



Dyadic Data Analysis with R

Part II: Applied Tutorial

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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	Cross-sectional APIM in R
15:30–15:45	<i>Short break</i>
15:45–16:45	Intensive longitudinal APIM in R
16:45–17:00	<i>Short break</i>
17:00–18:00	Exercises in R



Software and frameworks

SEM vs. MLM

- Many simple dyadic models can be represented in either framework.
- The best framework is the one that represents your conceptual model most naturally ([Ledermann & Kenny, 2017](#)).

SEM / DSEM is often more natural for

- Latent dyadic constructs (e.g., a CFM)
- Item-level measurement models for reflective measures
- Linked outcomes or equations [e.g., mediation; [Ledermann & Macho \(2009\)](#)]
- Short dynamic panels in wide-format [e.g., LD-APIM; [Gistelinck et al. \(2021\)](#)]
- Intensive lagged or coupled dynamics via DSEM/RDSEM (e.g., [Asparouhov et al., 2018](#))

MLM is often more natural for

- Parsimonious observed-variable models with modest numbers of dyads
- Nested grouping and flexible random-effect structures
- Observed-outcome growth or concurrent ILD models with flexible time trends
- Complex observed-variable regressions—interactions, polynomials, splines, and dyadic RSA—especially with repeated measures or additional nesting
- Specialized generalized mixed models in R, including zero-inflated, hurdle, and Tweedie models

([Asparouhov et al., 2018](#); [Asparouhov & Muthén, 2020](#); [Brooks et al., 2017](#); [del Rosario & West, 2025](#); [Driver et al., 2017](#); [Gistelinck et al., 2021](#); [Nestler et al., 2019](#); [Schönbrodt et al., 2018](#))

SEM vs. MLM: Missing data

- **MLM: Complete-case**
 - **Outcome missing:** Valid under MAR, MLM uses remaining observations
 - **Predictor missing:** Valid under MAR, if missingness does **not depend** on the outcome after accounting for predictors
- **SEM with FIML and joint likelihood**
 - Valid under MAR: Models predictors and outcomes jointly
- **MI: Imputation**
 - Handles missing outcomes, predictors, and auxiliary information
 - Must match the analysis and preserve person, dyad, role, and time structure

Include important predictors of missingness and missing values. FIML and MI cover more MAR situations than row omission; none automatically solves MNAR.

Ledermann & Kenny (2017); Hughes et al. (2019); Grund et al. (2018)

Why R

Why we teach R

- **Free to use:** no license fees or institutional access barriers
- **Open source:** statistical implementations can be inspected, audited, and adapted
- **Reproducible:** workflows can be rerun, reviewed, shared, and version-controlled
- **Extensible:** specialized methods integrate with data, graphics, and reporting

Current trade-offs

- **SEM/DSEM:** R spreads these capabilities across specialized packages
 - `lavaan`: fixed-wave and limited two-level SEM
 - `mlts` and `ctsem`: multivariate dynamic models
 - Dyadic DSEM in R remains cumbersome and limited
 - Mplus remains the most complete (non-open) option with DSEM capabilities
- **MLM/ILD:** `glmmTMB` and `brms` both model serial dependence
 - Neither directly offers a separable partner-by-time residual structure such as $UN \otimes AR(1)$
 - SAS `PROC MIXED` and SPSS `MIXED` do for Gaussian repeated-measures models

(Asparouhov et al., 2018; Asparouhov & Muthén, 2020; Bürkner, n.d.; Driver et al., 2017; IBM Corp., n.d.; Koslowski et al., 2025; Kristensen & McGillicuddy, 2023; lavaan project, n.d.; Merkle et al., n.d.; Mulder & Hamaker, 2021; SAS Institute Inc., n.d.)



Cross-sectional APIM in R

One possible workflow

1. Define dyads, distinguishability, and research questions
2. Prepare the data and validate the dyadic structure
3. Describe and visualize measures and observed relationships
4. Estimate the models
5. Verify model adequacy, distinguishability (if applicable), and robustness
6. Visualize, interpret, and report results

Synthesized from Kenny et al. (2006), Ledermann & Kenny (2015), and Stas et al. (2018).

One possible workflow

1. **Define dyads, distinguishability, and research questions**
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Synthesized from Kenny et al. (2006), Ledermann & Kenny (2015), and Stas et al. (2018).

The Dataset

Same as before:

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

Aggregated for cross-sectional analyses

Research Question

RQ: In romantic couples, is a person's self-efficacy linked to physical activity in both partners?

Measurement - predictor

Self-efficacy

Rough English translation of the original German item

“I am confident that I can be physically active tomorrow, even if it becomes difficult.”

Adapted from Sniehotta et al. (2005)

0 = *not at all true today*

5 = *completely true 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.

Distinguishable dyads

Distinguishing by gender

Workflow

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Load and inspect the raw data

```
1 library(dplyr) # for easier data-wrangling, exports functions like `select()`
2
3 raw_dyad_data <- readRDS("dyadic-person-means.rds") |>
4   dplyr::select(
5     couple_id, person_id, gender, efficacy, total_mvpa
6   )
7
8 # usually use head(raw_dyad_data), slide_table is a custom function for html tables on these slides
9 slide_table(raw_dyad_data[1:4,])
```

couple_id	person_id	gender	efficacy	total_mvpa
1.00	1.00	male	3.02	33.61
1.00	2.00	female	0.89	12.71
2.00	3.00	male	0.13	42.83
2.00	4.00	female	2.37	44.54

This dataset is stored as an R object. Other packages provide functions to import various formats, such as: `readxl::read_excel()`, `utils::read.csv()`, `haven::read_sav()`, `haven::read_sas()`

Create the required format and validate the data

For the distinguishable APIM we need to add:

- `efficacy_actor` and `efficacy_partner` columns
- Dummy coded numeric variables for the two roles

Validate things like:

- no dyad with more than two members,
- each dyad-member combination occurs only once (per occasion),
- gender labels are present and consistent
- you only have the type of dyad you expect

Create the required format and validate the data

We can use the `dyadMLM` package to help with data preparation and validation.

```
1 library(dyadMLM)
2
3 apim_distinguishable_data <- dyadMLM::prepare_dyad_data( # exported function from dyadMLM
4   data = raw_dyad_data,
5   dyad = couple_id,
6   member = person_id,
7   role = gender,
8   predictors = efficacy,
9   model_types = 'apim',
10  # if we want to fit an exchangeable model from the same data we can:
11  include_arbitrary_member_contrast = TRUE,
12  add_apim_gmc_predictors = TRUE,
13  seed = 123
14 )
15
16 print(apim_distinguishable_data)
```

Create the required format and validate the data

```
# dyadMLM data
# Rows: 72 | Dyads: 36 | Intensive longitudinal: no
# Structure: dyad = couple_id, member = person_id, role = gender
#
# Dyad compositions:
# female_x_male distinguishable 36 dyads
#
# Added columns:
# .composition                inferred dyad composition
# .composition_role           composition-specific member role
# .is_{role}                  composition-role indicator columns
# .member_contrast_arbitrary  composition-specific member contrasts coded
#                             -1/+1 in arbitrary direction for
#                             exchangeability-constrained random effects.
#                             Values are 0 for other compositions
# .{pred}_actor               APIM actor predictor: actor's original
#                             predictor values
# .{pred}_partner             APIM partner predictor: partner's original
#                             predictor values
# .{pred}_gmc                 APIM grand-mean-centered predictor source:
#                             original values minus the mean across all
#                             retained non-missing observations
# .{pred}_gmc_actor           APIM grand-mean-centered actor predictor:
```

Create the required format and validate the data

[Manual code →](#)

Looking at the columns immediately relevant to us:

```
1 head(apim_distinguishable_data) |>
2   dplyr::select(
3     couple_id, person_id, gender, .is_female, .is_male, .efficacy_gmc, .efficacy_gmc_actor, .efficacy_gmc_partner
4   ) |>
5   slide_table()
```

couple_id	person_id	gender	.is_female	.is_male	.efficacy_gmc	.efficacy_gmc_actor	.efficacy_gmc_partner	total
1.00	1.00	male	0.00	1.00	0.64	0.64	-1.49	
1.00	2.00	female	1.00	0.00	-1.49	-1.49	0.64	
2.00	3.00	male	0.00	1.00	-2.24	-2.24	-0.01	
2.00	4.00	female	1.00	0.00	-0.01	-0.01	-2.24	
3.00	5.00	female	1.00	0.00	0.96	0.96	-0.76	
3.00	6.00	male	0.00	1.00	-0.76	-0.76	0.96	

Workflow

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Create a wide view for role-specific exploration

The models will **NOT** use this dataset

```
1 apim_distinguishable_wide_data <- apim_distinguishable_data |>
2   dplyr::select(couple_id, gender, efficacy, total_mvpa) |>
3   tidyr::pivot_wider(
4     names_from = gender,
5     values_from = c(efficacy, total_mvpa)
6   )
7
8 slide_table(head(apim_distinguishable_wide_data))
```

couple_id	efficacy_male	efficacy_female	total_mvpa_male	total_mvpa_female
1.00	3.02	0.89	33.61	12.71
2.00	0.13	2.37	42.83	44.54
3.00	1.62	3.33	32.29	62.86
4.00	1.09	0.75	21.55	51.89
5.00	1.35	1.48	11.35	9.79
6.00	1.18	0.63	7.55	3.43

Describe focal variables per role

```
1 library(report)
2
3 apim_distinguishable_wide_data |>
4   dplyr::select(-couple_id) |>
5   report::report_table() |>
6   slide_table()
```

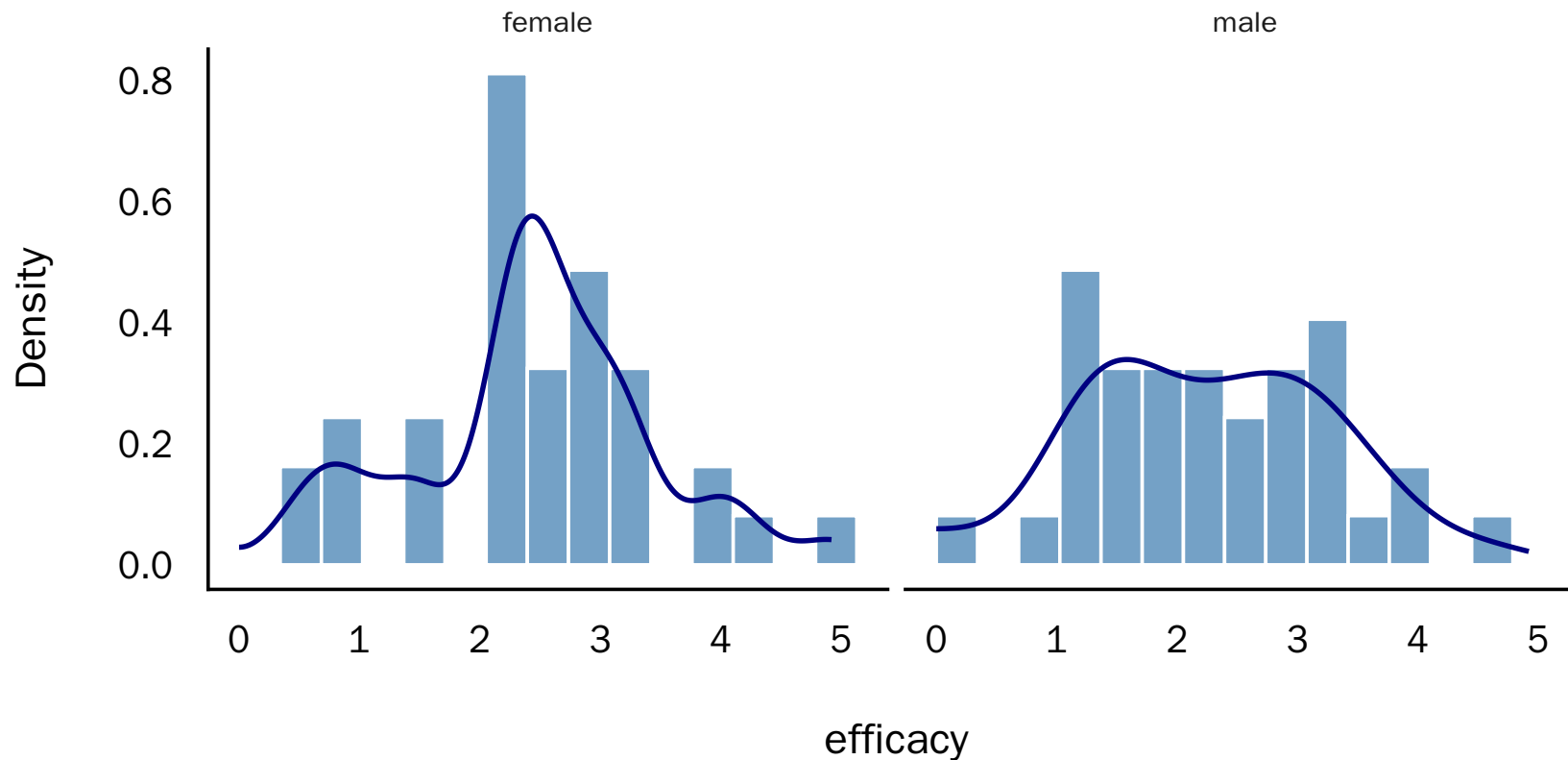
Variable	n_Obs	Mean	SD	Median	MAD	Min	Max	Skewness	Kurtosis	n_Missing
efficacy_male	36.00	2.29	0.99	2.32	1.18	0.13	4.60	0.16	-0.39	0.00
efficacy_female	36.00	2.46	1.01	2.39	0.85	0.46	4.92	0.01	0.28	0.00
total_mvpa_male	36.00	28.84	20.28	27.26	16.82	3.51	111.16	2.11	7.00	0.00
total_mvpa_female	36.00	33.58	24.39	29.85	20.90	3.43	126.35	1.74	4.80	0.00

Visualize focal variable by partner role

```
1 library(ggplot2)
2 library(see)
3
4 plot_role_histograms <- function(data, group, var) {
5   var_label <- rlang::as_label(rlang::enquo(var))
6
7   ggplot(
8     data,
9     aes(x = {{ var }}, y = after_stat(density))
10  ) +
11    geom_histogram(
12      bins = 15, boundary = 0,
13      fill = "steelblue", color = "white", alpha = 0.75
14    ) +
15    geom_density(
16      bounds = c(0, Inf), color = "navy", linewidth = 1.1
17    ) +
18    facet_wrap(vars({{ group }}), nrow = 1) +
19    labs(x = var_label, y = "Density") +
20    see::theme_modern(base_size = 16)
21 }
```

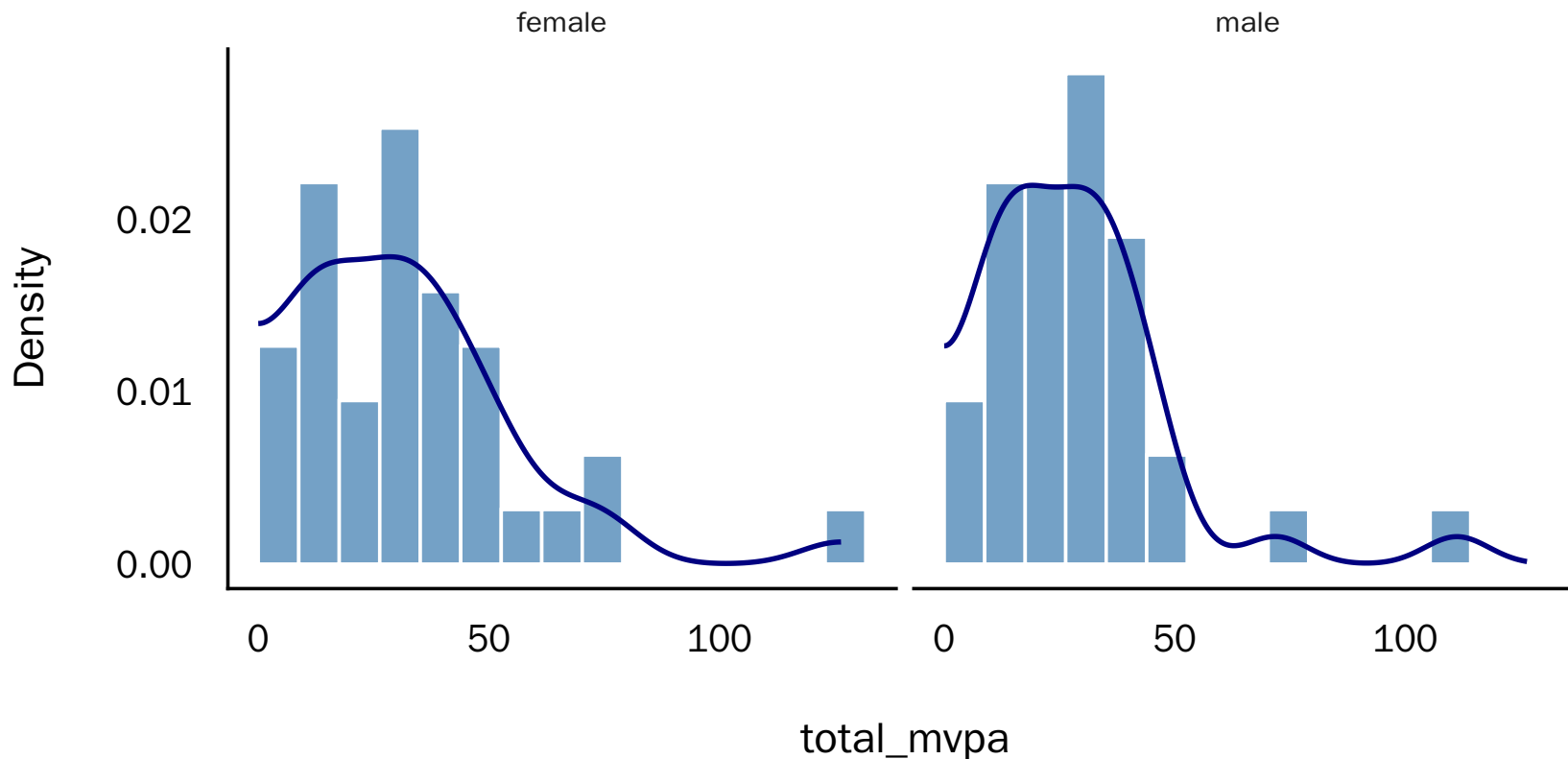
Visualize focal variable by partner role - Efficacy

```
1 plot_role_histograms(apim_distinguishable_data, gender, efficacy)
```



Visualize focal variable by partner role - MVPA

```
1 plot_role_histograms(apim_distinguishable_data, gender, total_mvpa)
```



Observed dyadic correlations

The wide data ensure that each couple contributes once.

```
1 library(correlation)
2 library(insight)
3
4 apim_distinguishable_wide_data |>
5   correlation::correlation(
6     select = c("efficacy_female", "total_mvpa_female"),
7     select2 = c("efficacy_male", "total_mvpa_male")
8   ) |>
9   summary() |>
10  insight::print_md(footer = "")
```

Correlation Matrix (pearson-method)

Parameter	efficacy_male	total_mvpa_male
efficacy_female	0.60***	0.43*
total_mvpa_female	0.42*	0.82***

Visualize partner similarity

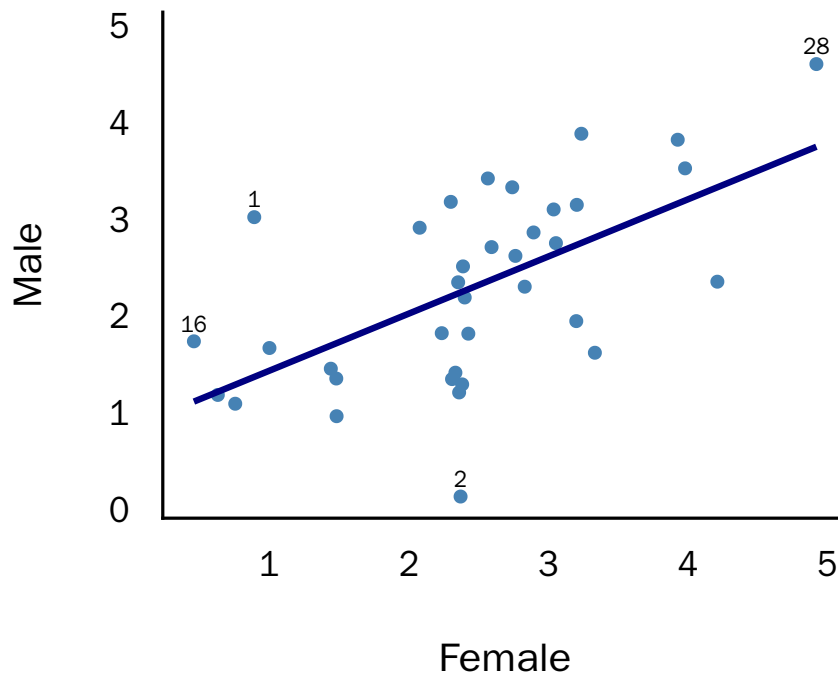
```
1 plot_partner_similarity <- function(data, x, y, id, title, n_mahalanobis = 3) {
2   x_name <- rlang::as_name(rlang::enquo(x))
3   y_name <- rlang::as_name(rlang::enquo(y))
4   xy <- cbind(data[[x_name]], data[[y_name]])
5   labels <- data |>
6     dplyr::mutate(
7       .distance = mahalanobis(xy, colMeans(xy), cov(xy))
8     ) |>
9     dplyr::distinct({{ id }}, .keep_all = TRUE) |>
10    dplyr::slice_max(.distance, n = n_mahalanobis, with_ties = FALSE)
11
12  ggplot(data, aes(x = {{ x }}, y = {{ y }})) +
13    geom_point(color = "steelblue") +
14    geom_smooth(method = "lm", se = FALSE, color = "navy") +
15    geom_text(
16      data = labels,
17      aes(label = {{ id }}),
18      vjust = -0.6, check_overlap = TRUE, size = 4
19    ) +
20    labs(title = title, x = "Female", y = "Male") +
21    scale_y_continuous(expand = expansion(mult = c(0.05, 0.12))) +
22    see::theme_modern(base_size = 16)
23 }
```

Visualize partner similarity

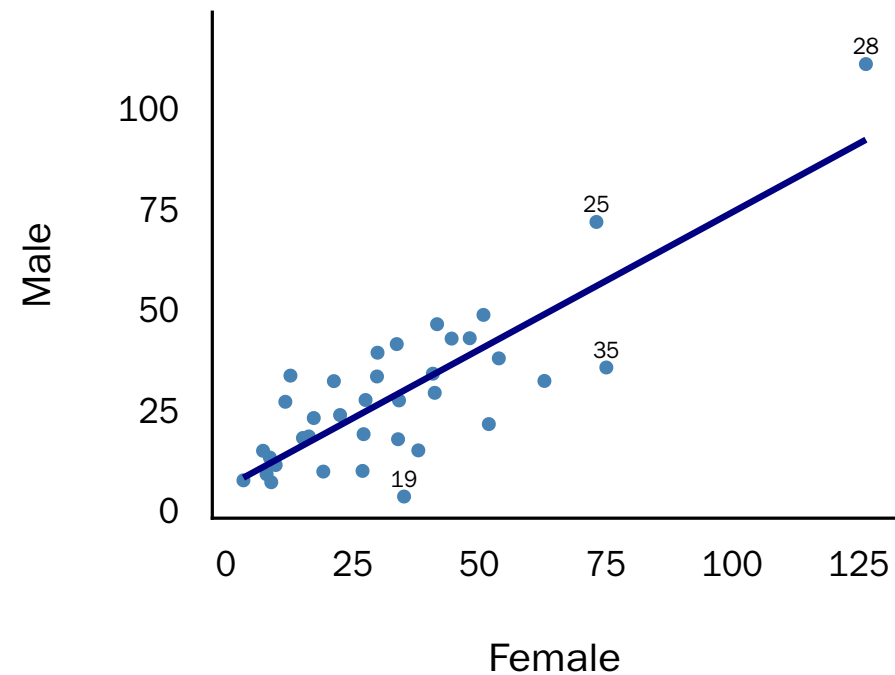
```
1 n_mahalanobis <- 4
2
3 see::plots(
4   plot_partner_similarity(
5     apim_distinguishable_wide_data,
6     efficacy_female, efficacy_male, couple_id, "Efficacy",
7     n_mahalanobis = n_mahalanobis
8   ),
9   plot_partner_similarity(
10    apim_distinguishable_wide_data,
11    total_mvpa_female, total_mvpa_male, couple_id, "Daily MVPA",
12    n_mahalanobis = n_mahalanobis
13  )
14 )
```

Visualize partner similarity

Efficacy



Daily MVPA

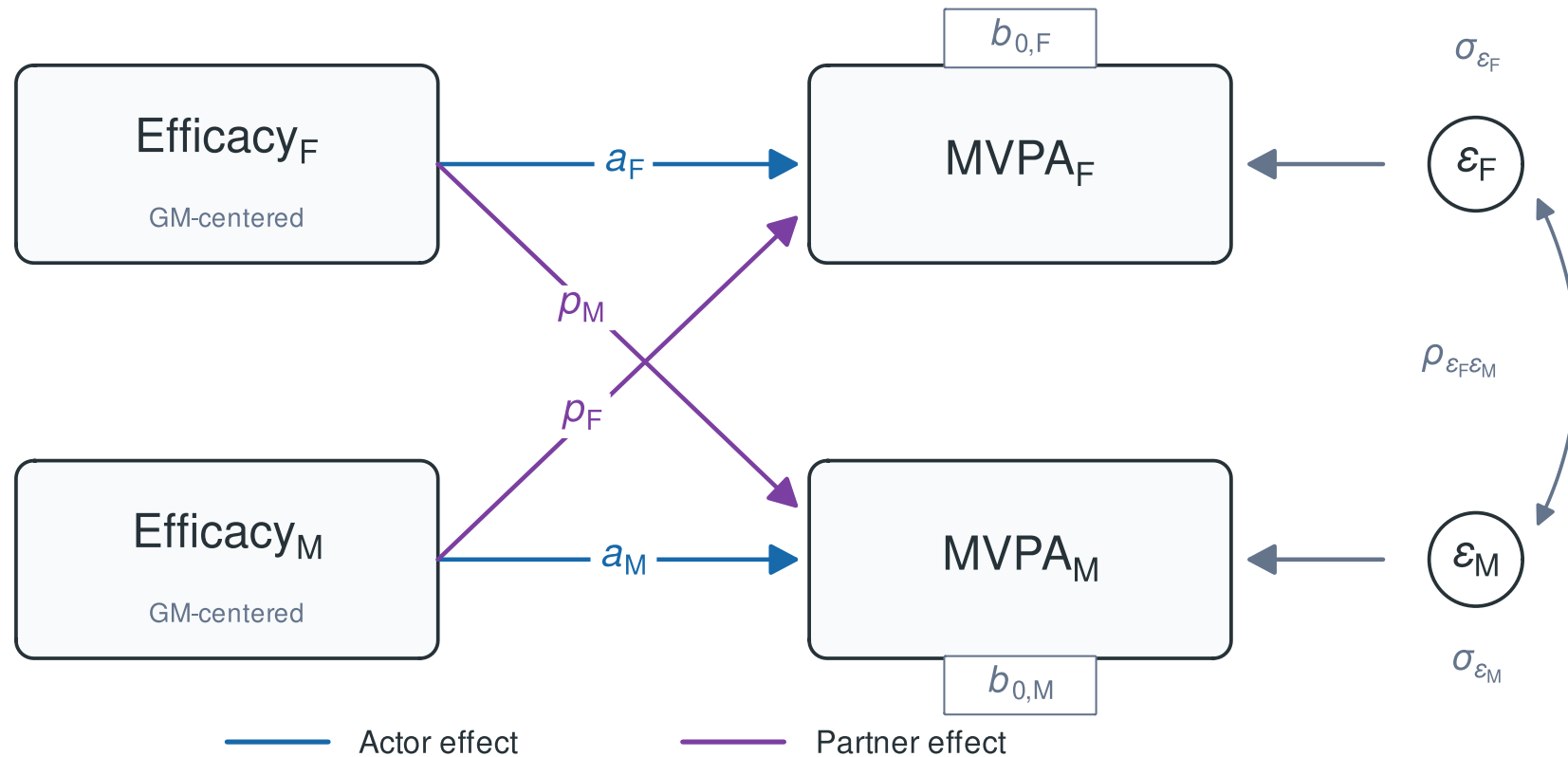


Labels: four largest Mahalanobis distances in each plot.

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Distinguishable APIM



The APIM starts with two member-specific equations

For each dyad i , each member with role $r \in \{M, F\}$ has their own predictor $X_{ri}^{(A)}$ and their partner's predictor $X_{ri}^{(P)}$:

$$Y_{M,i} = b_{0,M} + a_M \times X_{M,i}^{(A)} + p_M \times X_{M,i}^{(P)} + \epsilon_{M,i}$$
$$Y_{F,i} = b_{0,F} + a_F \times X_{F,i}^{(A)} + p_F \times X_{F,i}^{(P)} + \epsilon_{F,i}$$

- Actor effects - Partner effects

In long format, each equation applies to one member row of the dyad.

How can we combine these two equations into one model?

Role indicators combine the equations

The indicators $D_{M,ri}$ and $D_{F,ri}$ identify the male or female row:

$$\begin{aligned} Y_{ri} = & \underbrace{b_{0,M} \times D_{M,ri} + b_{0,F} \times D_{F,ri}}_{\text{role-specific intercepts}} \\ & + \underbrace{a_M \times D_{M,ri} \times X_{ri}^{(A)} + a_F \times D_{F,ri} \times X_{ri}^{(A)}}_{\text{role-specific actor effects}} \\ & + \underbrace{p_M \times D_{M,ri} \times X_{ri}^{(P)} + p_F \times D_{F,ri} \times X_{ri}^{(P)}}_{\text{role-specific partner effects}} + \epsilon_{ri}. \end{aligned}$$

For a male row: $D_M = 1$, $D_F = 0$. For a female row: the reverse.

Residuals remain correlated within dyads

The two member rows from the same dyad retain a joint residual structure:

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

Fitting the distinguishable APIM in glmmTMB

```
1 library(glmmTMB)
2
3 apim_distinguishable_model <- glmmTMB(
4   total_mvpa ~
5     # Role-specific intercepts
6     0 + .is_female + .is_male +
7
8     # Role-specific actor effects
9     .is_female:.efficacy_gmc_actor +
10    .is_male:.efficacy_gmc_actor +
11
12    # Role-specific partner effects
13    .is_female:.efficacy_gmc_partner +
14    .is_male:.efficacy_gmc_partner +
15
16    # Within-dyad residual covariance
17    (0 + .is_female + .is_male | couple_id),
18  dispformula = ~ 0,
19  family = gaussian(),
20  data = apim_distinguishable_data
21 )
22
23 summary(apim_distinguishable_model)
```

Fitting the distinguishable APIM in glmmTMB

```
Family: gaussian ( identity )
Formula:
total_mvpa ~ 0 + .is_female + .is_male + .is_female:.efficacy_gmc_actor +
  .is_male:.efficacy_gmc_actor + .is_female:.efficacy_gmc_partner +
  .is_male:.efficacy_gmc_partner + (0 + .is_female + .is_male |
  couple_id)
Dispersion: ~0
Data: apim_distinguishable_data
```

AIC	BIC	logLik	-2*log(L)	df.resid
605.4	625.9	-293.7	587.4	63

Random effects:

Conditional model:

Groups	Name	Variance	Std.Dev.	Corr
couple_id	.is_female	388.3	19.70	
	.is_male	286.0	16.91	0.79

Number of obs: 72, groups: couple_id, 36

Conditional model:

	Estimate	Std. Error	z value	Pr(> z)
.is_female	32.853	3.342	9.829	< 2e-16 ***

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Verify model adequacy, distinguishability, and robustness

1. Did estimation succeed?
2. Does the model reproduce the important data patterns?
3. Is distinguishability supported?
4. Are conclusions robust or driven by few dyads or consequential modeling choices? (sensitivity analyses)

Did estimation succeed / converge?

The model converged without warnings... a good first sign!

Other things to look out for in the model output:

- Estimated variances near 0 or correlations near ± 1 $\rightarrow$ possible boundary fit
- NaN or infinite estimates, standard errors, or model fit indices

Residual diagnostics / reproduction of data patterns

Residual diagnostics are not as straightforward anymore

- Linear models: straightforward checks
- Mixed models: residuals arise at multiple levels
- Generalized models: expectations depend on the family and link
- Dyadic models: partners' residuals are correlated

Solution: Compare the data with simulations from the fitted model.

DHARMa: one diagnostic scale across models

The `DHARMa` package ([Hartig, 2026](#)):

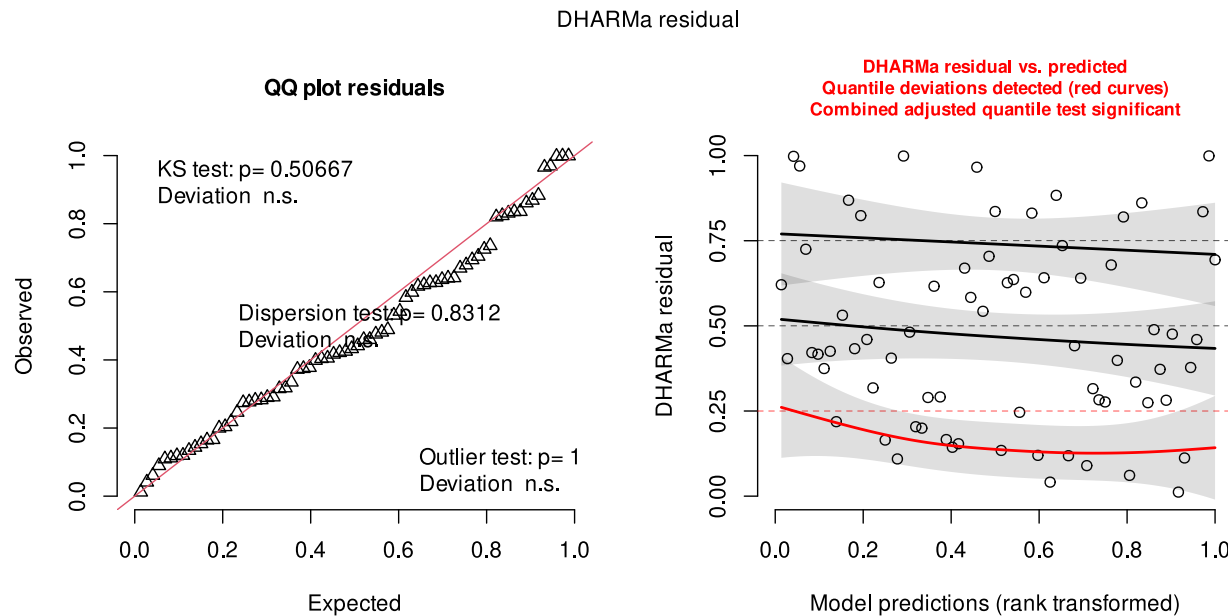
- Simulates outcomes from the fitted model
- Checks whether the observed residuals behave as expected under simulations from the fitted model.
- Adequate fit → approximately uniform, pattern-free residuals

One function works across many model families!

Simulate the full dyadic residual structure

```
1 library(DHARMA)
2
3 apim_distinguishable_dharma_residuals <- DHARMA::simulateResiduals(
4   fittedModel = apim_distinguishable_model,
5   n = 10000,
6
7   # Since our model uses dispformula = ~ 0, we cannot use DHARMA's default
8   # conditional simulations. With unconditional, the random-effects block representing
9   # our residuals is re-simulated.
10  simulateREs = "unconditional",
11
12  # Male and female residuals are correlated. DHARMA estimates this correlation
13  # from the simulations and rotates the residuals to "remove" it.
14  rotation = 'estimated',
15  seed = 123
16 )
```

Inspect DHARMa residuals



In this model:

- Uniformity and dispersion are plausible
- No simulation outliers
- A fitted-value pattern remains

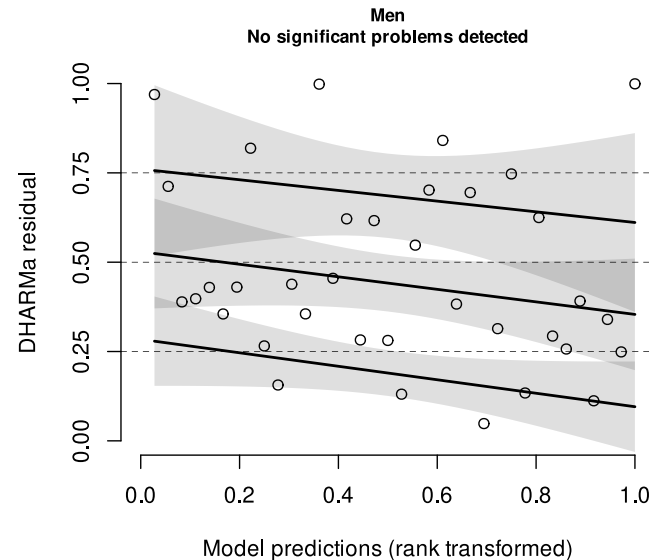
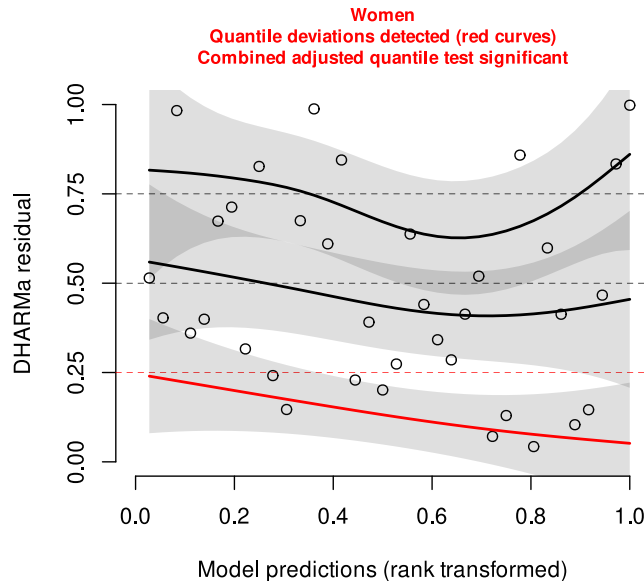
Next: inspect roles without rotation.

More targeted checks and guidance on interpretation of the plots: [DHARMa vignette](#).

Inspect DHARMA residuals by role

```
1 apim_distinguishable_female_dharma_residuals <- DHARMA::recalculateResiduals(  
2   apim_distinguishable_dharma_residuals,  
3  
4   # Recalculate from the same simulations for one role.  
5   # One observation per couple: no rotation needed.  
6   sel = ~ .is_female == 1,  
7   rotation = NULL,  
8   seed = 123  
9 )  
10  
11 apim_distinguishable_male_dharma_residuals <- DHARMA::recalculateResiduals(  
12   apim_distinguishable_dharma_residuals,  
13   sel = ~ .is_male == 1,  
14   rotation = NULL,  
15   seed = 123  
16 )
```

The fitted-value pattern appears among women



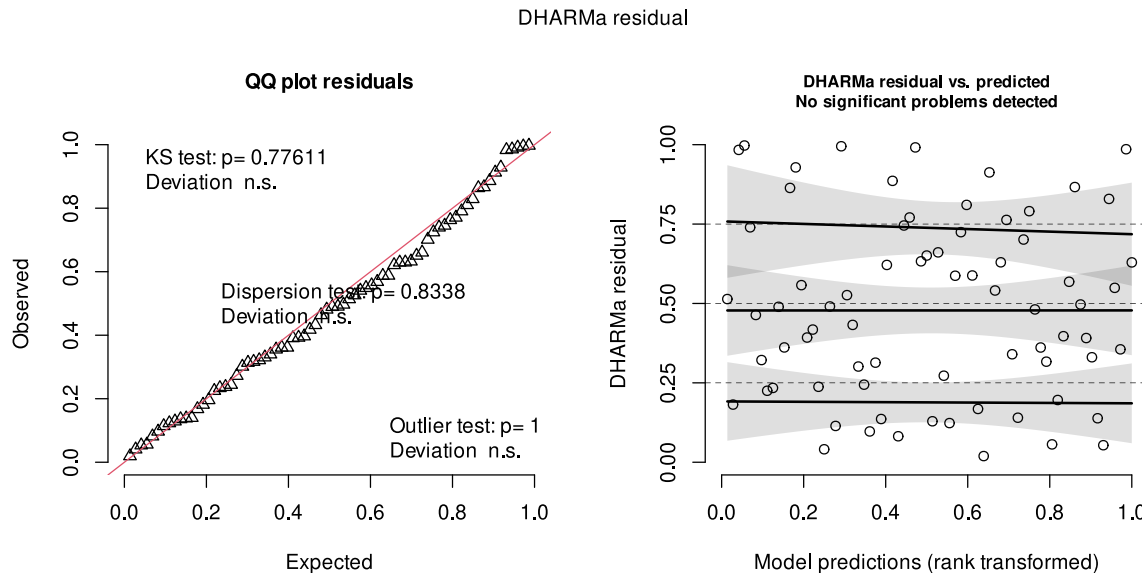
In this model:

- Pattern detected among women
- No comparable pattern among men

Next: try a defensible outcome scale.

More targeted checks and guidance on interpretation of the plots: [DHARMA vignette](#).

Square-root MVPA reduces the fitted-value pattern



Compared with raw MVPA:

- Uniformity and dispersion are plausible
- No simulation outliers
- No pooled fitted-value pattern

Substantive result unchanged:
actor effects remain positive and supported; partner effects remain unsupported.

In this example:

- **Sensitivity analysis:** square-root MVPA; conclusions unchanged
- **Primary analysis:** report the prespecified raw-MVPA model because the deviation was modest and minutes are directly interpretable
- **General rule:** larger or consequential diagnostic problems: revise main model

Transform—or change the outcome family?

- **Transformation may help** for a nonnegative, right-skewed outcome
 - Try `sqrt()` or `log1p()` (handles zeros)
 - Refit and rerun DHARMA; the histogram alone is not sufficient
- **A non-Gaussian family may be preferable**
 - Particularly for counts, proportions, bounded, or zero-heavy outcomes
 - Family and link choices require outcome-specific care
- **Workshop scope:** generalized models are not covered here

Test distinguishability

- Fit model with exchangeability constraints
 - Partial constraints can be very informative!
- Compare models
- Pool only if theoretically defensible, aligned with RQ and theory, and compatible with the data
 - Depending on goals you can also report the distinguishable model and report results from this analysis

However, non-significant comparisons are not proof that roles are identical.

Gistelinck et al. (2018)

Estimate and compare:

```
1 dyadMLM::compare_nested_models(  
2   apim_distinguishable_model, apim_exchangeable_comparison_model  
3 )
```

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
apim_exchangeable_comparison_model	5	604.25	615.64	-297.13	594.25	
apim_distinguishable_model	9	605.44	625.93	-293.72	587.44	6.8155

	Chi	Df	Pr(>Chisq)
apim_exchangeable_comparison_model			
apim_distinguishable_model		4	0.146

Conclusion (5% level): The likelihood-ratio test finds no clear improvement from
`apim\_exchangeable\_comparison\_model` to `apim\_distinguishable\_model` (p = 0.146). This does not establish
equal fit.

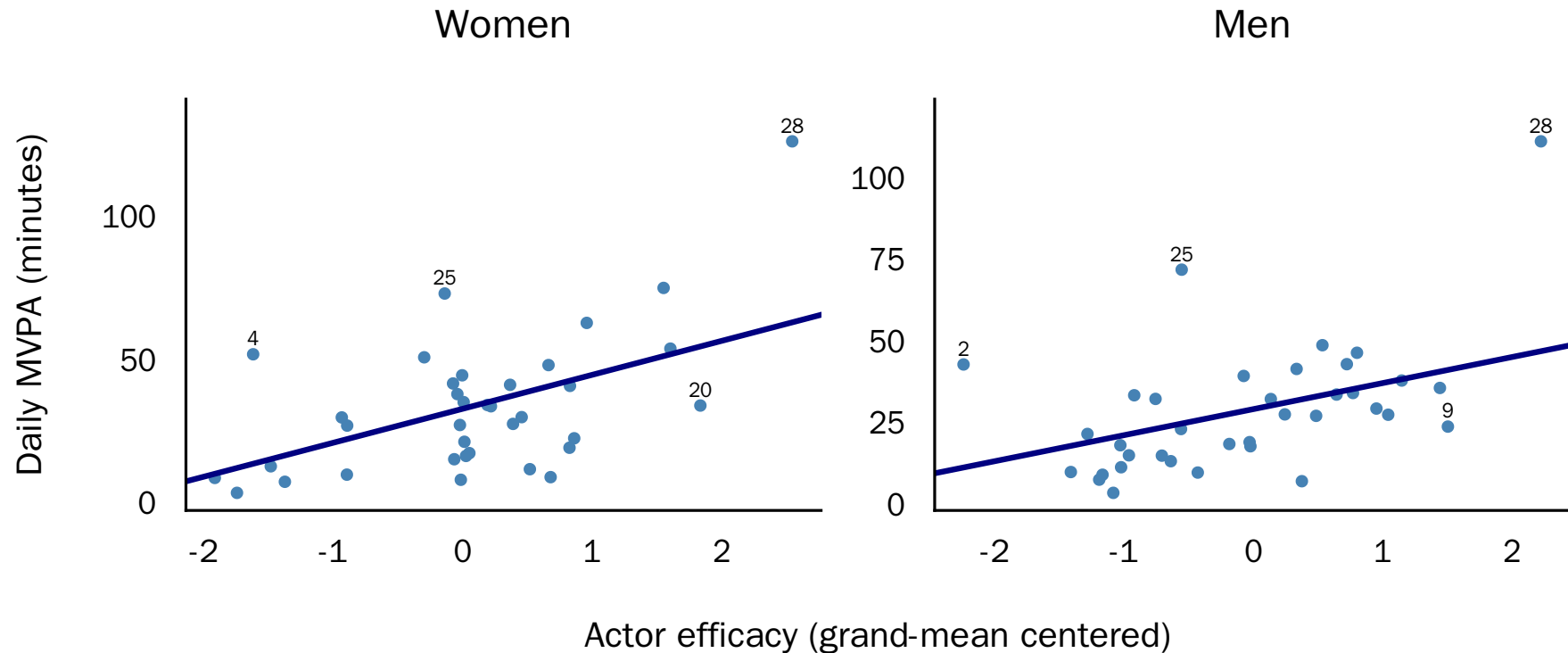
Test robustness - are conclusions driven by few dyads?

```
1 plot_actor_association <- function(data, model, role, title,
2                                   n_mahalanobis = 3) {
3   xy <- cbind(data$.efficacy_gmc_actor, data$total_mvpa)
4   labels <- data |>
5     dplyr::mutate(.distance = mahalanobis(xy, colMeans(xy), cov(xy))) |>
6     dplyr::slice_max(.distance, n = n_mahalanobis)
7   coefficients <- glmmTMB::fixef(model)$cond
8
9   ggplot(data, aes(.efficacy_gmc_actor, total_mvpa)) +
10     geom_point(color = "steelblue") +
11     geom_abline(intercept = coefficients[role],
12                slope = coefficients[paste0(role, ":", ".efficacy_gmc_actor")],
13                color = "navy", linewidth = 16 / 11) +
14     geom_text(
15       data = labels, aes(label = couple_id),
16       vjust = -0.6, check_overlap = TRUE, size = 4
17     ) +
18     labs(
19       title = title,
20       x = "Actor efficacy (grand-mean centered)",
21       y = "Daily MVPA (minutes)"
22     ) +
23     scale_y_continuous(expand = expansion(mult = c(0.05, 0.12))) +
24     see::theme_modern(base_size = 16) +
```

Test robustness - are conclusions driven by few dyads?

```
1 n_mahalanobis <- 4
2
3 see::plots(
4   plot_actor_association(
5     dplyr::filter(apim_distinguishable_data, gender == "female"),
6     apim_distinguishable_model, ".is_female", "Women",
7     n_mahalanobis = n_mahalanobis
8   ),
9   plot_actor_association(
10    dplyr::filter(apim_distinguishable_data, gender == "male"),
11    apim_distinguishable_model, ".is_male", "Men",
12    n_mahalanobis = n_mahalanobis
13  )
14 ) +
15 patchwork::plot_layout(
16   axes = "collect",
17   axis_titles = "collect"
18 )
```

Test robustness - are conclusions driven by few dyads?



Labels: four largest Mahalanobis distances in each plot.

Omitting Couple 28 changes the associations

```
1 apim_without_couple_28 <- update(  
2   apim_distinguishable_model,  
3   data = filter(apim_distinguishable_data, couple_id != 28)  
4 )  
5  
6 actor_sensitivity <- parameters::compare_parameters(  
7   `Full data` = apim_distinguishable_model,  
8   `Without Couple 28` = apim_without_couple_28,  
9   keep = "\\efficacy_gmc_actor"  
10 )
```

Actor slope	Full data	Without Couple 28
Women	11.87**	8.44*
Men	7.97 *	5.23

* $p < .05$; ** $p < .01$. Couple 28 was flagged in both visual screens. Its omission weakens both slopes; only the men's result crosses $p = .05$.

Other sensitivity analyses you could do

Fit a small set of (prespecified) models to test:

- coding decisions
- different plausible outcome families or transformations
- missing-data handling
- covariates with a substantive confounding or precision rationale

Workflow

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6. **Visualize, interpret, and report results**

Reporting results and answering the research question

```
1 library(parameters)
2
3 parameters::model_parameters(apim_distinguishable_model, effects = 'fixed') |>
4   insight::print_md(footer = "")
```

Fixed Effects

Parameter	Coefficient	SE	95% CI	z	p
is female	32.85	3.34	(26.30, 39.40)	9.83	< .001
is male	29.17	2.87	(23.55, 34.79)	10.17	< .001
is female × efficacy gmc actor	11.87	4.14	(3.75, 19.98)	2.87	0.004
is male × efficacy gmc actor	7.97	3.61	(0.89, 15.05)	2.21	0.027
is female × efficacy gmc partner	3.09	4.21	(-5.16, 11.34)	0.73	0.463
is male × efficacy gmc partner	4.05	3.55	(-2.91, 11.01)	1.14	0.254

In this sample, higher self-efficacy was associated with more of one's own MVPA for both women and men, but not clearly with the partner's MVPA.

Reporting results and answering the research question

Random effects in our model represent the residual structure

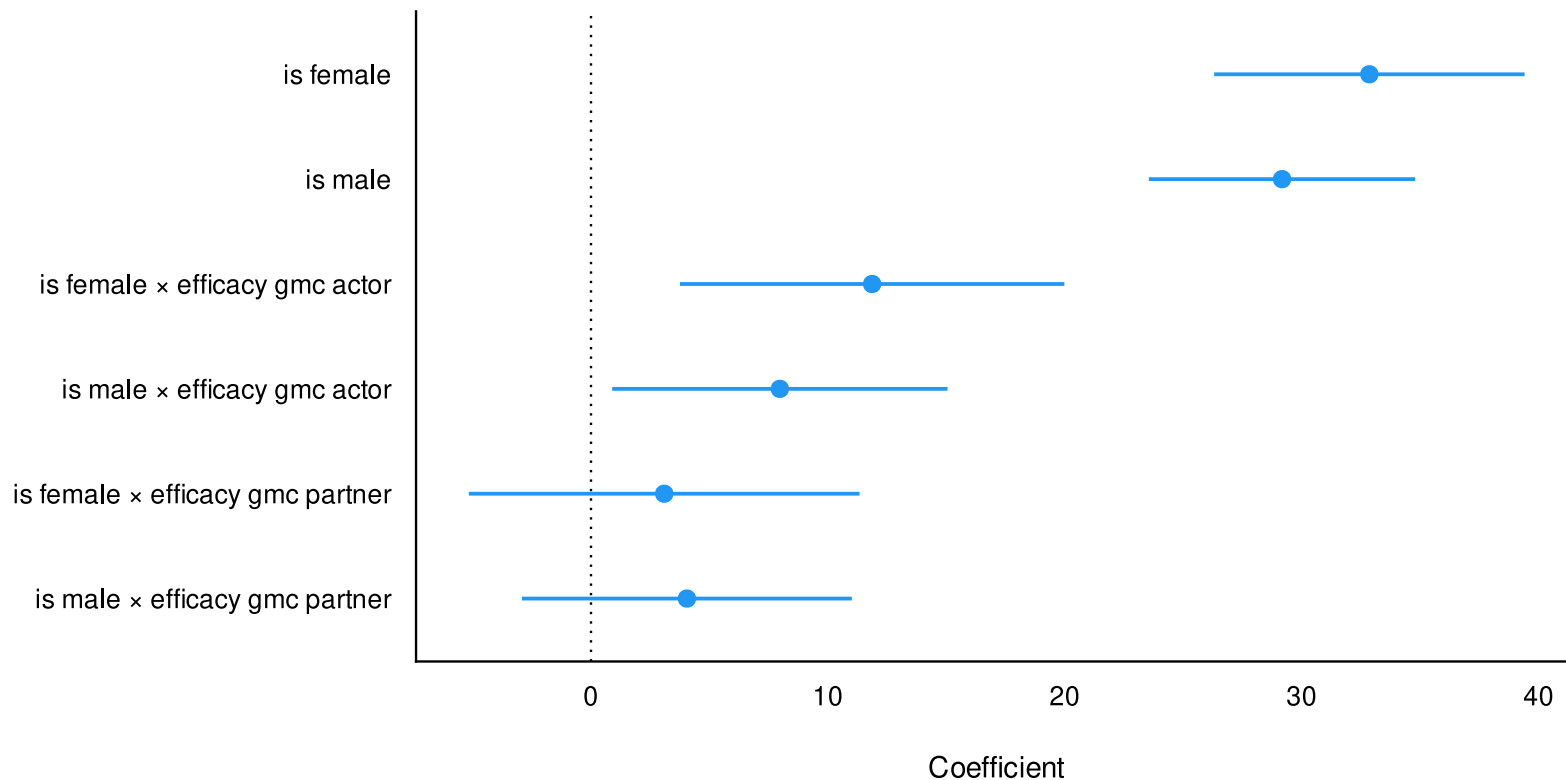
```
1 parameters::model_parameters(apim_distinguishable_model, effects = 'random') |>  
2   insight::print_md(footer = "")
```

Random Effects

Parameter	Coefficient	95% CI
SD (.is_female: couple_id)	19.70	(15.64, 24.83)
SD (.is_male: couple_id)	16.91	(13.42, 21.31)
Cor (.is_female~.is_male: couple_id)	0.79	

Visualize results

```
1 parameters::model_parameters(apim_distinguishable_model, effects = "fixed") |>  
2   plot()
```



What should be reported?

- **Analysis sample:** dyads and observations, exclusions, aggregation, and missing-data handling
- **Model specification:** outcome family and link, fixed effects, dyadic covariance structure, and equality constraints
- **Estimation and model decision:** estimator, software and version, convergence, boundary estimates, distinguishability comparison, and retained model
- **Results:** focal estimates with 95% confidence intervals in substantive units and the fitted variance-covariance parameters
- **Checks and interpretation:** residual diagnostics, influential dyads, prespecified sensitivity analyses, material changes, and causal limits



Short break!

Exchangeable dyads

The same model but constrained

Workflow

1. **Define dyads, distinguishability, and research questions**
2. Prepare the data and validate the dyadic structure
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Define dyads, distinguishability, and research questions

Same data and RQ, now with exchangeability constraints for illustration.

Workflow

1. Define dyads, distinguishability, and research questions
2. **Prepare the data and validate the dyadic structure**
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Create the required format and validate the data

You can use `dyadMLM::prepare_dyad_data()` to prepare and validate the data.

For exchangeable dyads, we can just omit the `role` argument.

```
1 apim_exchangeable_data <- dyadMLM::prepare_dyad_data(  
2   data = raw_dyad_data,  
3   dyad = couple_id,  
4   member = person_id,  
5   predictors = efficacy,  
6   model_types = 'apim',  
7   add_apim_gmc_predictors = TRUE,  
8   seed = 123  
9 )  
10  
11 print(apim_exchangeable_data)
```

If we want to estimate both distinguishable and exchangeable versions, we would pass `role` and set `include_arbitrary_member_contrast = TRUE`.

Create the required format and validate the data

```
# dyadMLM data
# Rows: 72 | Dyads: 36 | Intensive longitudinal: no
# Structure: dyad = couple_id, member = person_id
#
# Dyad compositions:
# assumed_exchangeable exchangeable 36 dyads
#
# Added columns:
# .composition                inferred dyad composition
# .composition_role           composition-specific member role
# .is_exchangeable            composition-role indicator columns
# .member_contrast_arbitrary  composition-specific member contrasts coded
#                             -1/+1 in arbitrary direction for
#                             exchangeability-constrained random effects.
#                             Values are 0 for other compositions
# .{pred}_actor               APIM actor predictor: actor's original
#                             predictor values
# .{pred}_partner             APIM partner predictor: partner's original
#                             predictor values
# .{pred}_gmc                 APIM grand-mean-centered predictor source:
#                             original values minus the mean across all
#                             retained non-missing observations
# .{pred}_gmc_actor           APIM grand-mean-centered actor predictor:
```

Create the required format and validate the data

Looking at the relevant columns:

```
1 head(apim_exchangeable_data) |>
2   dplyr::select(
3     couple_id, person_id, .member_contrast_arbitrary, .efficacy_gmc,
4     .efficacy_gmc_actor, .efficacy_gmc_partner, total_mvpa
5   ) |>
6   slide_table()
```

couple_id	person_id	.member_contrast_arbitrary	.efficacy_gmc	.efficacy_gmc_actor	.efficacy_gmc_partner	total_mvpa
1.00	1.00	-1.00	0.64	0.64	-1.49	
1.00	2.00	1.00	-1.49	-1.49	0.64	
2.00	3.00	-1.00	-2.24	-2.24	-0.01	
2.00	4.00	1.00	-0.01	-0.01	-2.24	
3.00	5.00	-1.00	0.96	0.96	-0.76	
3.00	6.00	1.00	-0.76	-0.76	0.96	

Workflow

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Describe focal variables (pooled)

No wide-view of the data is needed for exchangeable dyads. We can describe the data directly to obtain pooled estimates:

```
1 apim_exchangeable_data |>
2   dplyr::select(efficacy, total_mvpa) |>
3   report::report_table() |>
4   slide_table()
```

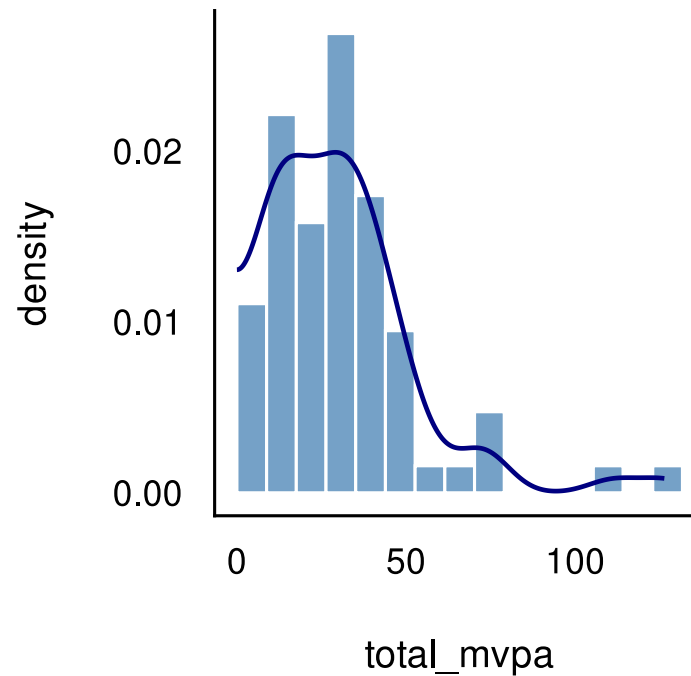
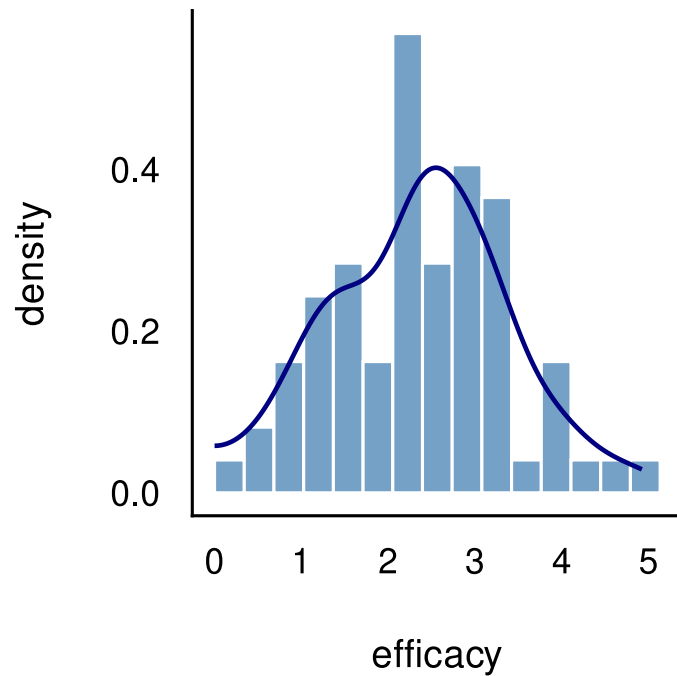
Variable	n_Obs	Mean	SD	Median	MAD	Min	Max	Skewness	Kurtosis	n_Missing
efficacy	72.00	2.38	0.99	2.38	1.06	0.13	4.92	0.09	-0.15	0.00
total_mvpa	72.00	31.21	22.40	27.55	18.67	3.43	126.35	1.89	5.34	0.00

Visualize focal variables

```
1 plot_pooled_histogram <- function(data, var) {  
2   var_label <- rlang::as_label(rlang::enquo(var))  
3  
4   ggplot(  
5     data,  
6     aes(x = {{ var }}, y = after_stat(density))  
7   ) +  
8     geom_histogram(  
9       bins = 15, boundary = 0,  
10      fill = "steelblue", color = "white", alpha = 0.75  
11    ) +  
12    geom_density(  
13      bounds = c(0, Inf), color = "navy", linewidth = 1.1  
14    ) +  
15    see::theme_modern(base_size = 16)  
16  }
```

Visualize focal variables

```
1 see::plots(  
2   plot_pooled_histogram(apim_exchangeable_data, efficacy),  
3   plot_pooled_histogram(apim_exchangeable_data, total_mvpa)  
4 )
```



Observed correlations

For exchangeable dyads, ICCs summarize partner similarity:

```
1 library(wbCorr)
2
3 apim_exchangeable_correlations <- wbCorr(
4   apim_exchangeable_data[,c('efficacy','total_mvpa')],
5   cluster = apim_exchangeable_data$couple_id
6 )
7
8 summary(apim_exchangeable_correlations, 'wb')
```

```
$merged_wb
      efficacy total_mvpa
efficacy  [0.60]      0.44**
total_mvpa 0.56***    [0.79]
```

```
$note
[1] "***p < 0.001, **p < 0.01, *p < 0.05"
```

Diagonal ICCs: expected correlation between partners on each variable

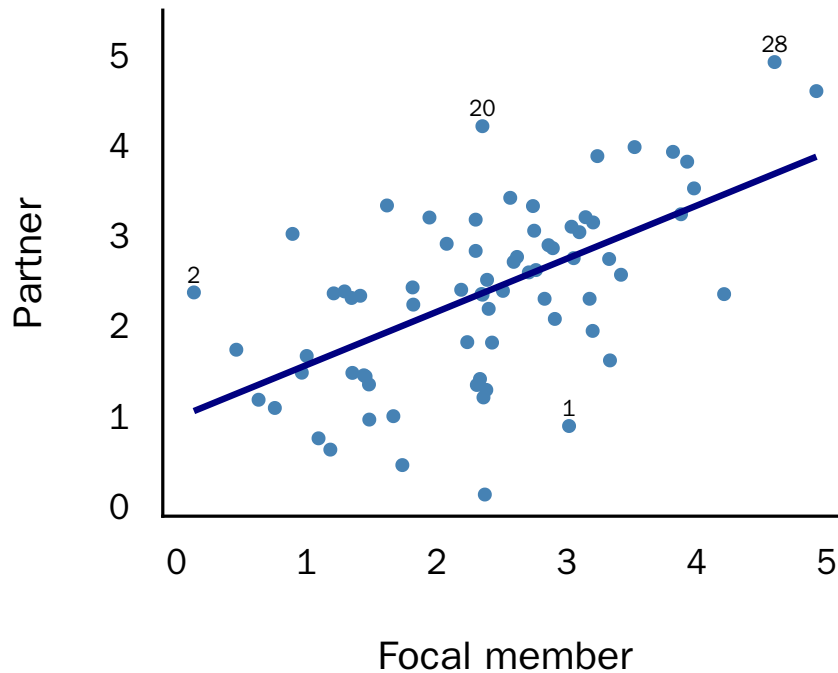
Off-diagonals: top right = within-couple correlation; bottom left = between-couple correlation

Visualize partner similarity

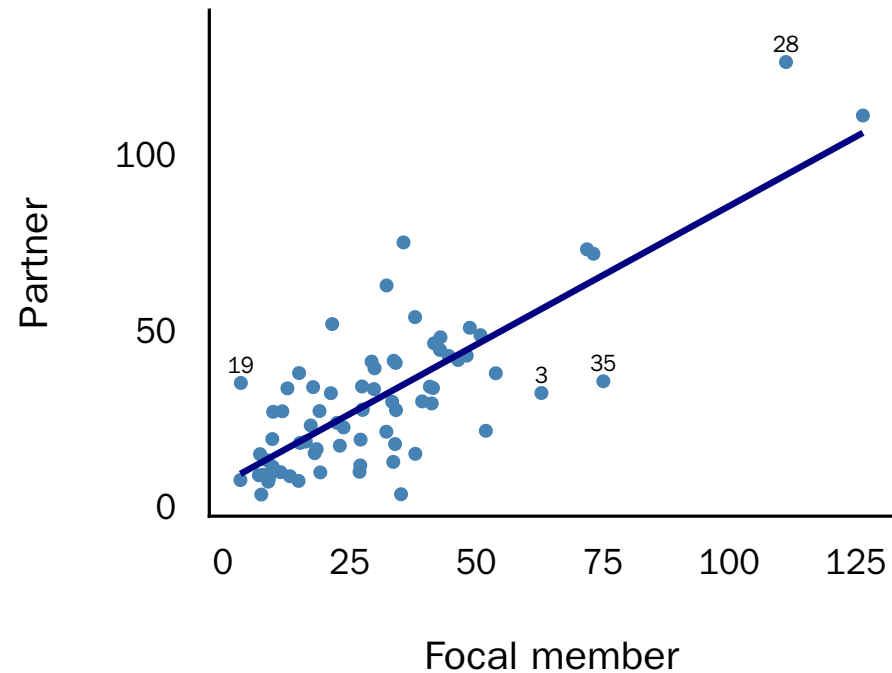
```
1 partner_similarity_data <- apim_exchangeable_data |>
2   dplyr::group_by(couple_id) |>
3   dplyr::mutate(
4     efficacy_partner = rev(efficacy),
5     total_mvpa_partner = rev(total_mvpa)
6   ) |>
7   dplyr::ungroup()
8
9 see::plots(
10   plot_partner_similarity(
11     partner_similarity_data,
12     efficacy, efficacy_partner, couple_id, "Efficacy",
13     n_mahalanobis = 4
14   ) +
15     labs(x = "Focal member", y = "Partner"),
16   plot_partner_similarity(
17     partner_similarity_data,
18     total_mvpa, total_mvpa_partner, couple_id, "Daily MVPA",
19     n_mahalanobis = 4
20   ) +
21     labs(x = "Focal member", y = "Partner")
22 )
```

Visualize partner similarity

Efficacy



Daily MVPA

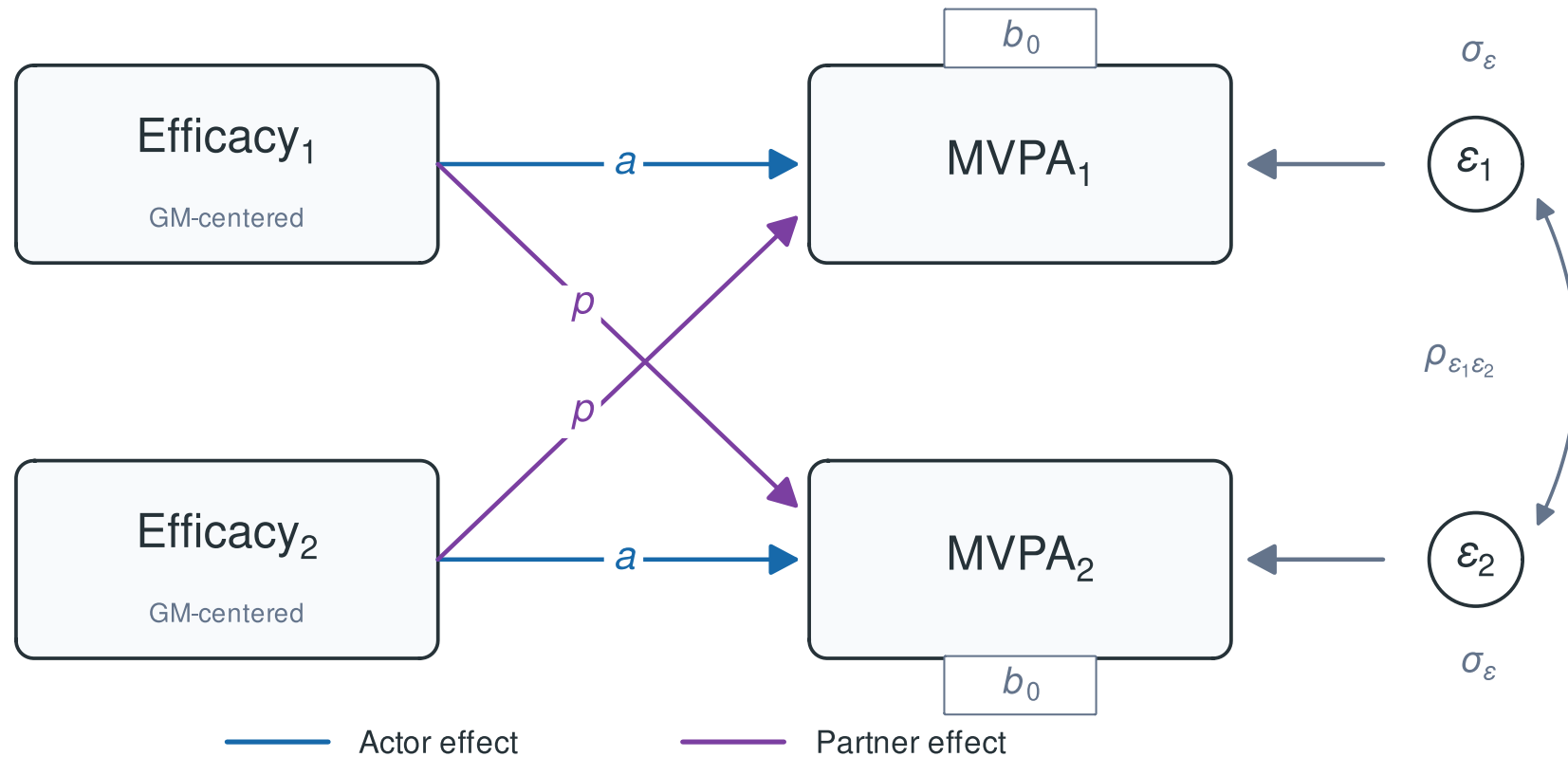


Each couple is shown twice—once in each orientation; labels mark the four largest dyad-level Mahalanobis distances.

Workflow

1. Define dyads, distinguishability, and research questions
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Exchangeable APIM



In MLM we constrain / pool by omitting terms

One single equation:

For each dyad i , each member j has their own predictor $X_{j,i}^{(A)}$ and their partner's predictor $X_{j,i}^{(P)}$:

$$Y_{j,i} = b_0 + a \times X_{j,i}^{(A)} + p \times X_{j,i}^{(P)} + \epsilon_{j,i}$$

- Actor effects - Partner effects

In long format, each equation applies to one member row of the dyad.

The tricky part: residuals need to remain correlated within dyads

- The two member rows from the same dyad retain a joint residual structure
- Both members now have the same residual variance (pooled)
- Position 1 and 2 within the dyad are arbitrary

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

Fitting the exchangeable APIM in glmmTMB

```
1 apim_exchangeable_model <- glmmTMB(  
2   total_mvpa ~  
3     # Pooled intercept  
4     1 +  
5  
6     # Pooled actor effect  
7     .efficacy_gmc_actor +  
8  
9     # Pooled partner effect  
10    .efficacy_gmc_partner +  
11  
12    #----- Within-dyad residual covariance (Sum/Deviation) -----  
13  
14    # Residuals of partners might be similar (positively correlated)  
15    (1 | couple_id) +  
16  
17    # Residuals of partners might move opposite (negatively correlated)  
18    (0 + .member_contrast_arbitrary | couple_id),  
19  
20    dispformula = ~ 0,  
21    family = gaussian(),  
22    data = apim_exchangeable_data  
23 )  
24
```

The mean-deviation parameterization

- The DIM is equivalent to the APIM
- The DIM represents member residuals using two uncorrelated components:
 - Mean block (`1 | couple_id`): $r_{Mi} = (\epsilon_{1i} + \epsilon_{2i})/2$; both members move together
 - Deviation block (`0 + .member_contrast_arbitrary | couple_id`):
 $r_{Di} = (\epsilon_{1i} - \epsilon_{2i})/2$; members move in opposite directions

Using this parametrization allows us to represent random effects and later in ILD even random slopes with the correct constraints.

We can later backtransform to the familiar person-level structure.

Workflow

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6. Visualize, interpret, and report results

Verify model adequacy, distinguishability, and robustness

Same as before:

1. Did estimation succeed?
2. Does the model reproduce the important data patterns?
3. Does a distinguishable model fit clearly better?
4. Are conclusions robust or driven by few dyads or consequential modeling choices? (sensitivity analyses)

Workflow

1. Define dyads, distinguishability, and research questions
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3. Describe and visualize measures and observed relationships
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5. Verify model adequacy, distinguishability, and robustness
6. **Visualize, interpret, and report results**

Reporting results and answering the research questions

```
1 parameters::model_parameters(apim_exchangeable_model, effects = 'fixed') |>  
2   insight::print_md(footer = "")
```

Fixed Effects

Parameter	Coefficient	SE	95% CI	z	p
(Intercept)	31.21	2.89	(25.54, 36.88)	10.79	< .001
efficacy gmc actor	10.34	2.04	(6.35, 14.34)	5.07	< .001
efficacy gmc partner	3.17	2.04	(-0.83, 7.17)	1.55	0.120

In the parsimonious exchangeable model, higher self-efficacy was associated with more of one's own MVPA, but not clearly with the partner's MVPA.

Reporting results and answering the research questions

```
1 parameters::model_parameters(apim_exchangeable_model, effects = 'random') |>  
2   insight::print_md(footer = "")
```

Random Effects

Parameter	Coefficient	95% CI
SD (Intercept: couple_id)	17.36	(13.78, 21.87)
SD (.member_contrast_arbitrary: couple_id)	6.48	

Often it is preferable to rotate the covariance back to the familiar member-level covariance matrix:

- Member residual variance: $\text{Var}(\epsilon_{1i}) = \text{Var}(\epsilon_{2i}) = \text{Var}(r_{Mi}) + \text{Var}(r_{Di})$
- Partner residual covariance: $\text{Cov}(\epsilon_{1i}, \epsilon_{2i}) = \text{Var}(r_{Mi}) - \text{Var}(r_{Di})$

Reporting results and answering the research questions

No need to do so by hand. Rotating back with `dyadMLM`:

```
1 dyadMLM::recover_exchangeable_covariance(apim_exchangeable_model)
```

Recovered exchangeable member-level covariance

```
Pair `pair_1`  
Shared:      us(1 | couple_id)  
Difference: us(0 + .member_contrast_arbitrary | couple_id)
```

Variance-covariance:

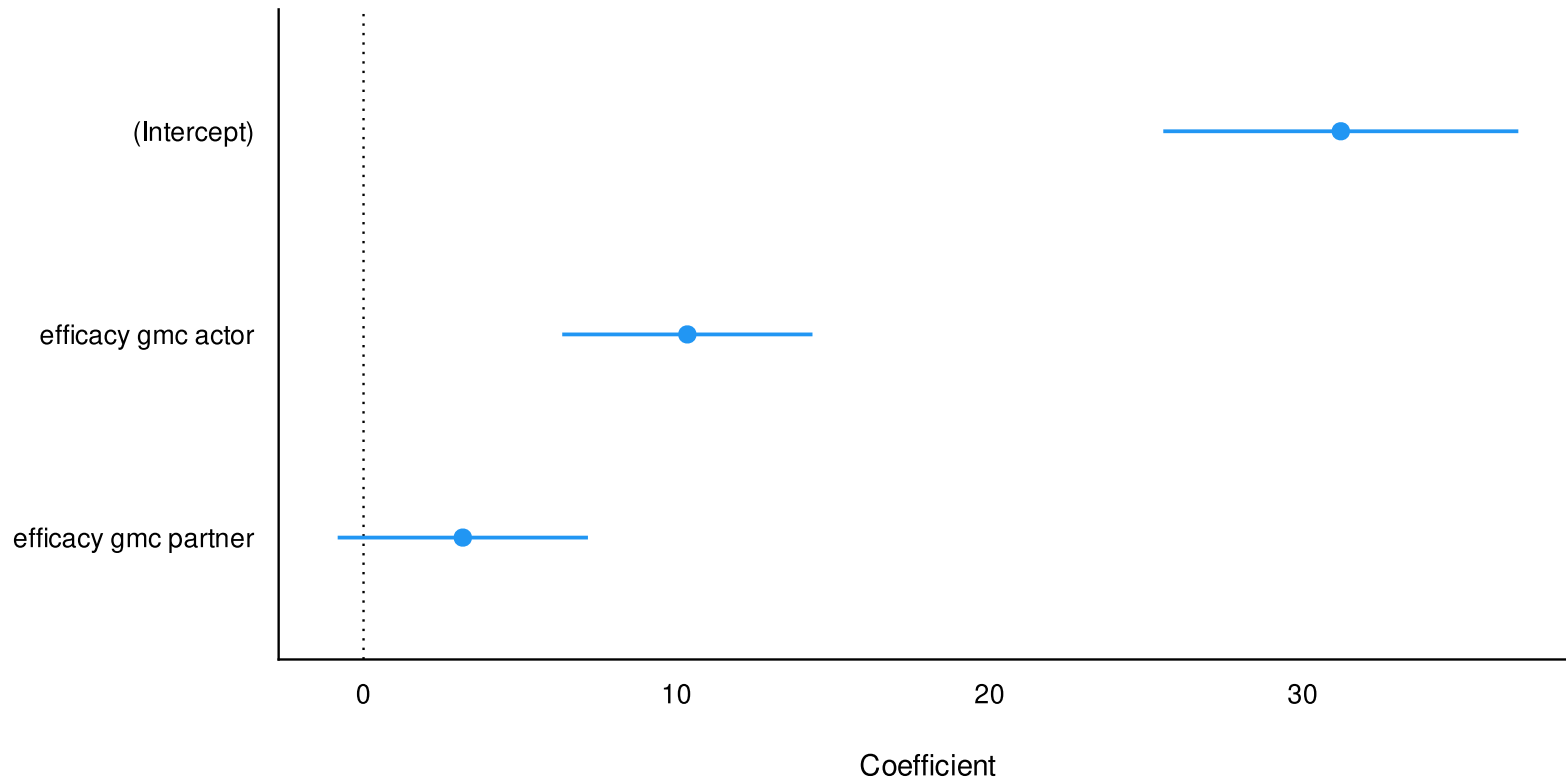
```
              1      2  
1 member1: (Intercept) 343.216 259.269  
2 member2: (Intercept) 259.269 343.216
```

Standard deviations and correlations:

```
              1      2  
1 member1: (Intercept) 18.526 0.755  
2 member2: (Intercept) 0.755 18.526
```

Visualize results

```
1 parameters::model_parameters(apim_exchangeable_model, effects = 'fixed') |>  
2 plot(show_intercept = TRUE)
```



Optional: DIM and DSM

Worked examples are available in the package vignettes of [dyadMLM](#).

Open the DIM vignette →

Open the DSM vignette →



Intensive longitudinal APIM

Intensive longitudinal APIM - Workflow

We can follow the same workflow. Additional possible ILD considerations:

- Check compliance / missingness
- Inspect and visualize paired trajectories and patterns
- Separate within- and between-person variation
 - Inspect ICCs and multilevel reliability where applicable
 - Model dyads on multiple levels
- Check and account for residual temporal dependence

Synthesized from Bolger & Laurenceau (2013), Revol et al. (2024), McNeish & Hamaker (2020), and del Rosario & West (2025).

Workflow

1. **Define dyads, distinguishability, and research questions**
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The Dataset

Same as before:

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

Not aggregated anymore

ILD Research Question

RQ: How are previous-day deviations and stable between-person differences in perceived behavioral control over next-day physical activity associated with one's own and one's partner's current-day MVPA?

Measurement - predictor

Perceived behavioral control (PBC) over next-day physical activity

Rough English translation of the original German item

“Being physically active tomorrow would/will be for me ...”

Adapted from Ajzen (1991)

0 = *impossible—crucial prerequisites are not met*

3 = *possible with some effort—several prerequisites are not met*

6 = *easily possible—all prerequisites are met*

- Lagged predictor: perceived behavioral control on day $t - 1$, MVPA on day t

Measurement - outcome

Device-based MVPA

Accelerometer-derived measure

Daily minutes of moderate-to-vigorous physical activity

- Days with less than 10 hours of awake wear time → NA
- Analyze $\log(\text{MVPA})$ to reduce right skew

Exponentiated coefficients describe multiplicative differences in MVPA.

Workflow

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Load the daily measures

We set MVPA to `NA` on days with less than 10 hours of weartime, center time at the middle of the study in full-study units, and select the needed variables.

```
1 raw_ild_dyad_data <- readRDS("dyadic-data.rds") |>
2   dplyr::mutate(
3     device_based_mvpa = dplyr::if_else(
4       awake_wear_minutes >= 600,
5       device_based_mvpa,
6       NA
7     ),
8     log_device_based_mvpa = log(device_based_mvpa),
9     diaryday_c = (diaryday - 27) / 54
10  ) |>
11  dplyr::select(
12    couple_id, person_id, diaryday, diaryday_c, gender,
13    pbc = perceived_behavioral_control,
14    device_based_mvpa, log_device_based_mvpa, awake_wear_minutes
15  ) |>
16  dplyr::arrange(couple_id, diaryday, person_id)
17
18  slide_table(head(raw_ild_dyad_data))
```

Load the daily measures

couple_id	person_id	diaryday	diaryday_c	gender	pbc	device_based_mvpa	log_device_based_mvpa	awake_w
1.00	1.00	0.00	-0.50	male	6.00	156.25	5.05	
1.00	2.00	0.00	-0.50	female	2.00	NA	NA	
1.00	1.00	1.00	-0.48	male	6.00	134.50	4.90	
1.00	2.00	1.00	-0.48	female	3.00	152.00	5.02	
1.00	1.00	2.00	-0.46	male	4.00	99.00	4.60	
1.00	2.00	2.00	-0.46	female	3.00	NA	NA	

Create the required format and validate the data

For ILD we **decompose** the predictor(s):

- Between-person component: Person mean centered on the mean of person means (stable)
 - $\bar{X}_{ri} - \bar{X}$
- Within-person component: Daily deviations from the person mean
 - $X_{ri,t} - \bar{X}_{ri}$

In this example we then lag the within-person component ($X_{ri,t-1}$)

Create the required format and validate the data

[Manual code →](#)

The `dyadMLM` package can handle centering alongside the construction and validation of the dyadic dataset:

```
1 ild_apim_data <- dyadMLM::prepare_dyad_data(  
2    data = raw_ild_dyad_data,  
3    dyad = couple_id,  
4    member = person_id,  
5    role = gender,  
6    time = diaryday,  
7    predictors = pbc,  
8    lag1_predictors = pbc,  
9    model_types = "apim",  
10   temporal_decomposition = "21",  
11   include_arbitrary_member_contrast = TRUE,  
12   seed = 123  
13 )  
14  
15 ild_apim_data <- ild_apim_data |>  
16   dplyr::mutate(  
17     diaryday_f = factor(diaryday, levels = 0:54)  
18   )  
19  
20 print(ild_apim_data)
```

Create the required format and validate the data

[Manual code →](#)

```
# dyadMLM data
# Rows: 3960 | Dyads: 36 | Intensive longitudinal: yes
# Structure:
#   dyad = couple_id, member = person_id, role = gender, time = diaryday
#
# Dyad compositions:
# female_x_male distinguishable 36 dyads
#
# Added columns:
#   .composition           inferred dyad composition
#   .composition_role      composition-specific member role
#   .is_{role}             composition-role indicator columns
#   .member_contrast_arbitrary composition-specific member contrasts coded
#                           -1/+1 in arbitrary direction for
#                           exchangeability-constrained random effects.
#                           Values are 0 for other compositions
#   .{pred}_lag1           lag-1 raw predictor values
#   .{pred}_cwp            within-person predictor: momentary deviations
#                           from each person's usual level
#   .{pred}_cwp_lag1       lag-1 within-person predictor: momentary
#                           deviations from each person's usual level
#   .{pred}_cbp            between-person predictor: stable differences
#                           from the average person's usual level
```

Workflow

1. Define dyads, distinguishability, and research questions
2. Prepare the data and validate the dyadic structure
3. **Describe and visualize measures and observed relationships**
4. Estimate the models
5. Verify model adequacy, distinguishability, and robustness
6. Visualize, interpret, and report results

Report measures

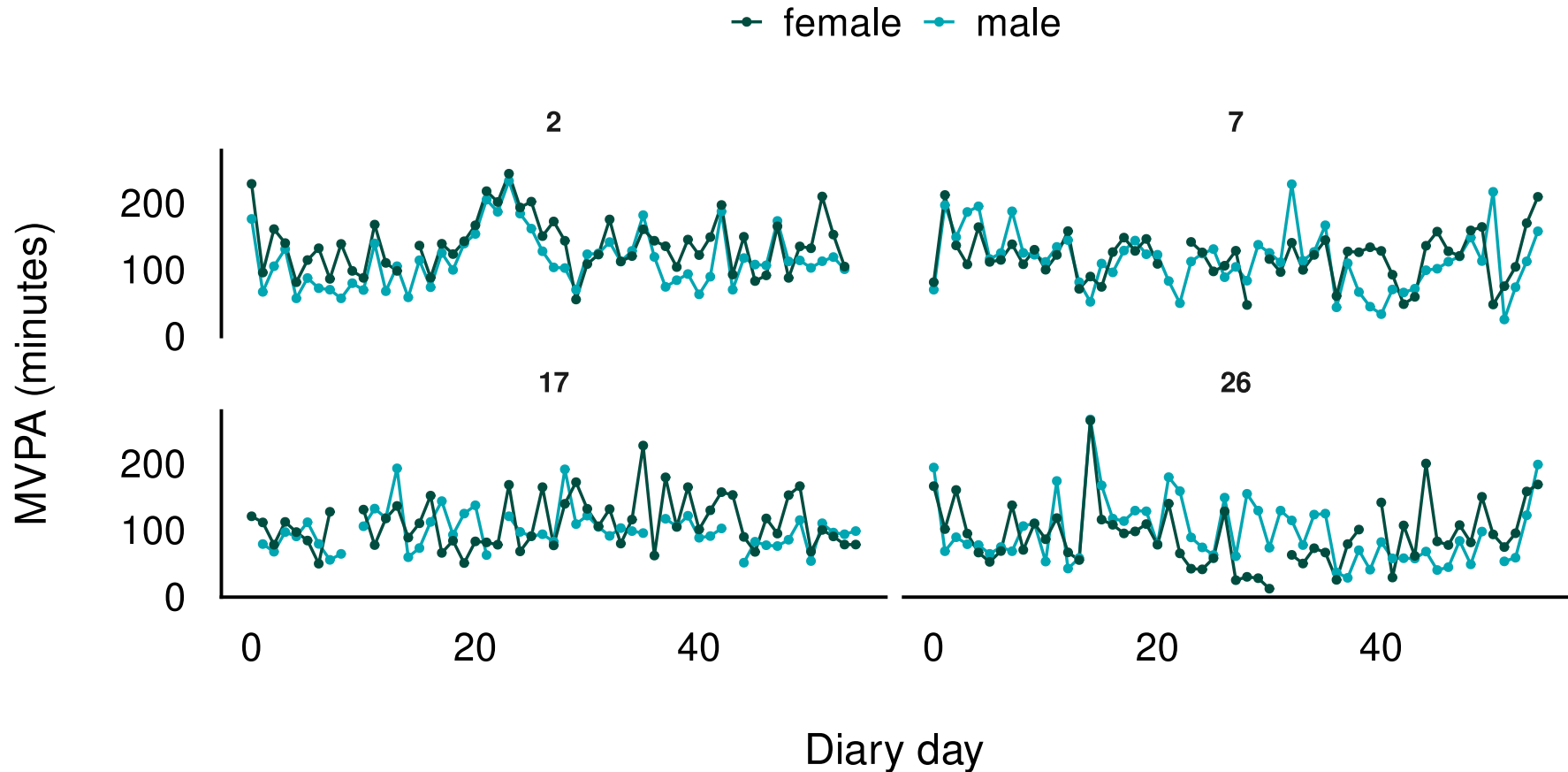
Among other things you may check and report:

- Missingness and general summary statistics
- ICCs
- Within- and between- person correlations (e.g., with `wbCorr`)
- Visualize outcome trajectories over time

Plot paired raw MVPA trajectories

```
1 raw_ild_dyad_data |>
2   dplyr::filter(couple_id %in% c(2, 7, 17, 26)) |>
3   ggplot(aes(diaryday, device_based_mvpa, color = gender,
4             group = person_id)) +
5   geom_line(linewidth = 0.65, na.rm = TRUE) +
6   geom_point(size = 1.1, na.rm = TRUE) +
7   facet_wrap(~ couple_id, ncol = 2) +
8   scale_color_manual(values = c(female = "#004D40", male = "#00A6B2")) +
9   scale_y_continuous(breaks = seq(0, 300, by = 100)) +
10  labs(x = "Diary day", y = "MVPA (minutes)", color = NULL) +
11  see::theme_modern(base_size = 16) +
12  theme(legend.position = "top")
```

Plot paired raw MVPA trajectories



Workflow

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Fitting the ILD APIM: Two member-specific equations

For dyad i at occasion t , superscripts W and B denote within-person and between-person components.

$$Y_{M,i,t} = b_{0,M} + a_M^W X_{M,i,t-1}^{(A,W)} + a_M^B X_{M,i}^{(A,B)} + p_M^W X_{M,i,t-1}^{(P,W)} + p_M^B X_{M,i}^{(P,B)} + u_{0,Mi} +$$

$$Y_{F,i,t} = b_{0,F} + a_F^W X_{F,i,t-1}^{(A,W)} + a_F^B X_{F,i}^{(A,B)} + p_F^W X_{F,i,t-1}^{(P,W)} + p_F^B X_{F,i}^{(P,B)} + u_{0,Fi} + \epsilon_F$$

Actor effects · Partner effects

- $u_{0,ri}$: stable member-within-dyad deviation
- $\epsilon_{r,it}$: occasion-specific residual
- **Optional random slope:** add $u_{A,ri} X_{r,i,t-1}^{(A,W)}$
- **Same stacking approach:** role indicators select the male or female equation

Repeated measures separate two covariance levels

Stable across occasions

`couple_id`

- Role-specific random intercepts
- Optional role-specific random slopes
- Partner covariance in stable levels or slopes

At each single occasion

`couple_id:diaryday`

- Partner-specific Gaussian residual variance
- Same-occasion residual correlation
- Independent across occasions unless modeled otherwise

Fitting the distinguishable ILD APIM with glmmTMB

```
1 ild_apim_distinguishable_model <- glmmTMB::glmmTMB(  
2    log_device_based_mvpa ~  
3  
4    # Role-specific fixed intercepts  
5    0 + .is_female + .is_male +  
6  
7    # Role-specific fixed time-slope  
8    .is_female:diaryday_c + .is_male:diaryday_c +  
9  
10   # ----- WITHIN PERSON APIM -----  
11   # Role-specific fixed actor- and partner effects  
12  
13   .is_female:.pbc_cwp_actor_lag1 +  
14   .is_male:.pbc_cwp_actor_lag1 +  
15  
16   .is_female:.pbc_cwp_partner_lag1 +  
17   .is_male:.pbc_cwp_partner_lag1 +  
18  
19   # ----- BETWEEN PERSON APIM -----  
20   # Role-specific fixed actor-and partner effects  
21  
22   .is_female:.pbc_cbp_actor +  
23   .is_male:.pbc_cbp_actor +  
24
```

Workflow

1. Define dyads, distinguishability, and research questions
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6. Visualize, interpret, and report results

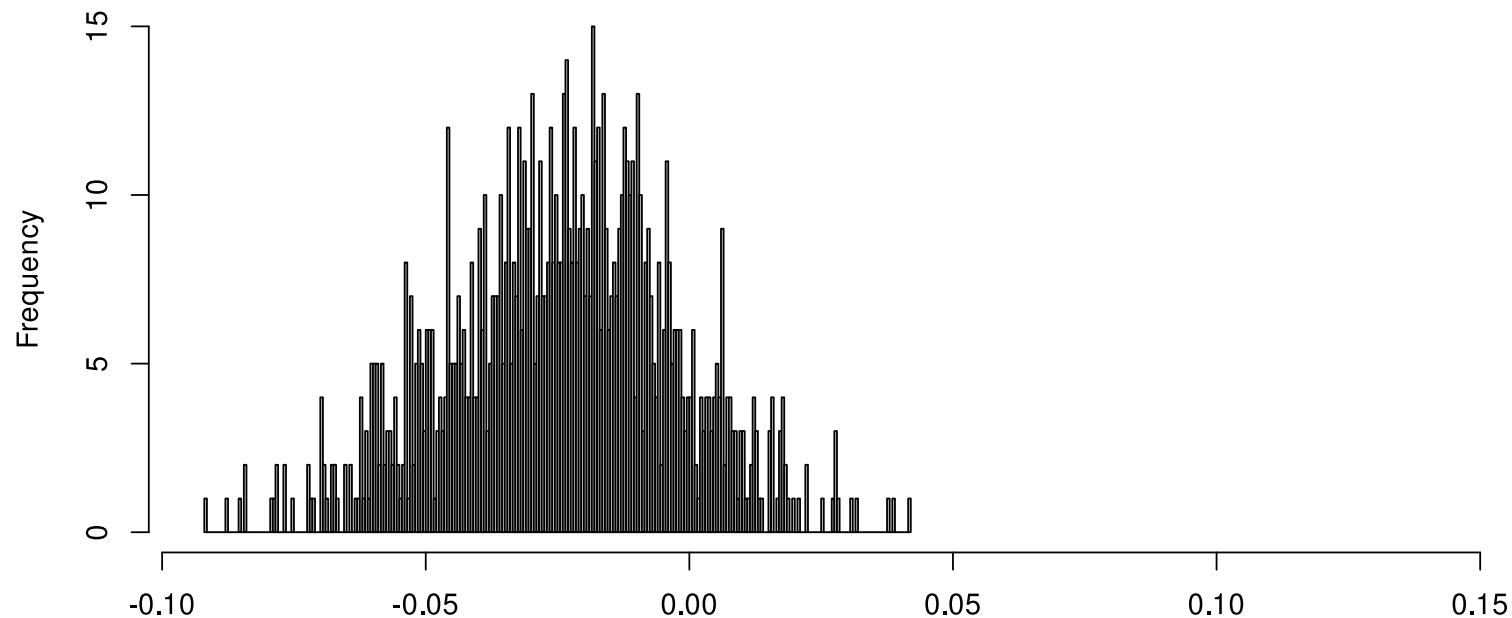
Testing for residual autocorrelation

```
1 ild_apim_no_ar_dharma <- simulate_ild_dharma(  
2   model = ild_apim_distinguishable_model,  
3   dyad = ild_apim_data$couple_id,  
4   member = ild_apim_data$person_id,  
5   time = ild_apim_data$diaryday,  
6   n = 1000,  
7   seed = 123  
8 )  
9  
10 diagnostic <- test_ild_lag1(  
11   ild_apim_no_ar_dharma,  
12   plot = TRUE  
13 )
```

The helper compares the observed consecutive-day correlation with correlations simulated from the fitted model.

Testing for residual autocorrelation

Consecutive-day lag-1 residual-dependence check



Simulated values; red = observed; $p < .001$

Add role-specific residual AR(1) processes

- Separate AR(1) series for the female and male partner
- Role-specific residual variability and persistence ρ
- Same-day partner covariance retained separately

```
1 ild_apim_distinguishable_ar1_model <- update(  
2    ild_apim_distinguishable_model,  
3    . ~ . +  
4      ar1(0 + .is_female:diaryday_f | couple_id) +  
5      ar1(0 + .is_male:diaryday_f | couple_id)  
6  )
```

```
1 glmmTMB::VarCorr(ild_apim_distinguishable_ar1_model)
```

The two AR(1) terms represent independent member-specific persistence. The dyad-day SDs and correlation describe the remaining same-day variation.

Add role-specific residual AR(1) processes

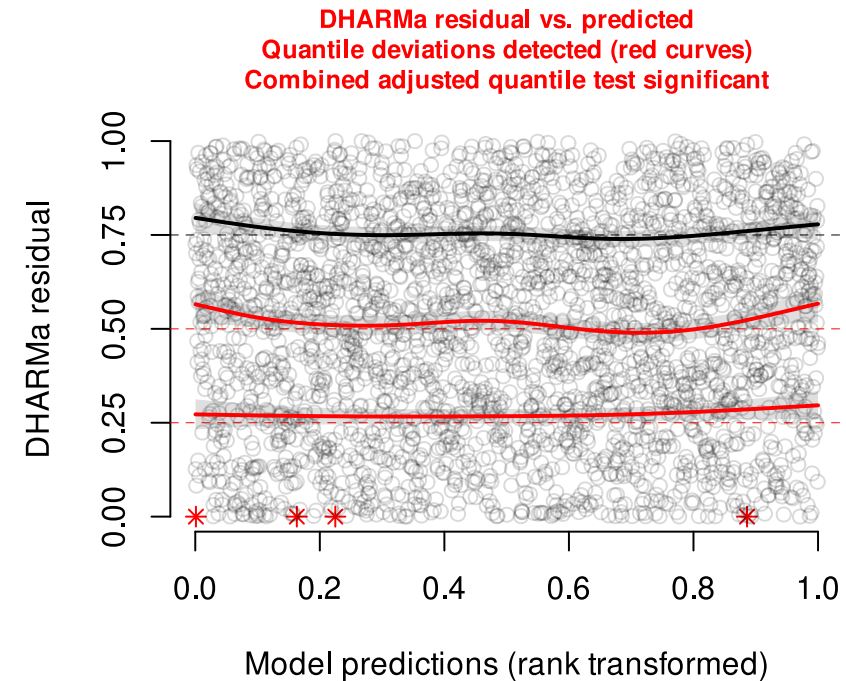
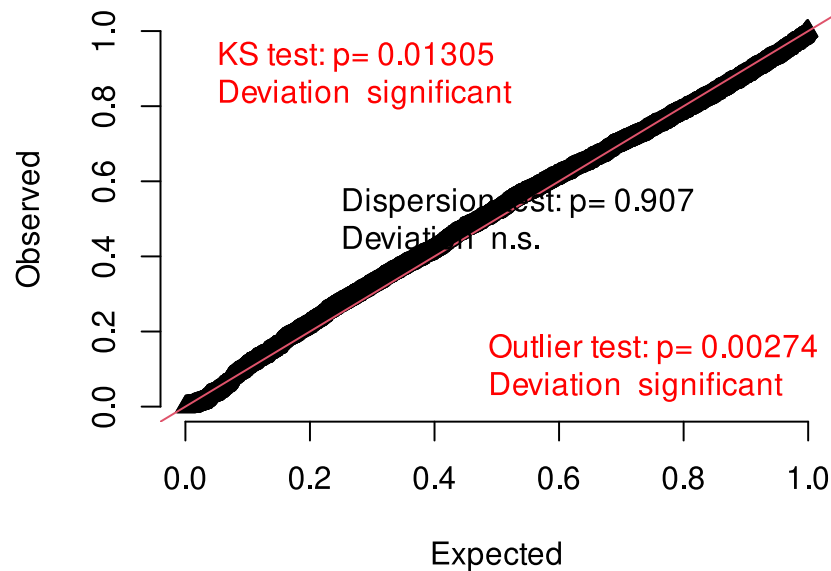
Conditional model:

Groups	Name	Std.Dev.	Corr
couple_id	.is_female	0.23723	
	.is_male	0.25925	0.343
couple_id.diaryday	.is_female	0.35352	
	.is_male	0.37559	0.388
couple_id.1	.is_female:diaryday_f1	0.23017	0.878 (ar1)
couple_id.2	.is_male:diaryday_f1	0.22912	0.814 (ar1)

Simulate residuals from the AR(1) model

DHARMa residual

QQ plot residuals

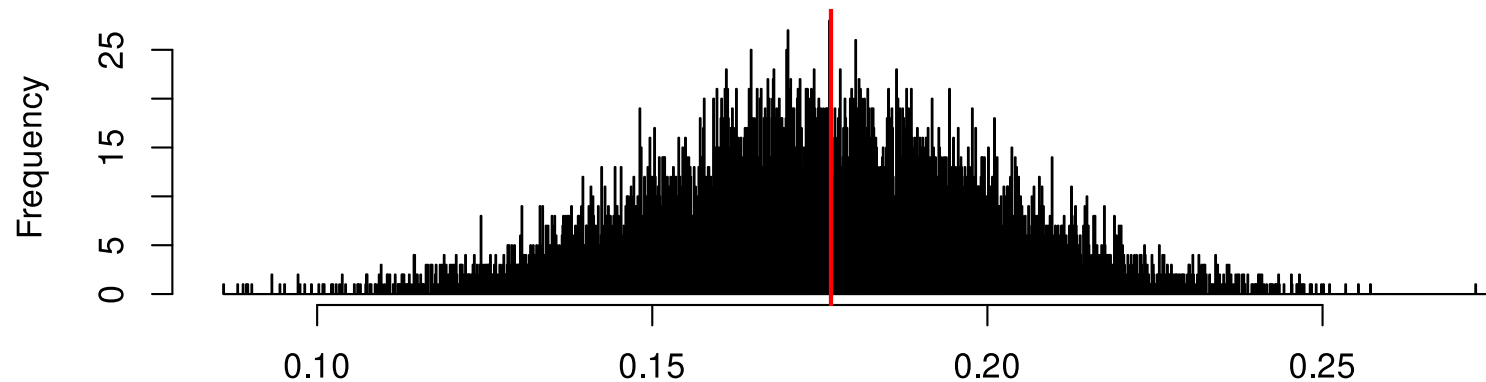


With almost 2,800 observations, DHARMa tests are very sensitive. Visual inspection becomes more meaningful.

Does the fitted AR(1) reproduce lag-1 dependence?

```
1 ild_apim_ar1_lag1_test <- test_ild_lag1(  
2    ild_apim_dharma_residuals,  
3    plot = TRUE  
4  )
```

Consecutive-day lag-1 residual-dependence check



Simulated values; red = observed; $p = .935$

The correlation need not become zero. It should be typical under simulations from the fitted AR(1) model.

Fit the exchangeable model with pooled AR(1)

```
1 ild_apim_exchangeable_ar1_model <- glmmTMB::glmmTMB(  
2    log_device_based_mvpa ~  
3      1 +  
4      diaryday_c +  
5      .pbc_cwp_actor_lag1 +  
6      .pbc_cwp_partner_lag1 +  
7      .pbc_cbp_actor +  
8      .pbc_cbp_partner +  
9  
10     # Couple-level variance-covariance structure  
11     (1 | couple_id) +  
12     (0 + .member_contrast_arbitrary | couple_id) +  
13  
14     # Occasion-level residual variance-covariance structure  
15     (1 | couple_id:diaryday) +  
16     (0 + .member_contrast_arbitrary | couple_id:diaryday) +  
17     ar1(0 + diaryday_f | couple_id:person_id),  
18     dispformula = ~ 0,  
19     family = gaussian(),  
20     data = ild_apim_data  
21 )  
22  
23 summary(ild_apim_exchangeable_ar1_model)
```

Each member retains a separate series, but residual variability and persistence ρ are pooled across members.

Fit the exchangeable model with pooled AR(1)

```
Family: gaussian ( identity )
Formula:
log_device_based_mvpa ~ 1 + diaryday_c + .pbc_cwp_actor_lag1 +
    .pbc_cwp_partner_lag1 + .pbc_cbp_actor + .pbc_cbp_partner +
    (1 | couple_id) + (0 + .member_contrast_arbitrary | couple_id) +
    (1 | couple_id:diaryday) + (0 + .member_contrast_arbitrary |
    couple_id:diaryday) + ar1(0 + diaryday_f | couple_id:person_id)
Dispersion:
~0
Data: ild_apim_data
```

AIC	BIC	logLik	-2*log(L)	df.resid
3052.4	3123.8	-1514.2	3028.4	2821

Random effects:

Conditional model:

Groups	Name	Variance	Std.Dev.	Corr
couple_id	(Intercept)	0.04350	0.2086	
couple_id.1	.member_contrast_arbitrary	0.03149	0.1774	
couple_id.diaryday	(Intercept)	0.09234	0.3039	
couple_id.diaryday.1	.member_contrast_arbitrary	0.04146	0.2036	
couple_id.person_id	diaryday_f1	0.05190	0.2278	0.85 (ar1)

Number of obs: 2833, groups:

Backtransform to member-level variance-covariance structure

```
1 dyadMLM::recover_exchangeable_covariance(ild_apim_exchangeable_ar1_model)
```

Recovered exchangeable member-level covariances (2 block pairs)

Pair `pair\_1`

Shared: us(1 | couple_id)

Difference: us(0 + .member_contrast_arbitrary | couple_id)

Variance-covariance:

	1	2
1 member1: (Intercept)	0.075	0.012
2 member2: (Intercept)	0.012	0.075

Standard deviations and correlations:

	1	2
1 member1: (Intercept)	0.274	0.160
2 member2: (Intercept)	0.160	0.274

Pair `pair\_2`

Shared: us(1 | couple_id:diaryday)

Difference: us(0 + .member_contrast_arbitrary | couple_id:diaryday)

Compare distinguishable and exchangeable models

This is a global test, partial constraints can be informative too!

```
1 dyadMLM::compare_nested_models(  
2   ild_apim_distinguishable_ar1_model,  
3   ild_apim_exchangeable_ar1_model  
4 )
```

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  
ild_apim_exchangeable_ar1_model    12 3052.4 3123.8 -1514.2   3028.4  
ild_apim_distinguishable_ar1_model  22 3040.9 3171.8 -1498.5   2996.9 31.487  
              Chi Df Pr(>Chisq)  
ild_apim_exchangeable_ar1_model  
ild_apim_distinguishable_ar1_model    10 0.0004873 ***  
---  
Signif. codes:  0 '***' 0.001 '**' 0.01 '*' 0.05 '.' 0.1 ' ' 1
```

Conclusion (5% level): The likelihood-ratio test provides evidence that

`ild\_apim\_distinguishable\_ar1\_model` fits better than `ild\_apim\_exchangeable\_ar1\_model` (p < 0.001).

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Report the retained distinguishable model

We exponentiate estimates from the log-transformed outcome to obtain geometric mean ratios (GMRs; representing multiplicative differences).

```
1 parameters::model_parameters(  
2   ild_apim_distinguishable_ar1_model,  
3   effects = 'fixed',  
4   exponentiate = TRUE  
5 ) |>  
6 insight::print_md(footer = "")
```

Report the retained distinguishable model

Fixed Effects

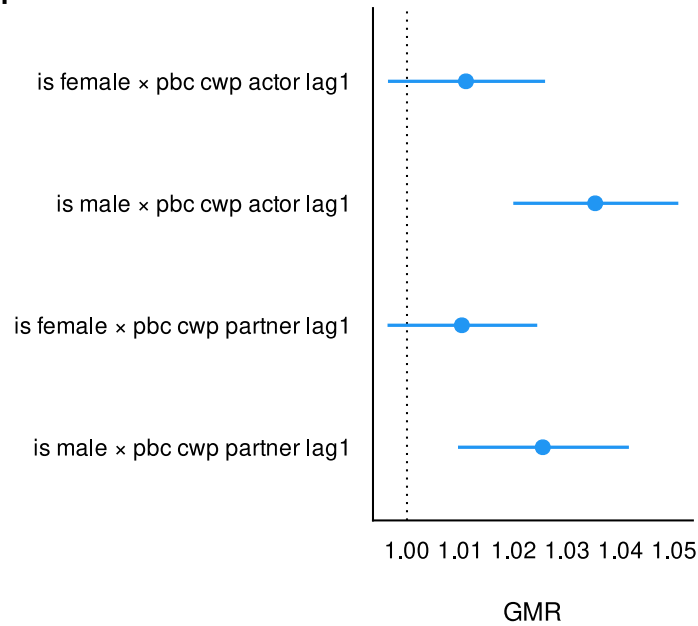
Parameter	Coefficient	SE	95% CI	z	p
is female	121.69	5.84	(110.77, 133.69)	100.11	< .001
is male	98.30	4.96	(89.05, 108.52)	90.94	< .001
is female × diaryday c	0.95	0.06	(0.84, 1.08)	-0.83	0.405
is male × diaryday c	0.98	0.06	(0.87, 1.10)	-0.38	0.705
is female × pbc cwp actor lag1	1.01	7.50e-03	(1.00, 1.03)	1.48	0.139
is male × pbc cwp actor lag1	1.04	7.88e-03	(1.02, 1.05)	4.55	< .001
is female × pbc cwp partner lag1	1.01	7.15e-03	(1.00, 1.02)	1.44	0.149
is male × pbc cwp partner lag1	1.03	8.16e-03	(1.01, 1.04)	3.15	0.002
is female × pbc cbp actor	0.98	0.06	(0.87, 1.11)	-0.29	0.769
is male × pbc cbp actor	1.11	0.06	(1.00, 1.24)	1.88	0.061
is female × pbc cbp partner	1.06	0.06	(0.96, 1.18)	1.19	0.233
is male × pbc cbp partner	1.01	0.07	(0.89, 1.15)	0.21	0.837

Report the retained distinguishable model

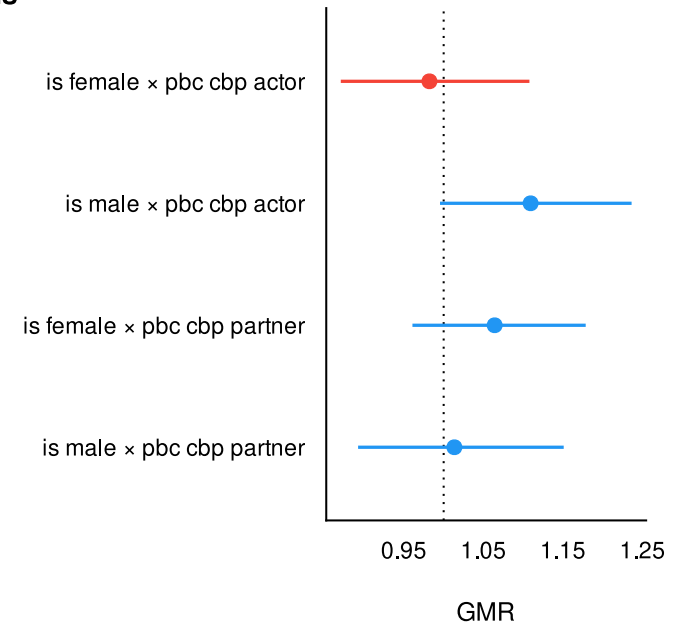
```
1 see::plots(  
2   parameters::model_parameters(  
3     ild_apim_distinguishable_ar1_model,  
4     effects = "fixed",  
5     exponentiate = TRUE,  
6     keep = "_cwp_"  
7   ) |> plot(),  
8   parameters::model_parameters(  
9     ild_apim_distinguishable_ar1_model,  
10    effects = "fixed",  
11    exponentiate = TRUE,  
12    keep = "_cbp_"  
13  ) |> plot(),  
14  n_columns = 2,  
15  tags = c("Within person", "Between persons")  
16 ) &  
17 ggplot2::labs(x = "GMR")
```

Report the retained distinguishable model

Within person



Between persons



Report the retained distinguishable model

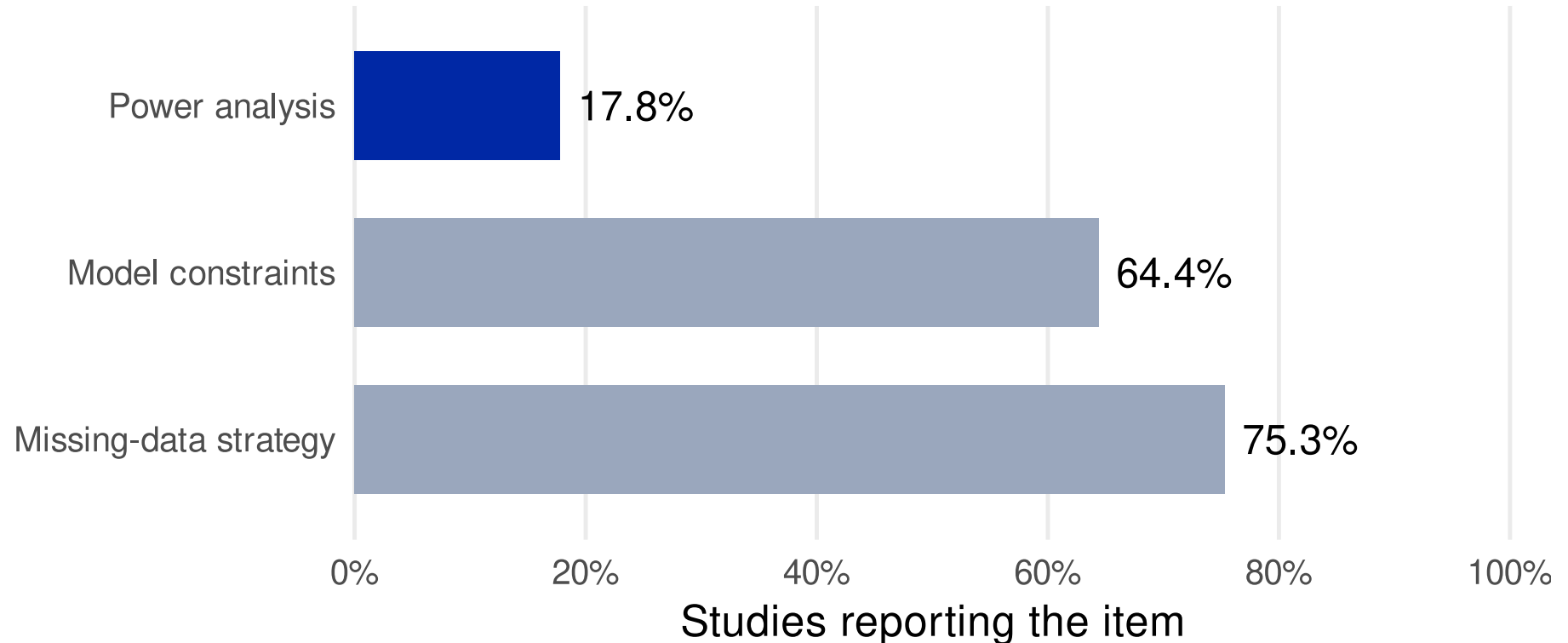
Within person: Men's MVPA was 3.5% higher when their own previous-day PBC was one point above usual, and 2.5% higher when their partner's was.

Between persons: There was no clear evidence of actor or partner associations.



General reporting practices for ILD APIM studies

Many studies lack complete reporting



Systematic review of 73 longitudinal APIM studies published from 2008–2025
([Mohammadzadeh Yazd et al., 2026](#)).

Make every dyadic analysis decision visible

1. **Preregister** actor and partner hypotheses and key analysis decisions.
2. **Explain missing data:** describe missingness and the handling strategy.
3. **Specify the full model:** roles and distinguishability, actor and partner paths, constraints, and covariance structure.
4. **Report reliability where applicable:** within- and between-level omega for multilevel item scales, e.g., `multilevelTools::omegaSEM()` ([Geldhof et al., 2014](#); [Wiley, 2025](#)).

Mohammadzadeh Yazd et al. (2026)

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

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- Bürkner, P.-C. (n.d.). *Autocorrelation structures*. Retrieved July 23, 2026, from <https://paulbuerkner.com/brms/reference/autocor-terms.html>
- del Rosario, K. S., & West, T. V. (2025). A Practical Guide to Specifying Random Effects in Longitudinal Dyadic Multilevel Modeling. *Advances in Methods and Practices in Psychological Science*, 8(3), 25152459251351286. <https://doi.org/10.1177/25152459251351286>



Appendix

Create the cross-sectional APIM variables manually

← Data preparation

- Explicit matching by couple and role
- Missing partner → NA

```
1 apim_manual_data <- raw_dyad_data |>
2   dplyr::mutate(
3     .is_female = as.numeric(gender == "female"),
4     .is_male = as.numeric(gender == "male"),
5     .efficacy_gmc = efficacy - mean(efficacy, na.rm = TRUE),
6     .efficacy_gmc_actor = .efficacy_gmc
7   )
8
9 partner_values <- apim_manual_data |>
10  dplyr::transmute(
11    couple_id,
12    gender = dplyr::recode(gender, female = "male", male = "female"),
13    .efficacy_gmc_partner = .efficacy_gmc
14  )
15
16 apim_manual_data <- apim_manual_data |>
17  dplyr::left_join(
18    partner_values,
19    by = c("couple_id", "gender"),
20    relationship = "one-to-one"
21  )
```

Decompose and lag perceived behavioral control manually

← Data preparation

```
1 pbc_components <- raw_ild_dyad_data |>
2   dplyr::arrange(couple_id, person_id, diaryday) |>
3   dplyr::group_by(couple_id, person_id) |>
4   dplyr::mutate(
5     .pbc_person_mean = mean(pbc, na.rm = TRUE),
6     .pbc_cwp = pbc - .pbc_person_mean,
7     .pbc_cwp_lag1 = dplyr::if_else(
8       diaryday == dplyr::lag(diaryday) + 1,
9       dplyr::lag(.pbc_cwp),
10      NA_real_
11   )
12 ) |>
13 dplyr::ungroup() |>
14 dplyr::mutate(
15   .pbc_cbp = .pbc_person_mean -
16     mean(
17       .pbc_person_mean[
18         !duplicated(paste(couple_id, person_id))
19       ],
20     na.rm = TRUE
21 )
22 )
```

Match actor and partner components manually

← Data preparation

```
1 partner_components <- pbc_components |>
2   dplyr::transmute(
3     couple_id,
4     diaryday,
5     gender = dplyr::recode(gender, female = "male", male = "female"),
6     .pbc_cwp_partner = .pbc_cwp,
7     .pbc_cwp_partner_lag1 = .pbc_cwp_lag1,
8     .pbc_cbp_partner = .pbc_cbp
9   )
10
11 i1d_manual_data <- pbc_components |>
12   dplyr::rename(
13     .pbc_cwp_actor = .pbc_cwp,
14     .pbc_cwp_actor_lag1 = .pbc_cwp_lag1,
15     .pbc_cbp_actor = .pbc_cbp
16   ) |>
17   dplyr::left_join(
18     partner_components,
19     by = c("couple_id", "diaryday", "gender"),
20     relationship = "one-to-one"
21   )
```

- Explicit day-role matching: independent of row order