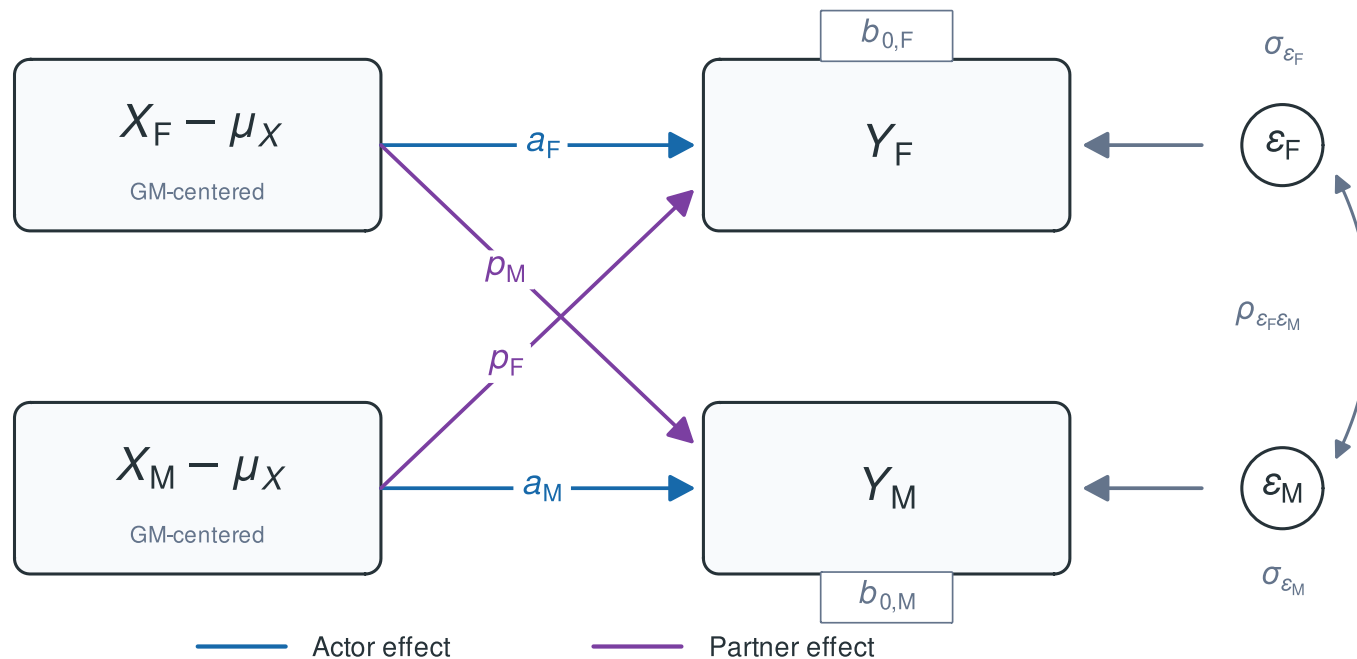
RQ1: Is a person's provided emotional support associated with (a) their own MVPA and (b) their partner's MVPA?

The distinguishable APIM



Actor and partner effects together explain some of the covariance between partners' outcomes.

The distinguishable APIM



Actor and partner effects together explain some of the covariance between partners' outcomes. → But some covariance may remain!

How to estimate actor and partner effects?

Conceptually, we are estimating these two equations in a single model: The member role is written first, and i indexes dyads.

$$Y_{\text{male},i} = b_{0,M} + b_{1,M} \times X_{\text{male},i} + b_{2,M} \times X_{\text{female},i} + \epsilon_{\text{male},i}$$

$$Y_{\text{female},i} = b_{0,F} + b_{1,F} \times X_{\text{female},i} + b_{2,F} \times X_{\text{male},i} + \epsilon_{\text{female},i}$$

Could we just use two separate models?

Could we just use two separate models?

Male model

```
1 male_model <- glmmTMB(  
2  
3   outcome_male ~ X_male + X_female,  
4  
5   data = data  
6 )
```

Female model

```
1 female_model <- glmmTMB(  
2  
3   outcome_female ~ X_female + X_male,  
4  
5   data = data  
6 )
```

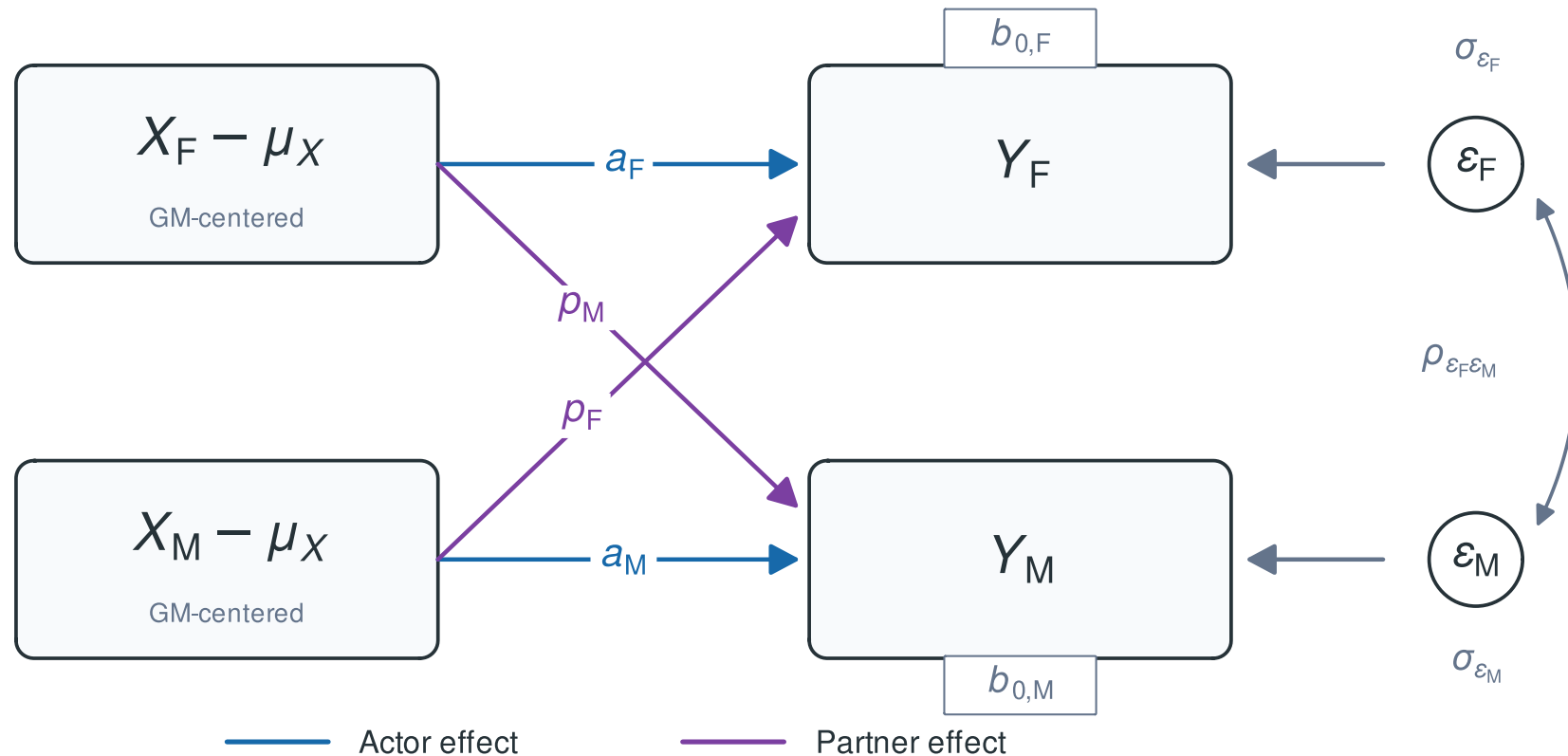
Could we just use two separate models?

Yes, we could! But separate fits:

- Do not directly test whether the actor or partner effects are equal
- Do not pool equal paths into a shared estimate, which can increase power
- Do not jointly estimate residual interdependence between partners
 - Joint modelling shows how much interdependence remains after accounting for the predictors

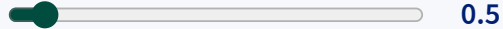
(Iida et al., 2018, pp. 67–69; Kenny & Cook, 1999, pp. 434, 439–440)

Residual interdependence in the distinguishable APIM

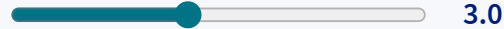


What remains after prediction?

Female residual variance, $\sigma^2_{\epsilon F}$



Male residual variance, $\sigma^2_{\epsilon M}$



Residual correlation, $\rho_{\epsilon F \epsilon M}$



Reset

Residual = observed – predicted

Line length shows each person's residual

Female: residual variance $\sigma^2_{\epsilon F} = 0.5$



Male: residual variance $\sigma^2_{\epsilon M} = 3.0$

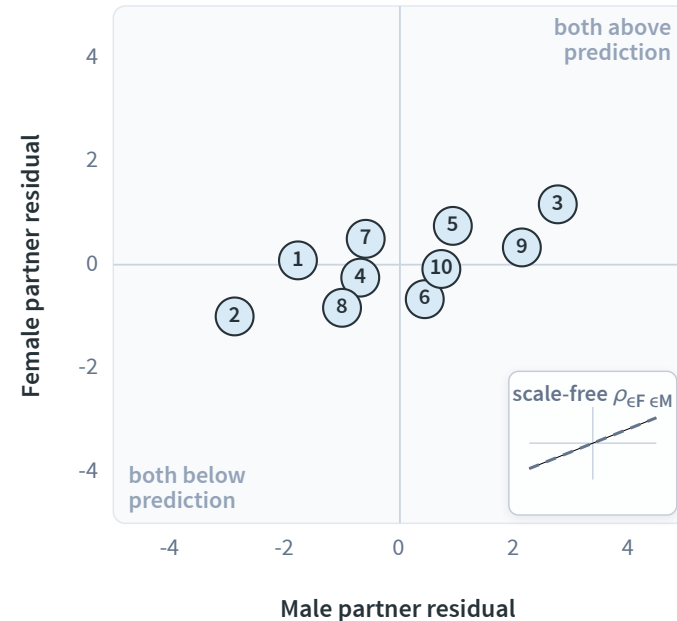


1 2 3 4 5 6 7 8 9 10

Illustrative dyad (arbitrary order)

Residual correlation: do partners move together?

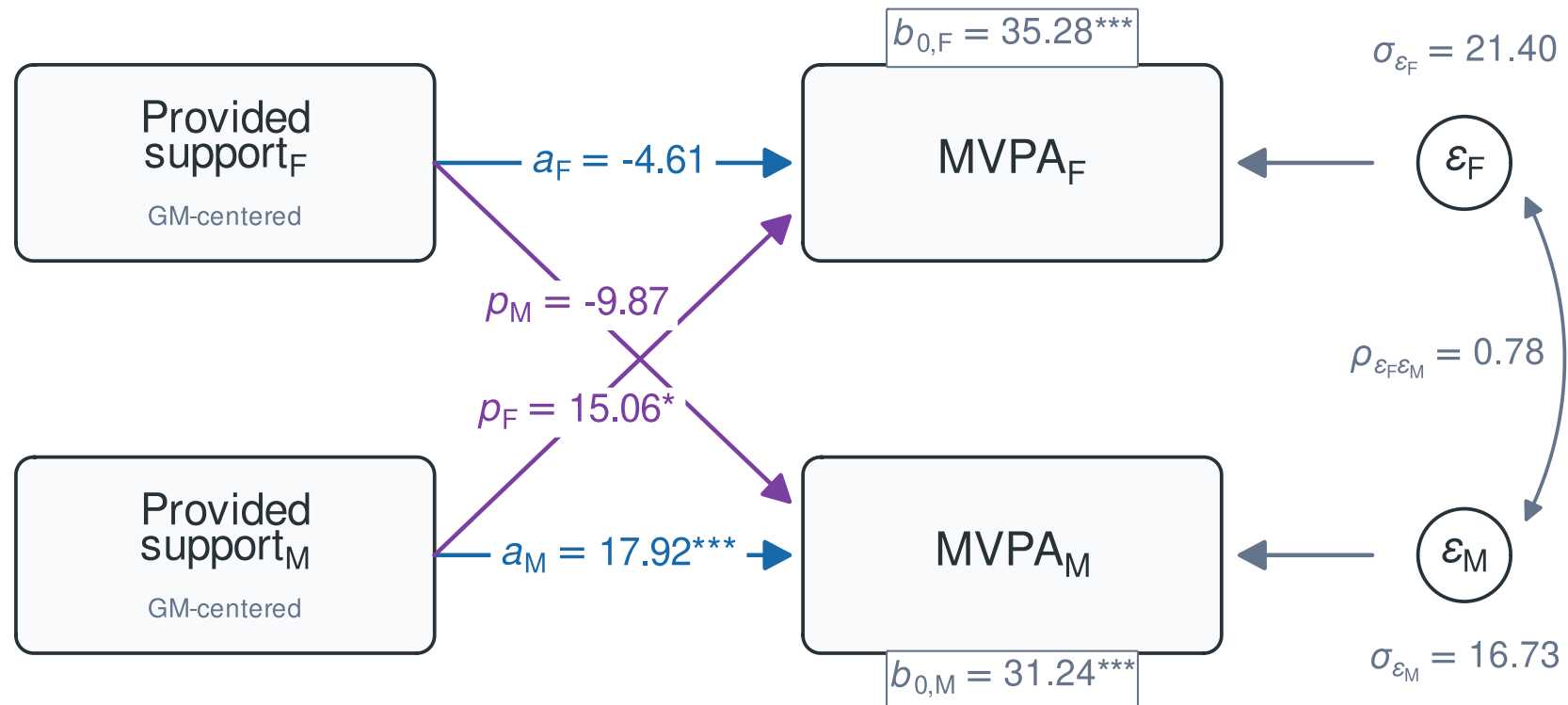
Each point pairs two partners; $\rho_{\epsilon F \epsilon M} = 0.7$ (positive association)



One linked set of dyads: changing a variance rescales one partner's residuals while preserving $\rho_{\epsilon F \epsilon M}$; changing $\rho_{\epsilon F \epsilon M}$ preserves both residual variances. The correlation guide is scale-free, not a fitted regression line.

Fitting the distinguishable APIM

Interpretation →



— Actor effect — Partner effect
 * $p < 0.05$; ** $p < 0.01$; *** $p < 0.001$

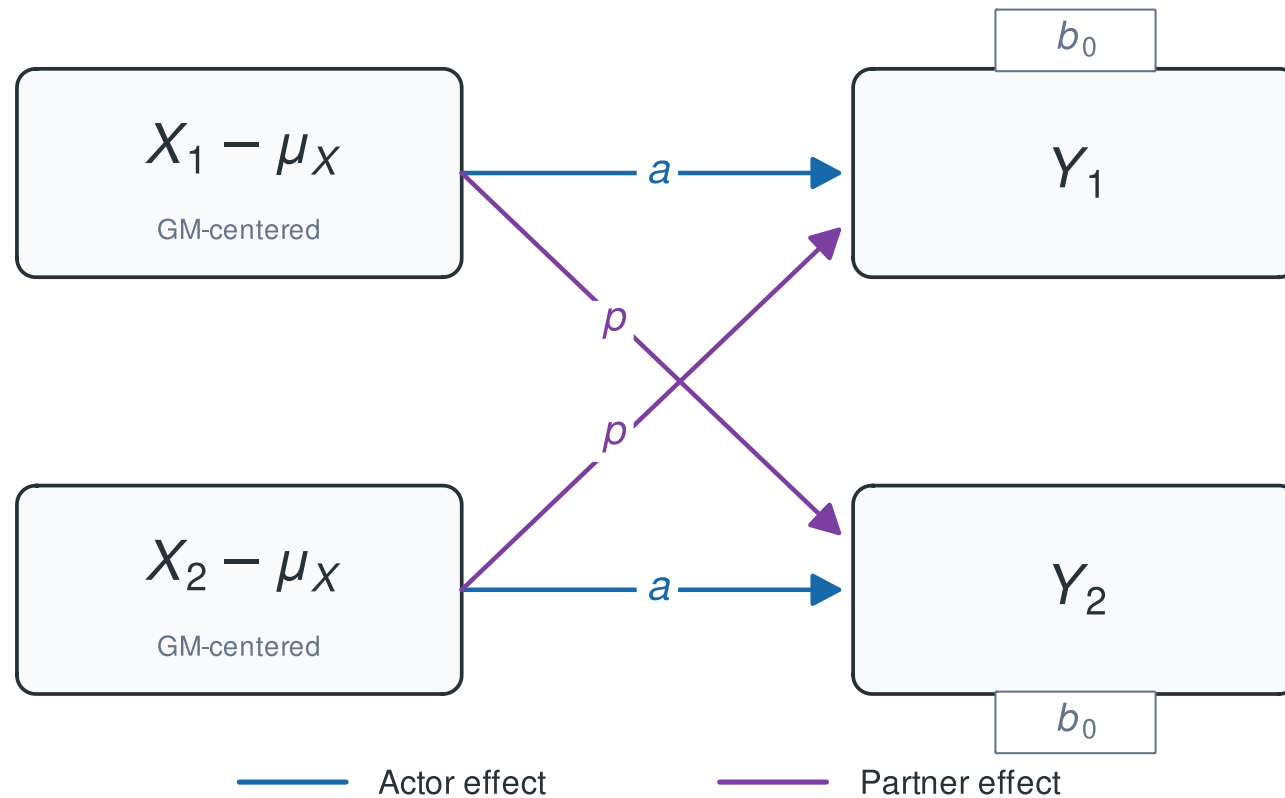
The exchangeable APIM

Sometimes:

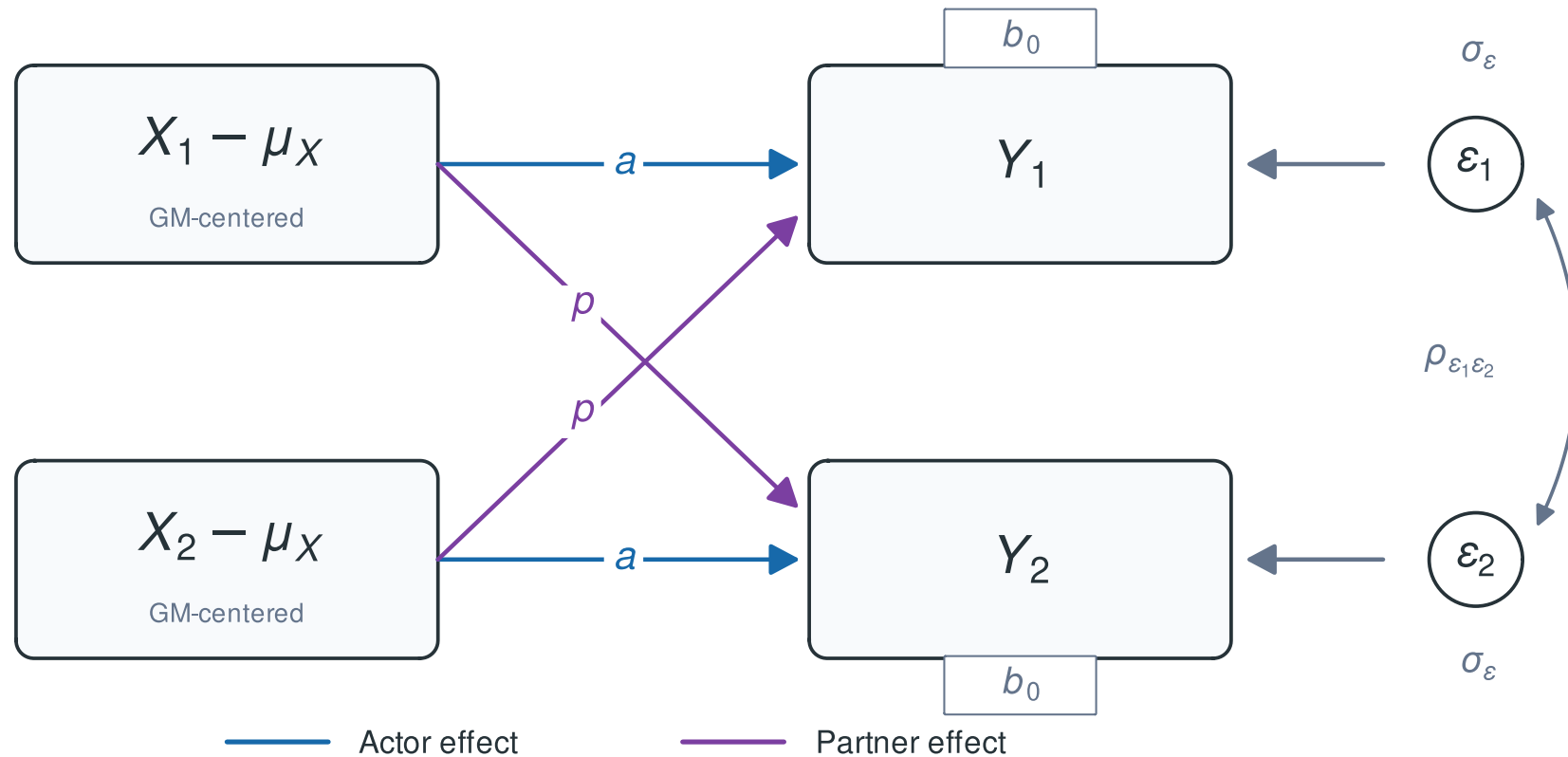
- Partners may not be theoretically meaningfully distinguishable
- No evidence of difference in effects → pool effects for greater power
- We want to formally test distinguishability

→ Then, we may fit an exchangeable model that imposes symmetry

The exchangeable APIM



The exchangeable APIM



Exchangeability constraints

Distinguishable APIM

Role-specific parameters

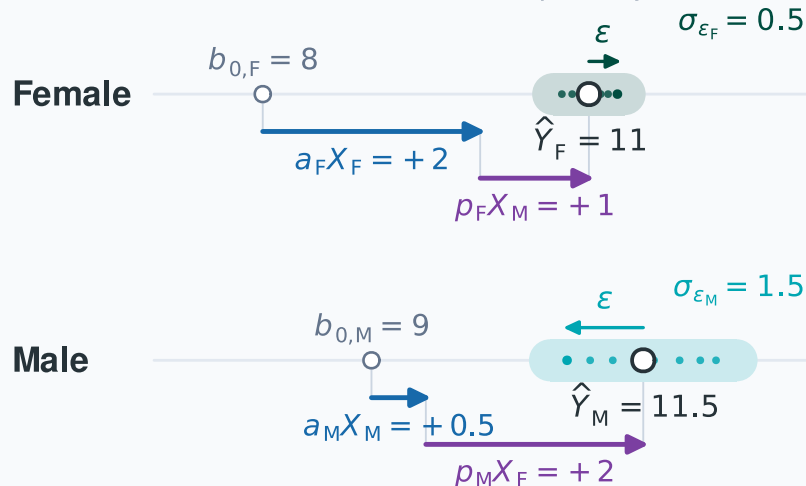
$$Y_F = b_{0,F} + a_F X_F + p_F X_M + \varepsilon_F$$

$$Y_M = b_{0,M} + a_M X_M + p_M X_F + \varepsilon_M$$

GM-centered example: $X_F = +1$, $X_M = +1$

Predictions and residual variation

σ_{ε_F} and σ_{ε_M} estimated separately



Exchangeable APIM

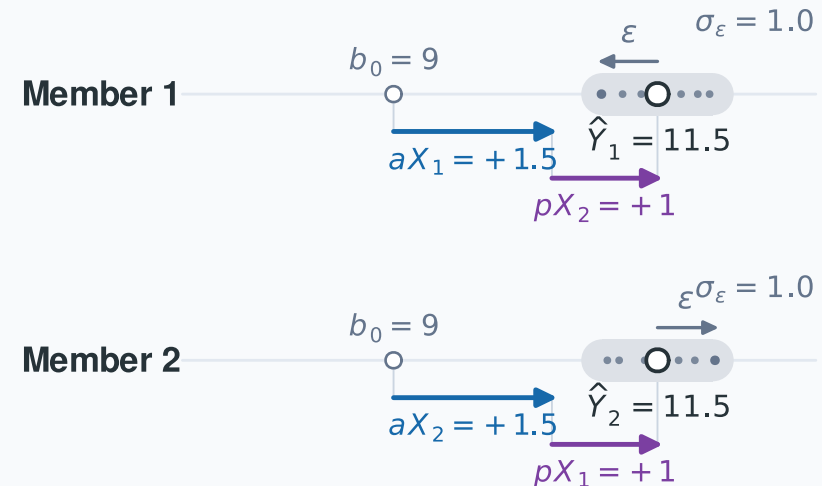
Shared parameters are refitted—not averaged

$$Y_i = b_0 + aX_i + pX_j + \varepsilon_i$$

GM-centered example: $X_1 = +1$, $X_2 = +1$

Predictions and residual variation

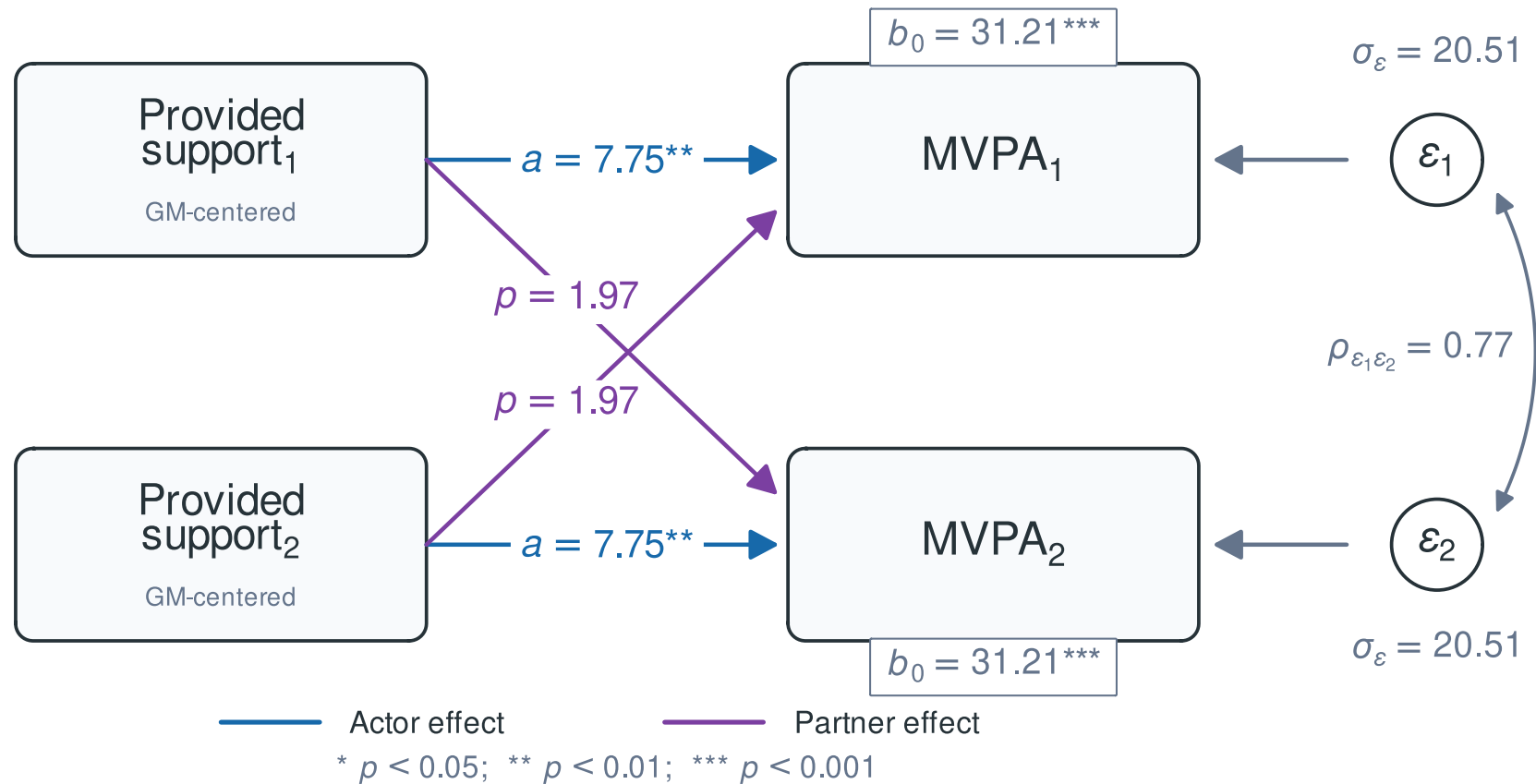
$\sigma_{\varepsilon_1} = \sigma_{\varepsilon_2} = \sigma_{\varepsilon}$



Symmetry constraints do not imply identical residuals; $\rho_{\varepsilon_F \varepsilon_M}$ and $\rho_{\varepsilon_1 \varepsilon_2}$ remain estimated.

Fitting the exchangeable APIM

Interpretation →



Testing exchangeability

```
1 library(dyadMLM)
2
3 compare_nested_models(
4   exchangeable_apim,
5   distinguishable_apim
6 )
```

Likelihood-ratio test for nested models fitted to equivalent data

Assumes mathematical nesting and an appropriate chi-squared reference distribution.

	Df	AIC	BIC	logLik	deviance	Chisq	Chi	Df	Pr(>Chisq)
exchangeable_apim	5	617.55	628.94	-303.78	607.55				
distinguishable_apim	9	611.59	632.08	-296.80	593.59	13.962		4	0.007418

```
exchangeable_apim
distinguishable_apim **
---
```

Signif. codes: 0 '***' 0.001 '**' 0.01 '*' 0.05 '.' 0.1 ' ' 1

Conclusion (5% level): The likelihood-ratio test provides evidence that `distinguishable\_apim` fits better than `exchangeable\_apim` (p = 0.00742).

Level-and-difference models

Dyad-individual model & dyadic score model

Shifting the analytical lens

Sometimes, actor and partner associations are not the primary interest.

Instead, we may want to understand:

- How couples compare with other couples
- How partners stand relative to one another within a couple

This shifts the focus to **dyadic levels and within-dyad differences**.

- For exchangeable dyads, use the **dyad-individual model (DIM)**
- For distinguishable dyads, use the **dyadic score model (DSM)**

RQ2 · Dyad levels and differences

RQ2: How are couples' average levels and partner differences in provided emotional support associated with the couple-average MVPA and partner differences in MVPA?

The dyad-individual model (DIM)

The DIM is:

- A re-parametrization of the **exchangeable** APIM!
- We decompose predictors into two variables:
 - Dyad mean (GM-centered): $\bar{X} - \mu_X$
 - Within-dyad member deviation: $X_i - \bar{X}$

In other words, these predictors express:

- A couple's average level compared with the average of all couples
- A partner's level compared with the average of their couple

DIM predictors are APIM predictors in disguise!

Provided support coordinates

Reset

APIM coordinates

Actor, x_{actor} 0.00

Partner, x_{partner} 0.00

DIM coordinates

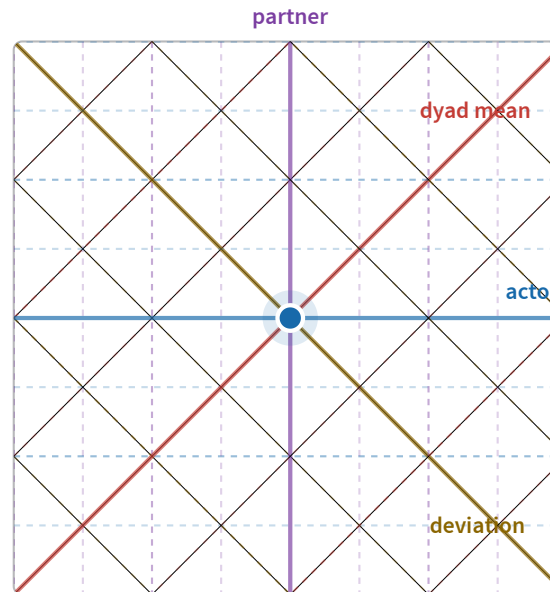
Dyad mean, x_{mean} 0.00

Member deviation, x_{dev} 0.00

$$x_{\text{mean}} = (x_{\text{actor}} + x_{\text{partner}}) / 2$$

$$x_{\text{dev}} = (x_{\text{actor}} - x_{\text{partner}}) / 2$$

APIM $7.75 \times 0.00 + 1.97 \times 0.00 = 0.00$
 DIM $9.72 \times 0.00 + 5.78 \times 0.00 = 0.00$
 Fitted slopes: $b_{\text{mean}} = a + p = 9.72$; $b_{\text{dev}} = a - p = 5.78$



Shared dyad level

Both members +1

$$b_{\text{mean}} = a + p$$

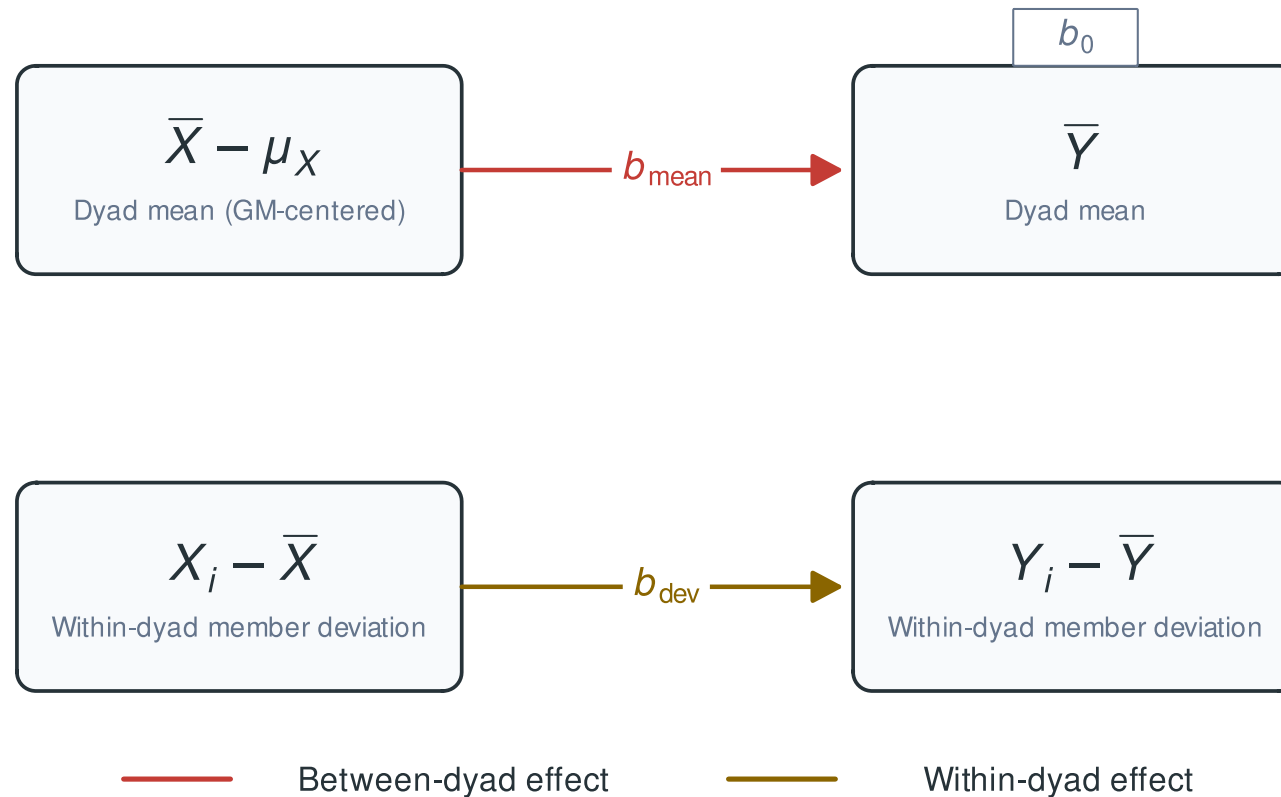
Within-dyad member deviation

Actor +1, partner -1

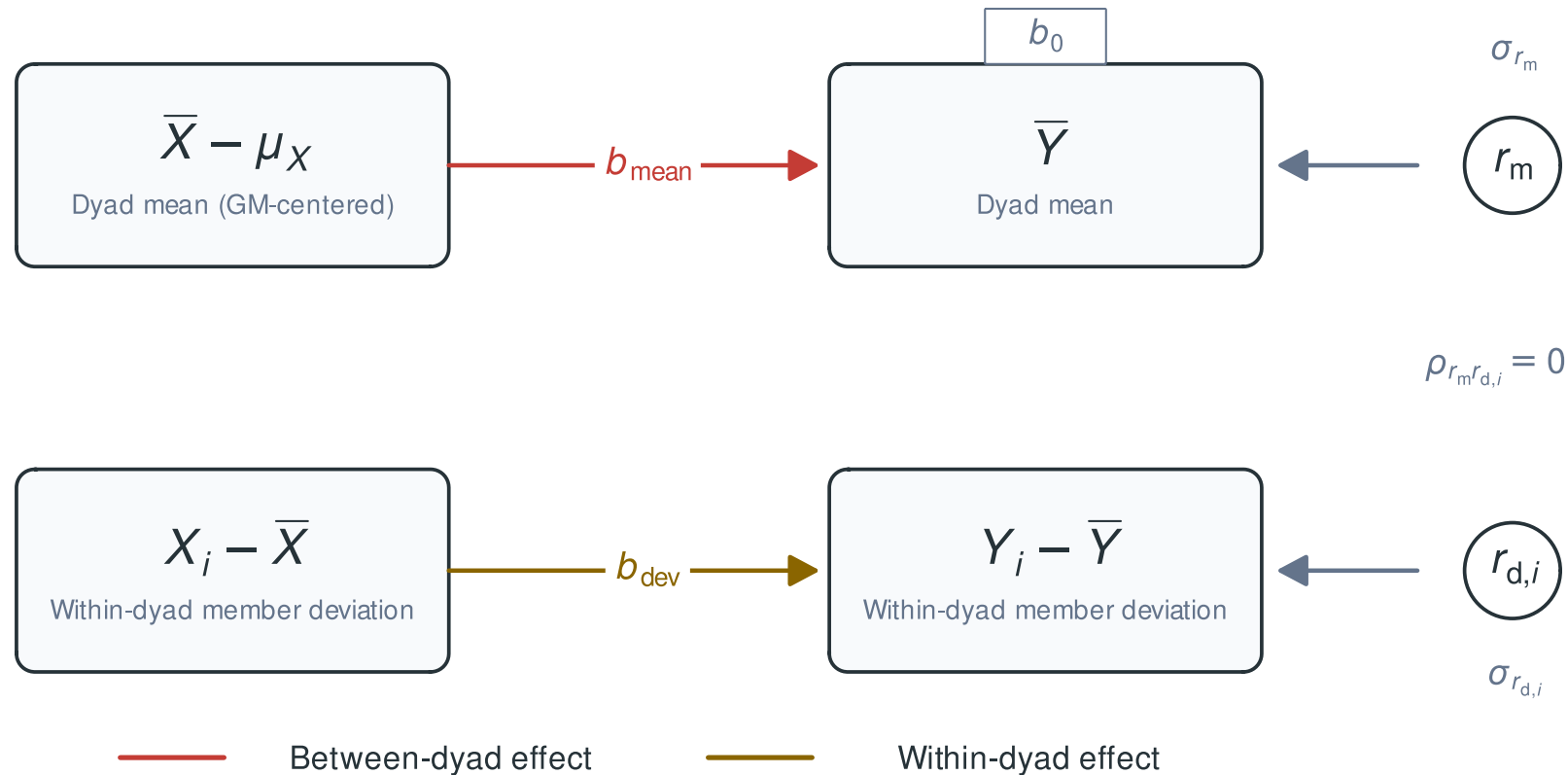
$$b_{\text{dev}} = a - p$$

Drag the dot or move either set of sliders.
Both equations give the same fitted change in MVPA.

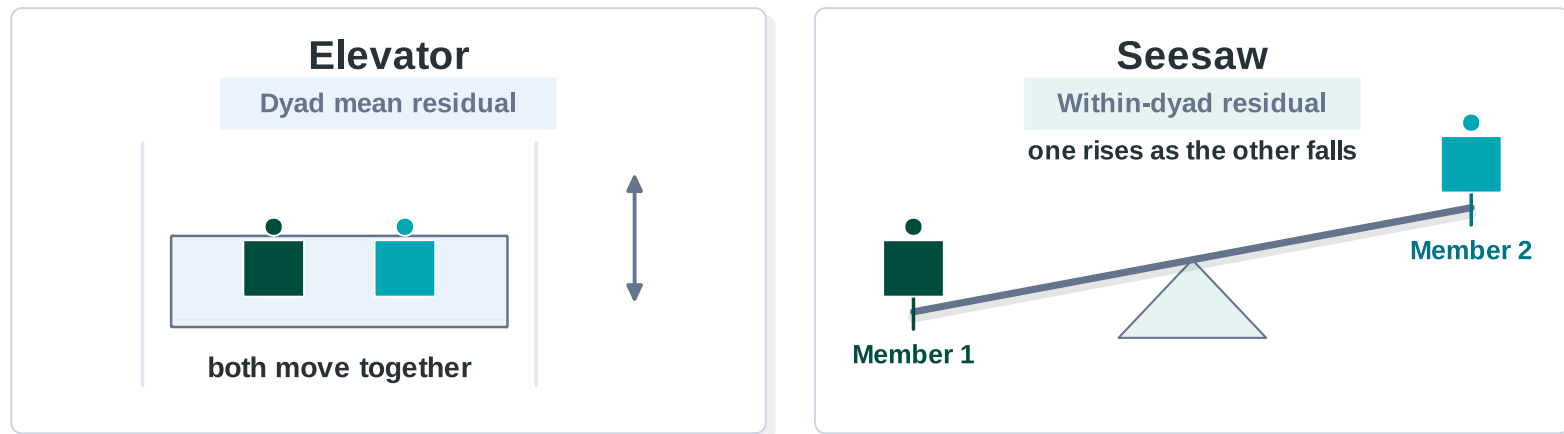
The DIM



The DIM



Why are the mean and deviation residuals uncorrelated?



Swap the arbitrary member labels: $r_M \mapsto r_M$ $r_D \mapsto -r_D$

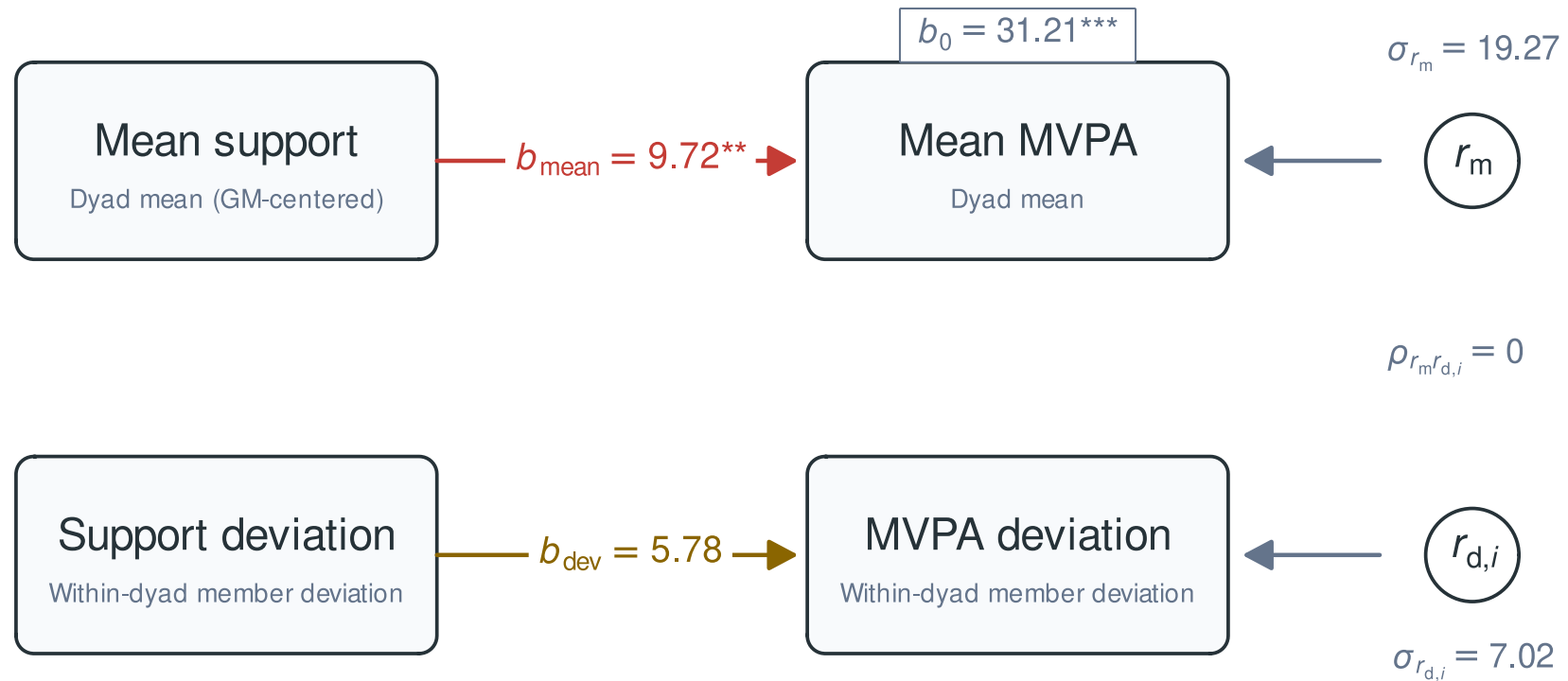
Exchangeability requires the same covariance after relabelling:

$$\text{Cov}(r_M, r_D) = \text{Cov}(r_M, -r_D) = -\text{Cov}(r_M, r_D) \implies \text{Cov}(r_M, r_D) = 0$$

Zero does not mean independent partners: $\text{Cov}(e_1, e_2) = \text{Var}(r_M) - \text{Var}(r_D)$
Their residual association is encoded by the relative elevator and seesaw variances.

Fitting the DIM

Interpretation →



— Between-dyad effect — Within-dyad effect
 * $p < 0.05$; ** $p < 0.01$; *** $p < 0.001$

DIM to exchangeable APIM coefficients

- Once we fit an APIM, we have already fitted a DIM—and vice versa.
- We can transform values from a fitted APIM into DIM values.

DIM to exchangeable APIM coefficients

The intercept is omitted; APIM predictors are grand-mean centered.

For a focal person, let $X_{\text{self}} = 1$, $X_{\text{partner}} = 1$,
so that in DIM coordinates: $X_{\text{mean}} = 1$, $X_{\text{dev,self}} = 0$.

So,

$$\hat{Y}_{\text{self}} = 1 \times a + 1 \times p$$

implies

$$\hat{Y}_{\text{self}} = 1 \times b_{\text{mean}} + 0 \times b_{\text{dev}} = b_{\text{mean}}.$$

Therefore,

$$b_{\text{mean}} = a + p.$$

DIM to exchangeable APIM coefficients

The intercept is omitted; APIM predictors are grand-mean centered.

For a focal person, let $X_{\text{self}} = 1$, $X_{\text{partner}} = -1$,

so that in DIM coordinates: $X_{\text{mean}} = 0$, $X_{\text{dev,self}} = 1$.

So,

$$\hat{Y}_{\text{self}} = 1 \times a + (-1) \times p$$

implies:

$$\hat{Y}_{\text{self}} = 0 \times b_{\text{mean}} + 1 \times b_{\text{dev}} = b_{\text{dev}}.$$

Therefore,

$$b_{\text{dev}} = a - p.$$

DIM to exchangeable APIM coefficients

Provided support coordinates

Reset

APIM coordinates

Actor, x_{actor} 0.00

Partner, x_{partner} 0.00

DIM coordinates

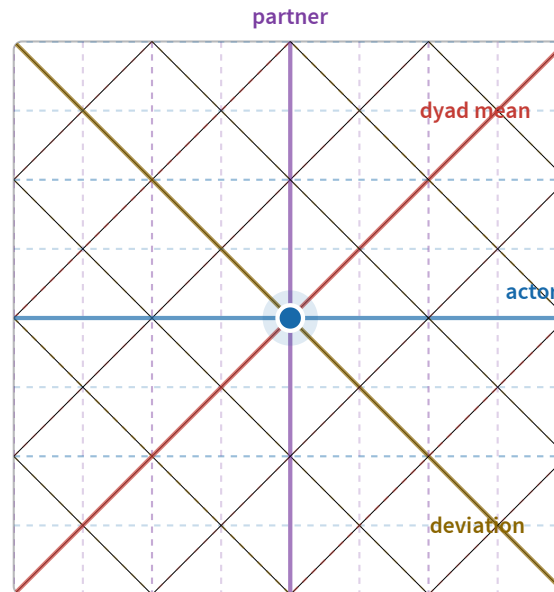
Dyad mean, x_{mean} 0.00

Member deviation, x_{dev} 0.00

$$x_{\text{mean}} = (x_{\text{actor}} + x_{\text{partner}}) / 2$$

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APIM $7.75 \times 0.00 + 1.97 \times 0.00 = 0.00$
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Shared dyad level

Both members +1

$$b_{\text{mean}} = a + p$$

Within-dyad member deviation

Actor +1, partner -1

$$b_{\text{dev}} = a - p$$

Drag the dot or move either set of sliders.
Both equations give the same fitted change in MVPA.

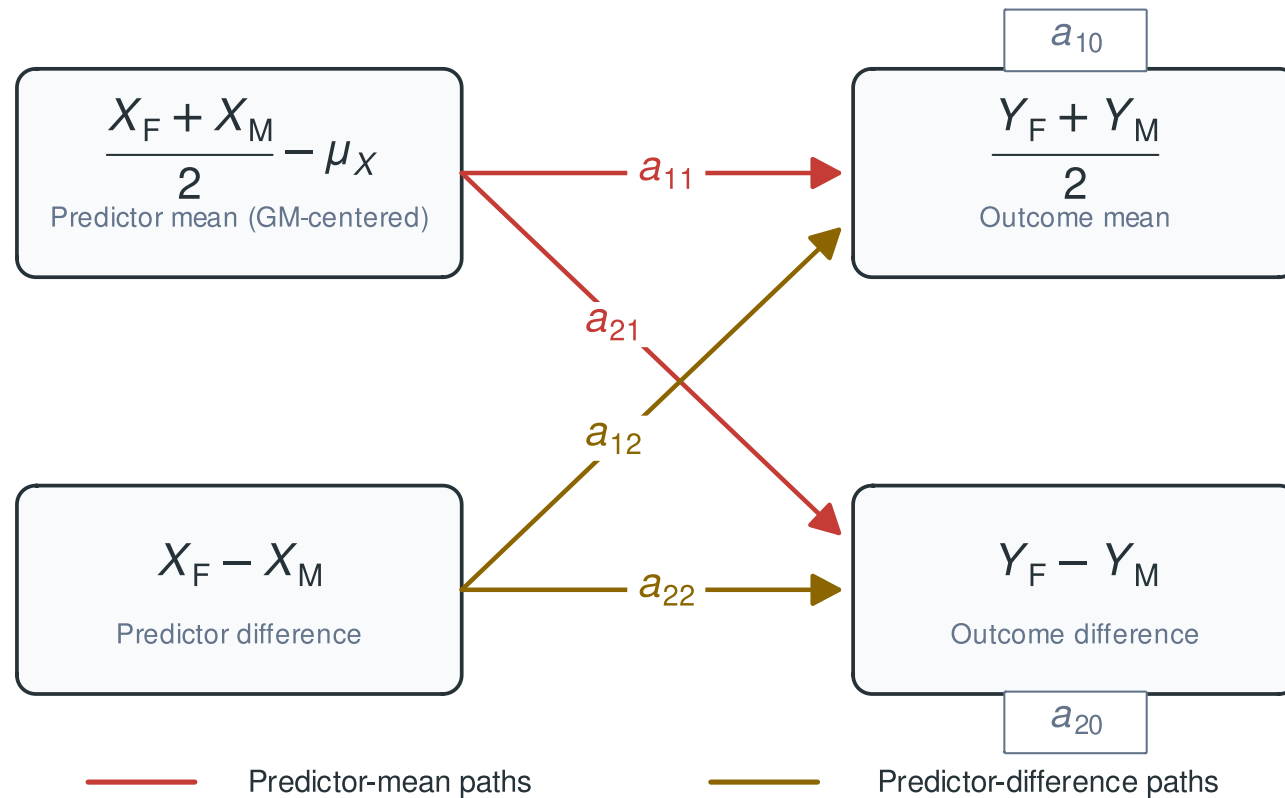
The dyadic score model (DSM)

What if we want DIM-style interpretation but have distinguishable dyads?

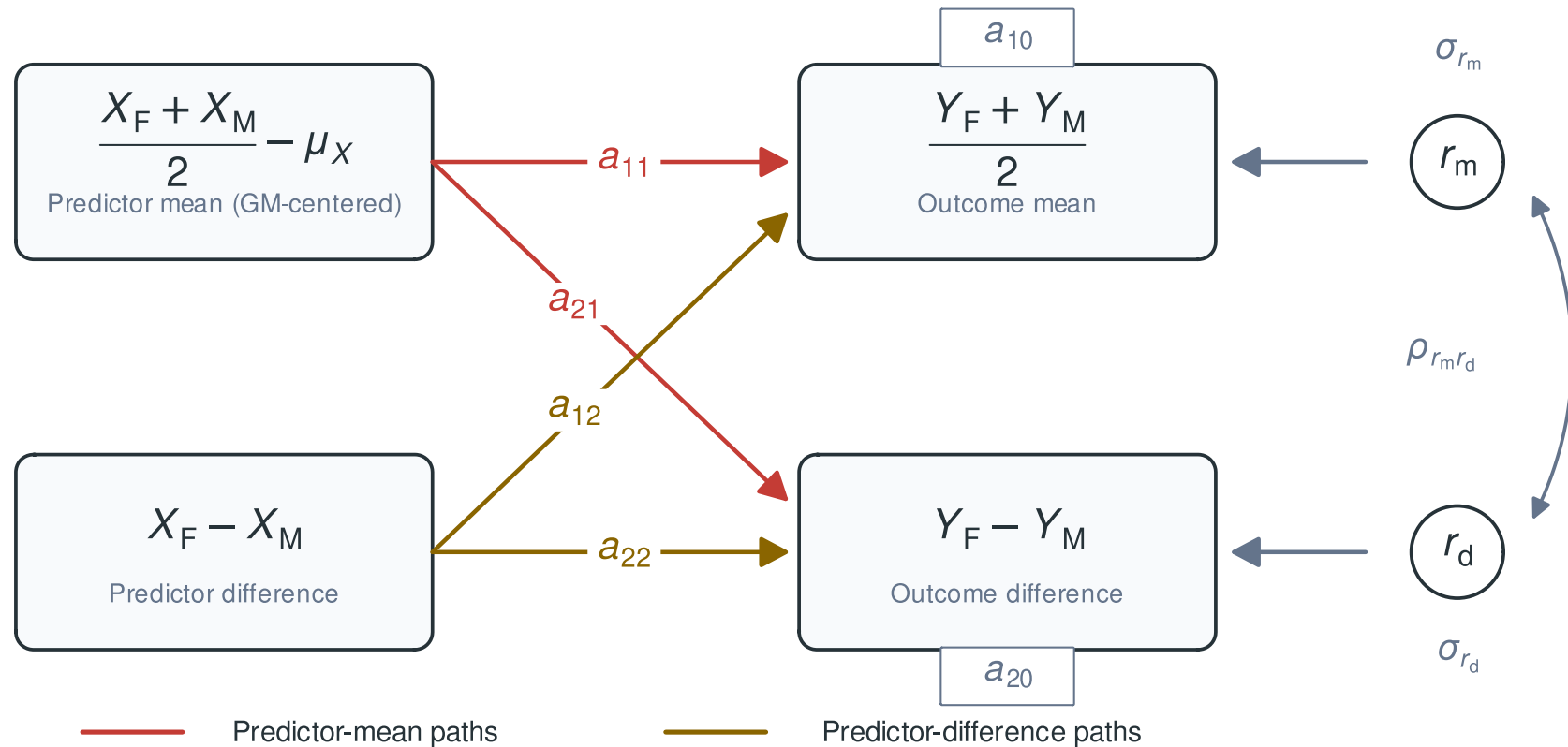
The DSM is:

- The unconstrained distinguishable version of the DIM
- A re-parametrization of the distinguishable APIM
- **DIM**: deviation from the couple mean $X_i - \bar{X}$
 - opposite for each partner
- **DSM**: meaningful directed differences $X_{\text{female}} - X_{\text{male}}$
 - repeated for both partners

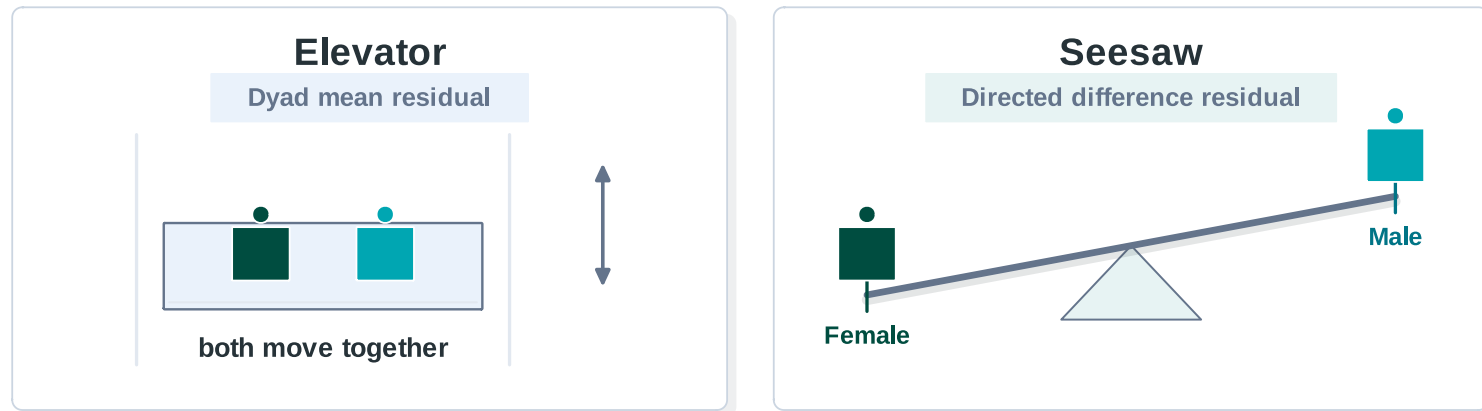
The DSM



The DSM



Why may the DSM mean and difference residuals correlate?



Substantive labels:

$$D_Y = Y_F - Y_M$$

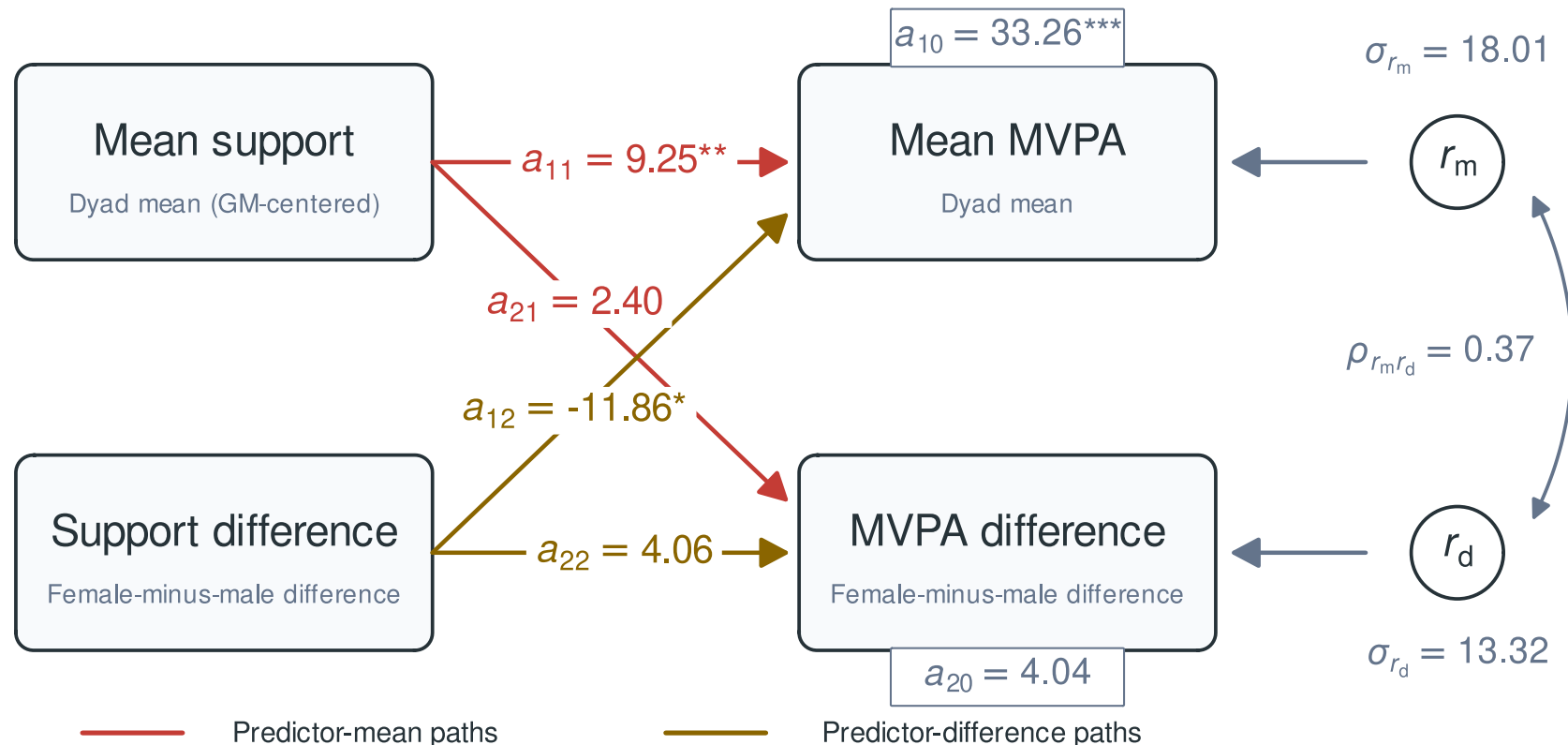
Swapping Female and Male changes the meaning and sign of the difference, so label-swapping is not a symmetry of the DSM.

$\text{Cov}(r_M, r_D)$ is not constrained to zero.

A positive $\rho_{r_M r_D}$ means: couples whose outcomes are higher than predicted on average also tend to have a larger female-male difference than predicted.

Fitting the DSM

Interpretation →



* $p < 0.05$; ** $p < 0.01$; *** $p < 0.001$

DSM to distinguishable APIM coefficients

- Once we fit a DSM, we have already fitted a distinguishable APIM—and vice versa.
- We can back-transform the DSM fixed effects into APIM coefficients:

$$b_{0,F} = a_{10} + \frac{1}{2}a_{20},$$

$$b_{0,M} = a_{10} - \frac{1}{2}a_{20},$$

$$b_{1,F} = \frac{1}{2}a_{11} + a_{12} + \frac{1}{4}a_{21} + \frac{1}{2}a_{22},$$

$$b_{1,M} = \frac{1}{2}a_{11} - a_{12} - \frac{1}{4}a_{21} + \frac{1}{2}a_{22},$$

$$b_{2,F} = \frac{1}{2}a_{11} - a_{12} + \frac{1}{4}a_{21} - \frac{1}{2}a_{22},$$

$$b_{2,M} = \frac{1}{2}a_{11} + a_{12} - \frac{1}{4}a_{21} - \frac{1}{2}a_{22}.$$

Here, b_1 is the actor effect and b_2 is the partner effect. The APIM predictors and DSM couple mean now use the same pooled grand-mean reference, so no additional centering adjustment is needed for the intercepts.

Common fate model

Modeling dyadic constructs

When the construct is dyadic

Sometimes, a construct describes the **couple as a unit**, rather than either partner individually.

- Both partners report on the same dyadic phenomenon.
- Differences between their reports are not the substantive focus.
- Interest lies in the couple's underlying dyadic level.

For our data example:

- Collaborative planning as a dyadic predictor
- Joint physical activity as a dyadic outcome

RQ3 · Shared dyadic constructs

RQ3: How is collaborative planning associated with joint physical activity in romantic couples?

Measurement - CFM predictor

Dyadic predictor: collaborative planning

Rough English translation of the original German item

“We have already planned precisely for tomorrow when, where, and how we will be physically active together.”

Adapted from Scholz et al. (2008)

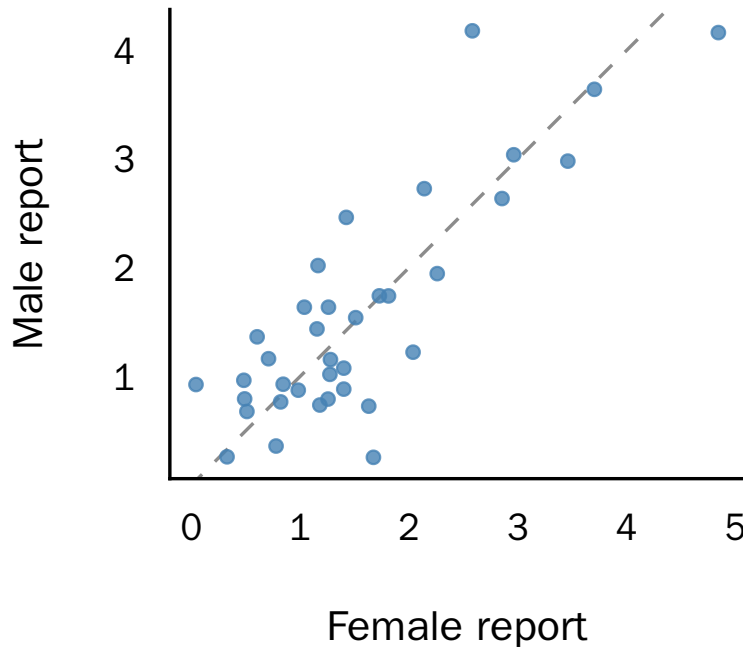
0 = *not at all true today*

5 = *completely true today*

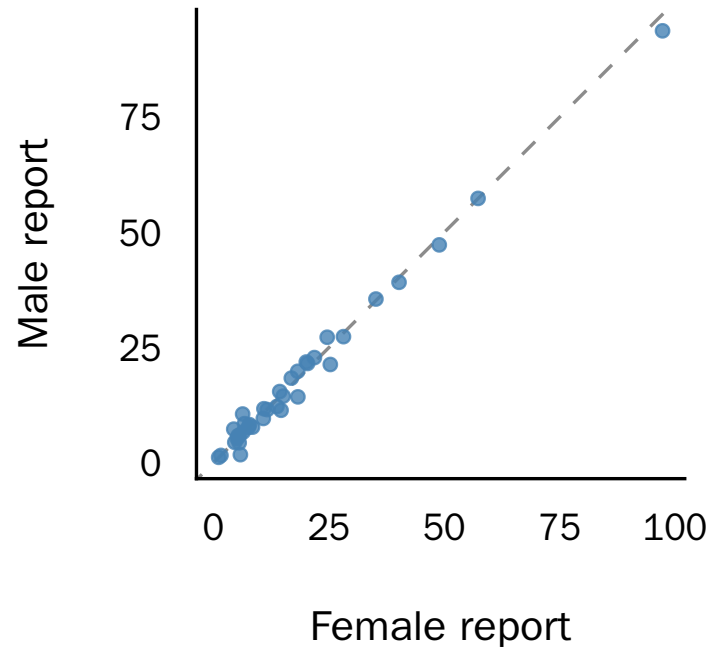
We aggregate each person's ratings into their **average daily collaborative planning** across the 55 days.

Do partners report similar dyadic levels?

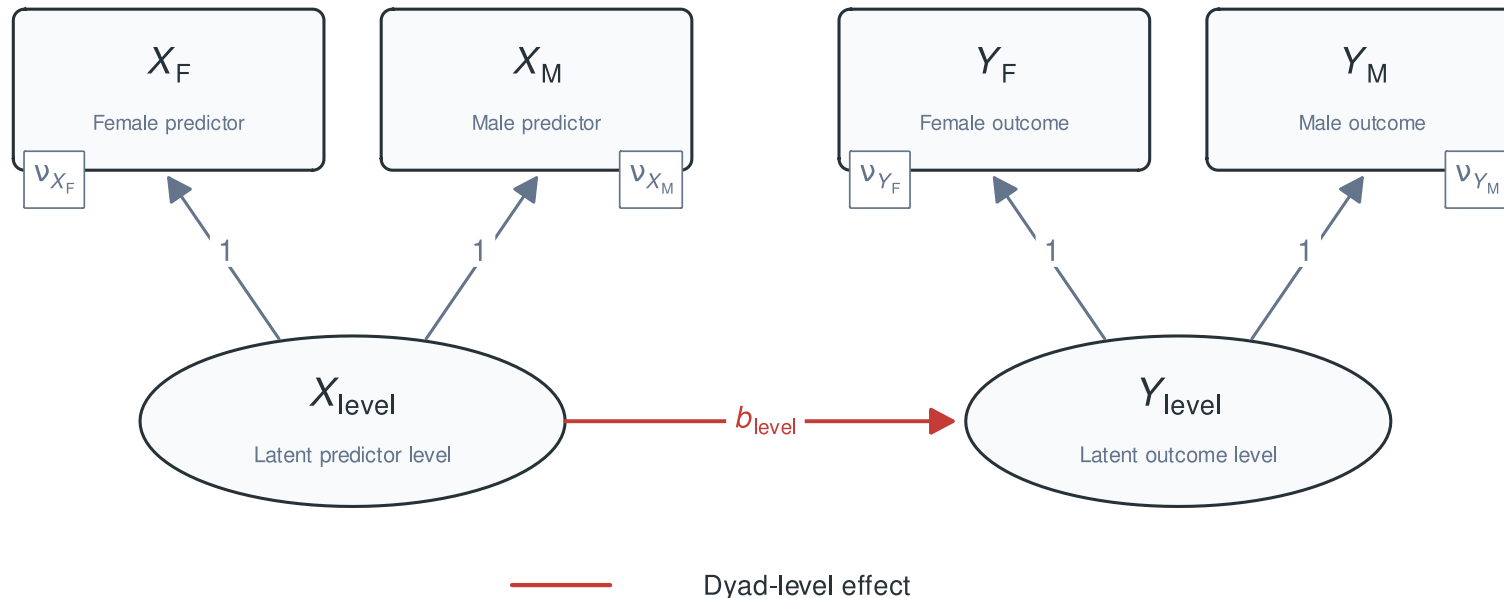
Collaborative planning (0–5)



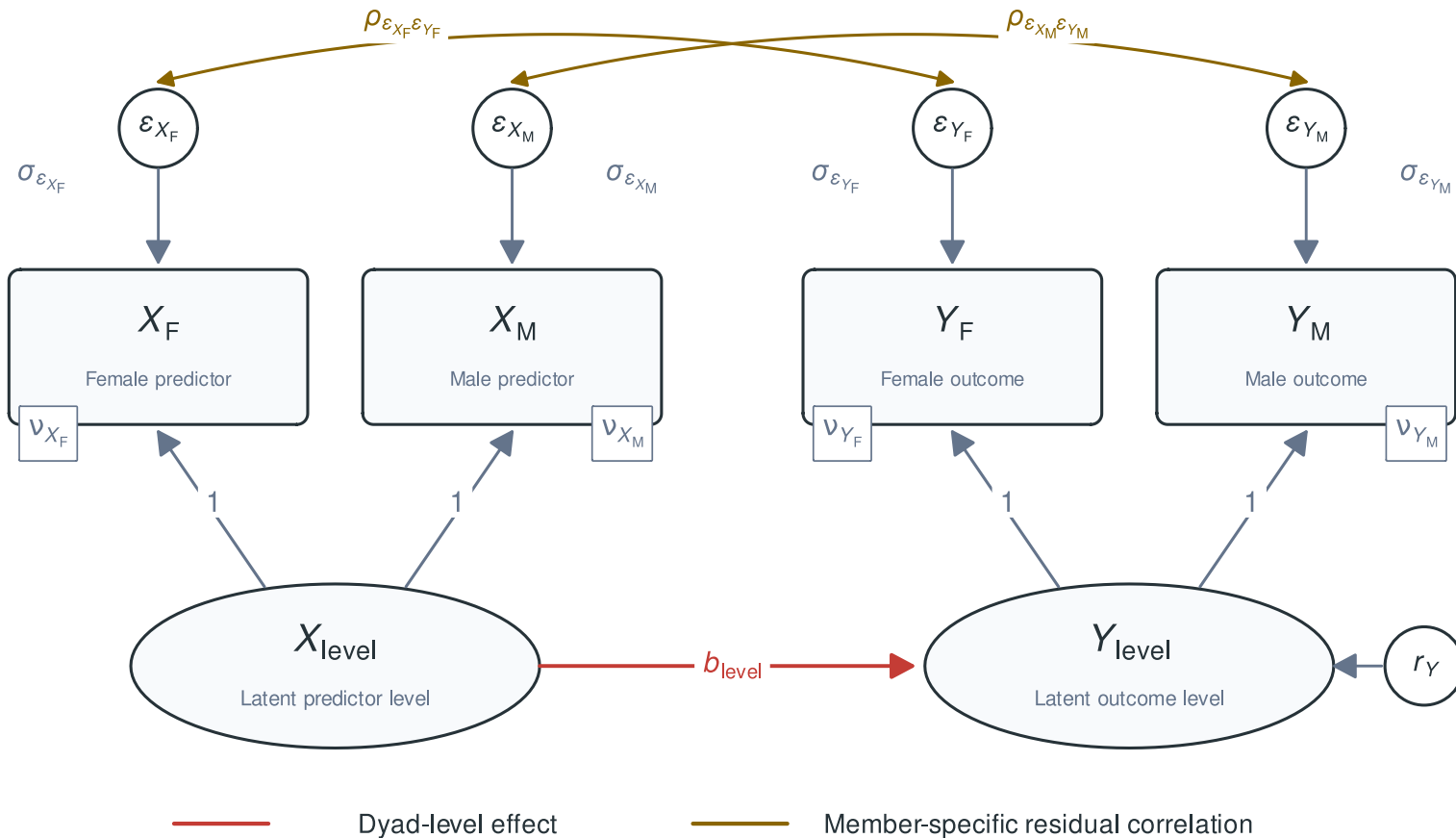
Joint MVPA (minutes/day)



The distinguishable CFM

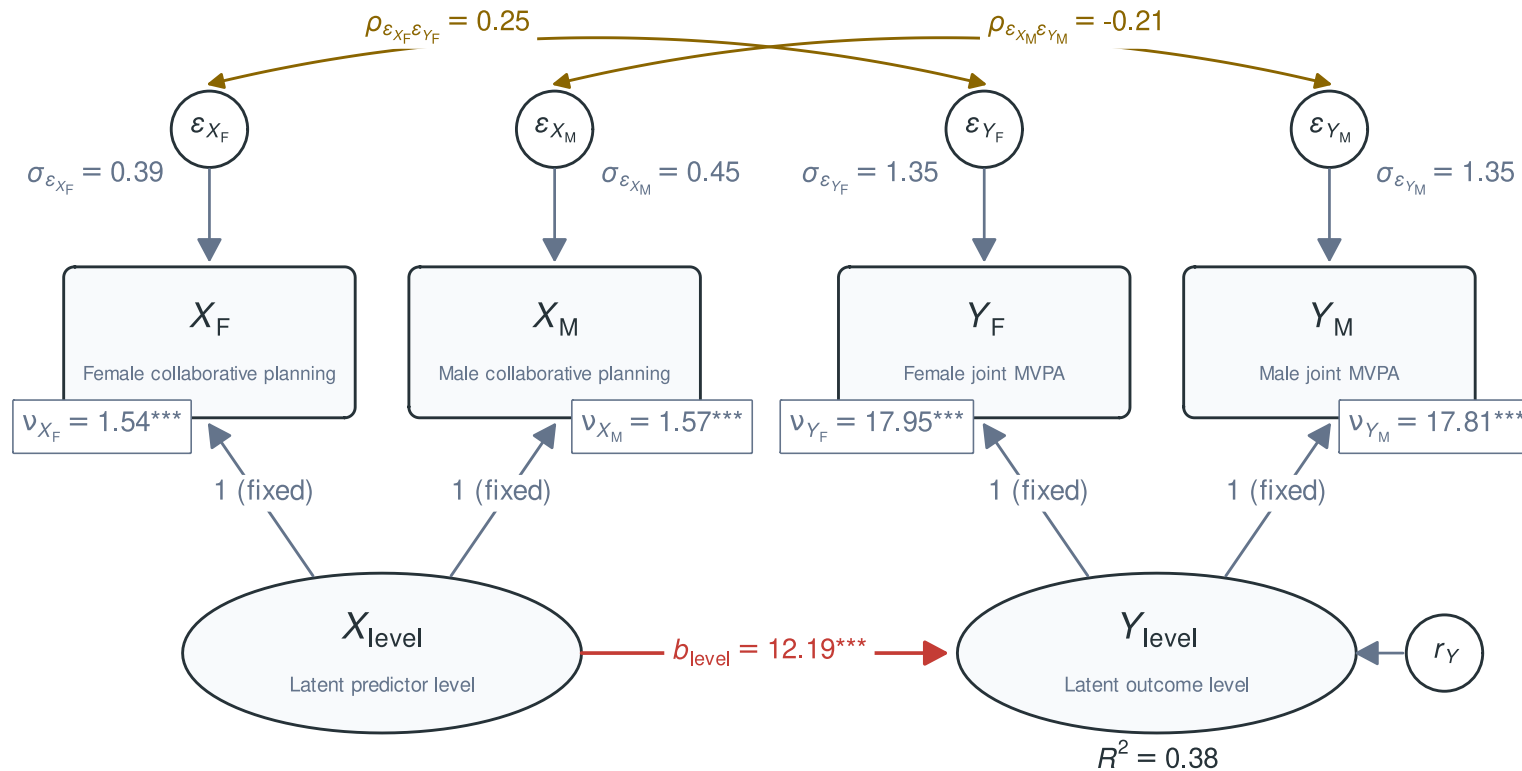


The distinguishable CFM



Fitted distinguishable CFM

Model constraint: The female and male joint-MVPA residual variances were constrained equal to obtain admissible fit.



— Dyad-level effect — Member-specific residual correlation

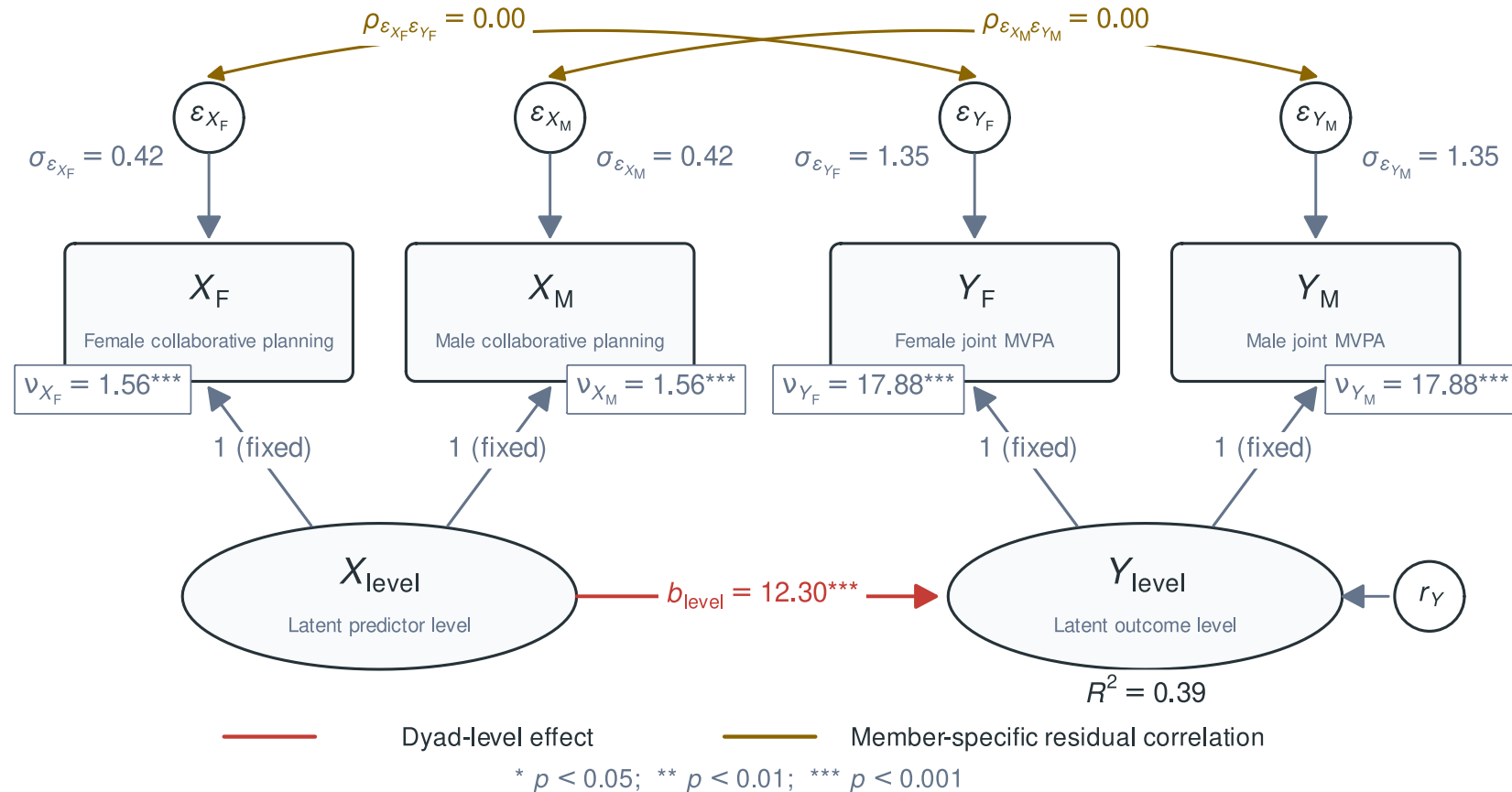
* $p < 0.05$; ** $p < 0.01$; *** $p < 0.001$

When should we model a CFM as exchangeable?

- Partner positions are arbitrary, or theory and the data support treating the measurement process as invariant across roles.
- Swapping the partner labels should then leave the model unchanged.
- We constrain corresponding partner parameters to be equal:
 - **intercepts:** the same expected report level
 - **residual variances:** the same amount of indicator-specific variation
 - **same-member residual associations:** the same residual predictor–outcome association for both partners

Ledermann & Macho (2009); Peugh et al. (2013)

Fitted CFM with partner-role equality constraints



Likelihood-ratio test of the remaining partner-role equality constraints: $\Delta\chi^2(4) = 0.65, p = .958$; no detectable loss of fit.

RQ3 result

RQ3: In this small observational sample, a one-unit higher latent collaborative-planning level was associated with 12.30 more minutes of joint MVPA per day at the couple level ($R^2 = 0.39$).

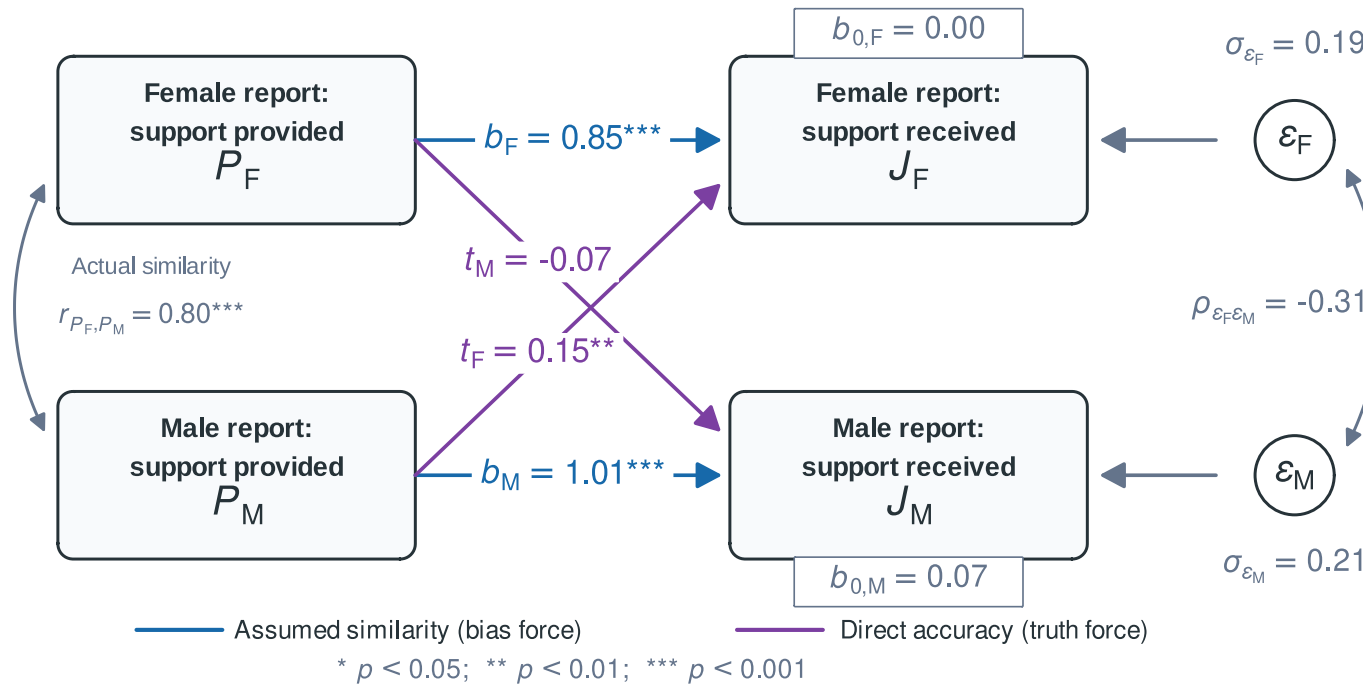
Other interesting dyadic models to consider

Other dyadic models and designs

- **Truth and Bias model:** Separates direct accuracy in judging a partner from directional bias and assumed-similarity bias ([West & Kenny, 2011](#)).
- **Mutual-influence model:** Tests whether partners' outcomes directly and reciprocally influence one another ([Kenny, 1996](#)).
- **APIM mediation model:** Traces whether actor and partner associations operate through either partner's mediator ([Ledermann et al., 2011](#)).
- **Dyadic response surface analysis:** Tests whether partner similarity, discrepancy, or particular combinations of scores relate to an outcome ([Schönbrodt et al., 2018](#)).
- **One-with-many and Social Relations models:** Extend dyadic analysis to repeated relationships with several partners or round-robin groups, separating person and relationship components ([Kenny et al., 2006](#); [Kenny & La Voie, 1984](#)).
- **Network models:** Explain the formation and evolution of ties within an interconnected group, including reciprocity, transitivity, and actor-oriented network change ([Holland & Leinhardt, 1981](#); [Snijders, 2001](#)).

The Truth and Bias model

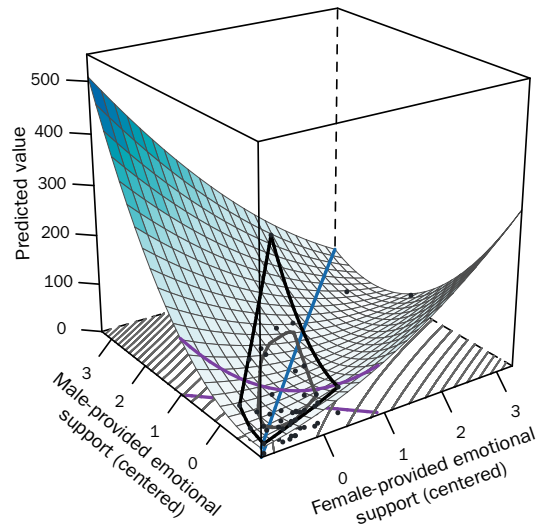
(Kenny & Acitelli, 2001; West & Kenny, 2011)



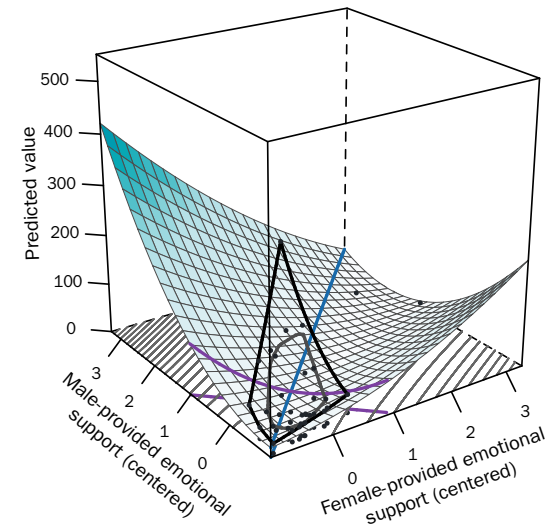
- The partner's report is the researcher-defined “truth”, not necessarily an objective truth.
- After truth-mean centering, b_0 is **directional bias**.

Dyadic response surface analysis (Schönbrodt et al., 2018)

Female total MVPA (min/day)



Male total MVPA (min/day)



- **Line of incongruence** curves upward; no clear slope or curvature along the **line of congruence**.
- **Interpretation:** No similarity-benefit pattern; instead, some evidence of a dissimilarity pattern.

Q&A and discussion

Questions?

- Discuss the different approaches briefly with your neighbor: which ones might be most relevant for your own data/research questions? (ca. 5 min)
- Share with the group.

Prepare for later exercises in R

- Go to <https://pascal-kueng.github.io/dyadMLM/workshop/>
- Link is also in the Teams channel
- Download and unzip all workshop materials
- Start R from that folder (by opening one of the files)

Run this in the console to ensure all relevant packages are installed and up to date:

```
1 source("00_setup.R")
```

References

- Amireault, S., & Godin, G. (2015). The godin–shephard leisure-time physical activity questionnaire: Validity evidence supporting its use for classifying healthy adults into active and insufficiently active categories. *Perceptual and Motor Skills*, 120(2), 604–622. <https://doi.org/10.2466/03.27.PMS.120v19x7>
- Bolger, N., Zuckerman, A., & Kessler, R. C. (2000). Invisible support and adjustment to stress. *Journal of Personality and Social Psychology*, 79(6), 953–961. <https://doi.org/10.1037/0022-3514.79.6.953>
- Höhener, P. S., Tobias, R., Allen, J. M., Küng, P., & Scholz, U. (2026). Effectiveness of smartphone-based dyadic interventions to increase physical activity in romantic couples: Microrandomized trial. *JMIR mHealth and uHealth*, 14, e67136. <https://doi.org/10.2196/67136>
- Holland, P. W., & Leinhardt, S. (1981). An exponential family of probability distributions for directed graphs. *Journal of the American Statistical Association*, 76(373), 33–50. <https://doi.org/10.1080/01621459.1981.10477598>
- Iida, M., Seidman, G., & Shrout, P. E. (2018). Models of interdependent individuals versus dyadic processes in relationship research. *Journal of Social and Personal Relationships*, 35(1), 59–88. <https://doi.org/10.1177/0265407517725407>
- Kenny, D. A. (1996). Models of Non-Independence in Dyadic Research. *Journal of Social and Personal Relationships*, 13(2), 279–294. <https://doi.org/10.1177/0265407596132007>
- Kenny, D. A., & Acitelli, L. K. (2001). Accuracy and bias in the perception of the partner in a close relationship. *Journal of Personality and Social Psychology*, 80(3), 439–448. <https://doi.org/10.1037/0022-3514.80.3.439>
- Kenny, D. A., & Cook, W. (1999). Partner effects in relationship research: Conceptual issues, analytic difficulties, and illustrations. *Personal Relationships*, 6(4), 433–448. <https://doi.org/10.1111/j.1475-6811.1999.tb00202.x>
- Kenny, D. A., Kashy, D. A., & Cook, W. L. (2006). *Dyadic data analysis*. Guilford Press.

Continue with the applied tutorial

Thank you for your attention!

Continue to Part II: Applied Tutorial →



Appendix

Interpreting the distinguishable APIM

[← Results](#)

Red estimates are not statistically distinguishable from zero at $\alpha = .05$. Their numerical translations are shown only to demonstrate how APIM coefficients are interpreted; they should not be treated as evidence of a nonzero effect.

Intercepts: When both partners' support scores equal the pooled sample mean:

- $b_{0,F}$: Predicted female MVPA is 35.28 minutes.
- $b_{0,M}$: Predicted male MVPA is 31.24 minutes.

Female MVPA, holding the male partner's support constant:

- a_F : One-unit higher female support is associated with 4.61 fewer minutes of her own MVPA.
- p_F : One-unit higher male support is associated with 15.06 additional minutes of female MVPA.

Male MVPA, holding the female partner's support constant:

- a_M : One-unit higher male support is associated with 17.92 additional minutes of his own MVPA.
- p_M : One-unit higher female support is associated with 9.87 fewer minutes of male MVPA.

Residual correlation ($\rho = .78$): When the female's MVPA is higher than predicted, the male's MVPA also tends to be higher than predicted, and likewise for being lower. This is the remaining within-couple interdependence after accounting for both support scores.

Interpreting the exchangeable APIM

[← Results](#)

Red estimates are not statistically distinguishable from zero at $\alpha = .05$. Their numerical translations are shown only to demonstrate how APIM coefficients are interpreted; they should not be treated as evidence of a nonzero effect.

The intercept, actor effect, partner effect, and residual SD are **pooled across members**.

Pooled intercept: When both partners' support scores equal the pooled sample mean:

- b_0 : Predicted MVPA is 31.21 minutes for either member position.

Pooled effects: For either member, holding the other support score constant:

- a : One-unit higher own support is associated with 7.75 additional minutes of own MVPA.
- p : One-unit higher partner support is associated with 1.97 additional minutes of own MVPA.

Pooling means that the same coefficients are used for both member positions. It does not require the two members to have identical predictions because their own and partner support scores may differ.

Residual correlation ($\rho = .77$): When one member's MVPA is higher than predicted, the partner's MVPA also tends to be higher than predicted, and likewise for being lower. The residual correlation remains freely estimated even though the other parameters are pooled.

Interpreting the fitted DIM

[← Results](#)

Red estimates are not statistically distinguishable from zero at $\alpha = .05$. Their numerical translations are shown only to demonstrate how DIM coefficients are interpreted; they should not be treated as evidence of a nonzero effect.

Intercepts: For a couple with an average support mean:

- b_0 : Predicted couple-mean MVPA is 31.21 minutes.
- The member-deviation intercept is constrained to zero: a member with no support deviation has no predicted MVPA deviation from the couple mean.

Holding the **members' support deviations fixed**, a one-unit higher couple-mean support score is associated with:

- b_{mean} : 9.72 additional minutes of couple-mean MVPA.

Holding couple-mean support at the **sample average**, a one-unit larger member support deviation from the couple mean is associated with:

- b_{dev} : A 5.78-minute larger member MVPA deviation from the couple mean. Thus, a member whose support is one unit above the couple mean is predicted to have MVPA 5.78 minutes above the couple mean.

Residual correlation: Exchangeability constrains the correlation between the residual couple mean and residual member deviation to zero. Thus, couples whose MVPA is higher than predicted on average are not expected to tilt systematically toward either arbitrarily labeled member in residual MVPA. This is a model constraint, not an empirical finding, and it does not imply that the two partners' residuals are independent.

Interpreting the fitted DSM

[← Results](#)

Red estimates are not statistically distinguishable from zero at $\alpha = .05$. Their numerical translations are shown only to demonstrate how DSM coefficients are interpreted; they should not be treated as evidence of a nonzero effect.

Intercepts: For a couple with an average support mean and no female–male support difference:

- a_{10} : Predicted couple-mean MVPA is 33.26 minutes.
- a_{20} : The female is predicted to be 4.04 minutes more active than the male.

Holding the **female–male support difference at zero**, a one-unit higher couple-mean support score is associated with:

- a_{11} : 9.25 additional minutes of couple-mean MVPA.
- a_{21} : A 2.40-minute larger female–male MVPA difference. Thus, when couple-mean support is one unit above the sample average, the predicted difference is $4.04 + 2.40 = 6.44$ minutes.

Holding couple-mean support at the **sample average**, a one-unit larger female–male support difference is associated with:

- a_{12} : 11.86 fewer minutes of couple-mean MVPA.
- a_{22} : A 4.06-minute larger female–male MVPA difference. Thus, when the female–male support difference is one unit, the predicted difference is $4.04 + 4.06 = 8.10$ minutes.

Residual correlation ($\rho = .37$): Couples with higher-than-predicted mean MVPA also tend to show a more positive-than-predicted female–male MVPA difference; residual MVPA therefore tilts toward the female.

Exchangeable CFM: constraints and degrees of freedom

Positions 1 and 2 are arbitrary. The model must be unchanged when they are swapped ([Ledermann & Macho, 2009](#); [Peugh et al., 2013](#)).

$$\begin{aligned}\nu_{X_1} &= \nu_{X_2}, & \nu_{Y_1} &= \nu_{Y_2} \\ \sigma_{\epsilon_{X_1}}^2 &= \sigma_{\epsilon_{X_2}}^2, & \sigma_{\epsilon_{Y_1}}^2 &= \sigma_{\epsilon_{Y_2}}^2 \\ \text{Cov}(\epsilon_{X_1}, \epsilon_{Y_1}) &= \text{Cov}(\epsilon_{X_2}, \epsilon_{Y_2})\end{aligned}$$

- All four loadings remain fixed to 1.
- Ordinary wide-data $\mathbf{df} = 6$; $\mathbf{df} = 0$ against the exchangeable saturated model.
- Usual exchangeability test: $\Delta df = 5$; here: $\Delta df = 4$ ($\sigma_{\epsilon_Y}^2$ is already equal).

Distinguishable APIM: residual covariance

Within-dyad residual covariance block (shared across dyads):

$$\text{Cov} \begin{pmatrix} \epsilon_{Fi} \\ \epsilon_{Mi} \end{pmatrix} = \Sigma_{\epsilon} = \begin{bmatrix} \sigma_{\epsilon_F}^2 & \rho_{\epsilon_F \epsilon_M} \sigma_{\epsilon_F} \sigma_{\epsilon_M} \\ \rho_{\epsilon_F \epsilon_M} \sigma_{\epsilon_F} \sigma_{\epsilon_M} & \sigma_{\epsilon_M}^2 \end{bmatrix}$$

Residual covariance matrix for all dyads (first three shown):

$$\Sigma_{\text{model}} = \begin{bmatrix} \Sigma_{\epsilon} & \mathbf{0} & \mathbf{0} & \cdots \\ \mathbf{0} & \Sigma_{\epsilon} & \mathbf{0} & \cdots \\ \mathbf{0} & \mathbf{0} & \Sigma_{\epsilon} & \cdots \\ \vdots & \vdots & \vdots & \ddots \end{bmatrix}$$

Exchangeable APIM: residual covariance

For arbitrary member positions 1 and 2, the residual variances must be equal:

$$\text{Cov} \begin{pmatrix} \epsilon_{1i} \\ \epsilon_{2i} \end{pmatrix} = \Sigma_{\epsilon, \text{exch}} = \begin{bmatrix} \sigma_{\epsilon}^2 & \rho_{\epsilon_1 \epsilon_2} \sigma_{\epsilon}^2 \\ \rho_{\epsilon_1 \epsilon_2} \sigma_{\epsilon}^2 & \sigma_{\epsilon}^2 \end{bmatrix}$$

- The equal diagonal elements express exchangeability.
- The off-diagonal element still allows residual interdependence.
- Across dyads, these blocks form the same block-diagonal model matrix as on the previous slide.

DIM: residual covariance

$$r_{Mi} = \bar{\epsilon}_i = \frac{\epsilon_{1i} + \epsilon_{2i}}{2},$$

$$r_{D,mi} = \epsilon_{mi} - r_{Mi} \quad (m = 1, 2), \quad r_{D,1i} = \frac{\epsilon_{1i} - \epsilon_{2i}}{2} = -r_{D,2i}.$$

Using the arbitrary orientation $r_{Di} = r_{D,1i}$, exchangeability gives:

$$\text{Cov} \begin{pmatrix} r_{Mi} \\ r_{Di} \end{pmatrix} = \begin{bmatrix} \sigma_{r_M}^2 & 0 \\ 0 & \sigma_{r_D}^2 \end{bmatrix}.$$

Back-transform to the exchangeable APIM: partner covariance need not be zero.

$$\begin{bmatrix} \sigma_{r_M}^2 + \sigma_{r_D}^2 & \sigma_{r_M}^2 - \sigma_{r_D}^2 \\ \sigma_{r_M}^2 - \sigma_{r_D}^2 & \sigma_{r_M}^2 + \sigma_{r_D}^2 \end{bmatrix} = \begin{bmatrix} \sigma_{\epsilon}^2 & \rho_{\epsilon_1 \epsilon_2} \sigma_{\epsilon}^2 \\ \rho_{\epsilon_1 \epsilon_2} \sigma_{\epsilon}^2 & \sigma_{\epsilon}^2 \end{bmatrix}.$$

DSM: residual covariance

With distinguishable roles, the directed difference may covary with the mean:

$$r_{Mi} = \frac{\epsilon_{Fi} + \epsilon_{Mi}}{2}, \quad r_{Di} = \epsilon_{Fi} - \epsilon_{Mi}.$$

$$\text{Cov} \begin{pmatrix} r_{Mi} \\ r_{Di} \end{pmatrix} = \begin{bmatrix} \sigma_{r_M}^2 & \rho_{r_M r_D} \sigma_{r_M} \sigma_{r_D} \\ \rho_{r_M r_D} \sigma_{r_M} \sigma_{r_D} & \sigma_{r_D}^2 \end{bmatrix}.$$

Back-transform to the distinguishable APIM, with $c_{MD} = \rho_{r_M r_D} \sigma_{r_M} \sigma_{r_D}$.

$$\begin{bmatrix} \sigma_{r_M}^2 + \frac{1}{4}\sigma_{r_D}^2 + c_{MD} & \sigma_{r_M}^2 - \frac{1}{4}\sigma_{r_D}^2 \\ \sigma_{r_M}^2 - \frac{1}{4}\sigma_{r_D}^2 & \sigma_{r_M}^2 + \frac{1}{4}\sigma_{r_D}^2 - c_{MD} \end{bmatrix} = \begin{bmatrix} \sigma_{\epsilon_F}^2 & \rho_{\epsilon_F \epsilon_M} \sigma_{\epsilon_F} \sigma_{\epsilon_M} \\ \rho_{\epsilon_F \epsilon_M} \sigma_{\epsilon_F} \sigma_{\epsilon_M} & \sigma_{\epsilon_M}^2 \end{bmatrix}.$$