

Exchangeable Dyads: Model Specification and Back-Transformation

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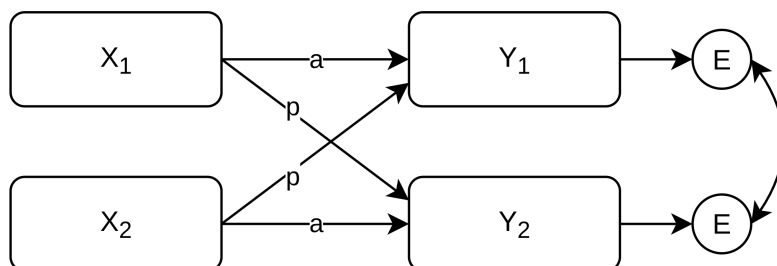
Full GitHub repository: The full repository contains the tutorial source files, reusable helper functions, model code, rendered PDFs, and additional information: <https://github.com/Pascal-Kueng/05DyadicDataAnalysis>

1 Background

Exchangeable dyads do not have substantively meaningful partner roles. Partner labels are arbitrary, and flipping the labels should not change the model interpretation.

For intensive longitudinal data, an exchangeable APIM needs to model:

- pooled fixed effects, because the two partner labels are not substantively different;
- pooled average time trends and pooled actor/partner effects;
- stable between-dyad differences in average levels and slopes;
- partner deviations from those dyad-level effects, because the two people in a dyad are still distinct repeated-observation units;
- correlations among the dyad-level random effects and among the partner deviation random effects;
- same-day residual interdependence between partners after fixed and random effects have been accounted for;
- a residual structure that remains invariant when the arbitrary partner labels are switched.



`prepare_interdep_data()` creates the APIM and DIM predictors together. Omitting `role` states the exchangeability assumption, while `seed` makes its arbitrary member contrast reproducible.

2 Data structure

```
exchangeable_raw <- tibble(
  coupleID = rep(31:32, each = 6),
  userID = rep(c("31_1", "31_2", "32_1", "32_2"), each = 3),
  diaryday = rep(0:2, 4),
  closeness = c(5.2, 5.5, 5.1, 4.8, 5.0, 5.3,
                4.9, 5.1, 5.0, 5.4, 5.2, 5.5),
  provided_support = c(4.1, 4.5, 4.3, 3.9, 4.2, 4.4,
                      4.0, 4.3, 4.1, 4.6, 4.5, 4.7)
)

df_long_dim <- prepare_interdep_data(
  data = exchangeable_raw,
  group = coupleID,
  member = userID,
  time = diaryday,
  predictors = provided_support,
  model_type = c("apim", "dim"),
  seed = 123
) |>
  rename_interdep_for_tutorial(
    predictor = "provided_support"
  ) |>
  mutate(
    diaryday_c = diaryday - mean(diaryday)
  )
```

Table 1: Example person-day structure for an exchangeable dyad

coupleID	userID	diaryday	idiff	provided_support	provided_actor	provided_partner	provided_dyad_mean	cwp_actor	cbp_partner	cwp_dyad_mean
31	31_1	0	-1	-0.2000000	-0.2666667	-0.2333333	0.0333333			
31	31_1	1	-1	0.2000000	0.0333333	0.1166667	0.0833333			
31	31_1	2	-1	0.0000000	0.2333333	0.1166667	-0.1166667			
31	31_2	0	1	-0.2666667	-0.2000000	-0.2333333	-0.0333333			
31	31_2	1	1	0.0333333	0.2000000	0.1166667	-0.0833333			
31	31_2	2	1	0.2333333	0.0000000	0.1166667	0.1166667			
32	32_1	0	-1	-0.1333333	0.0000000	-0.0666667	-0.0666667			
32	32_1	1	-1	0.1666667	-0.1000000	0.0333333	0.1333333			
32	32_1	2	-1	-0.0333333	0.1000000	0.0333333	-0.0666667			
32	32_2	0	1	0.0000000	-0.1333333	-0.0666667	0.0666667			
32	32_2	1	1	-0.1000000	0.1666667	0.0333333	-0.1333333			
32	32_2	2	1	0.1000000	-0.0333333	0.0333333	0.0666667			

idiff is constant within person and opposite within dyad. Its sign has no substantive meaning. The tutorial helper drops the .i_ prefix while retaining the package's cwp_actor, cbp_partner, and cwp_dyad_mean ordering; only the long within_dyad_deviation suffix is shortened to dev.

3 glmmTMB model

```
model_exch_long_apim_glmmTMB <- glmmTMB(
  closeness ~ 1 +
```

```

# Pooled fixed effects: no gender-specific intercepts or slopes.
diaryday_c +
provided_support_cwp_actor +
provided_support_cwp_partner +
provided_support_cbp_actor +
provided_support_cbp_partner +

# Dyad-level means and slopes.
(1 + diaryday_c +
  provided_support_cwp_actor +
  provided_support_cwp_partner | coupleID) +

# Partner deviations from the dyad-level effects.
# This block is kept separate from the dyad-level block so that the
# common/couple-mean and deviation components are independent.
(0 + idiff +
  I(idiff * diaryday_c) +
  I(idiff * provided_support_cwp_actor) +
  I(idiff * provided_support_cwp_partner) | coupleID) +

# Same-day residual interdependence:
# Independent common and member-deviation components imply homogeneous
# residual variance and covariance.
(1 | coupleID:diaryday) + (0 + idiff | coupleID:diaryday),

# The residual variance is represented by the homcs block above.
# Without dispformula = ~ 0, glmmTMB would add a second independent
# residual variance on top of the dyadic residual covariance structure.
# For families without a residual, dispformula should NOT be set to zero.
dispformula = ~ 0,
family = gaussian(),
data = df_long_dim
)

```

The residual block could also be written as independent common/deviation terms:

```

(1 | coupleID:diaryday) +
(0 + idiff | coupleID:diaryday)

```

With `idiff = +1/-1`, this has one common variance and one deviation variance, which rotate back to one homogeneous residual variance and one residual covariance.

4 brms model

```

formula_exch_long_apim <- bf(
  closeness ~ 1 +

  # Pooled fixed effects.
  diaryday_c +
  provided_support_cwp_actor +
  provided_support_cwp_partner +
  provided_support_cbp_actor +
  provided_support_cbp_partner +

  # Dyad-level means and slopes.
  (1 + diaryday_c +
    provided_support_cwp_actor +
    provided_support_cwp_partner | coupleID) +

  # Partner deviations from the dyad-level effects.
  (0 + idiff +
    I(idiff * diaryday_c) +
    I(idiff * provided_support_cwp_actor) +
    I(idiff * provided_support_cwp_partner) | coupleID) +

```

```

# Native residual correlation between the two partners on the same day.
# We use unstr() instead of cs() because brms currently restricts cs()
# residual correlations to be positive. With exactly two members per group
# (dyads), unstr() is equivalent here because only one residual correlation
# is estimated. For triads or larger groups, unstr() would no longer impose
# the compound-symmetry constraint.
unstr(time = idiff, gr = coupleID:diaryday)

# No sigma formula is specified here. Thus, sigma ~ 1 is implied,
# meaning one homogeneous residual variance for both partners.
# If sigma is modelled with its own formula, brms estimates the sigma
# coefficients on the log scale, so those coefficients must be exponentiated
# before reporting them as residual SDs.
)

priors_exch_long_apim <- c(
  prior(normal(4, 2), class = "Intercept"),
  prior(normal(0, 2), class = "b"),
  prior(exponential(1), class = "sd"),
  prior(lkj(2), class = "cor"),
  prior(student_t(3, 0, 1.5), class = "sigma"),
  prior(lkj(2), class = "cortime")
)

model_exch_long_apim <- brm(
  formula = formula_exch_long_apim,
  data = df_long_dim,
  family = gaussian(link = identity),
  prior = priors_exch_long_apim,
  chains = 4,
  cores = 4,
  iter = 2000,
  warmup = 1000,
  seed = 123,
  file = file.path("brms_cache", "model_apim_ind_long_apim")
)

```

5 Back-transformation

The model estimates a common/couple-mean block and an `idiff` deviation block. For exchangeable dyads, the full APIM random-effects matrix is recovered by rotating these two blocks:

$$\text{Var}(A) = \text{Var}(B) = \Sigma_{\text{common}} + \Sigma_{\text{idiff}}$$

$$\text{Cov}(A, B) = \Sigma_{\text{common}} - \Sigma_{\text{idiff}}$$

This exact rotation assumes that the common/couple-mean and `idiff` deviation random-effect blocks are independent.

The helper function `summarize_exchangeable_apim_brms()` used below is defined in `00_R_Functions/ReportModels.R` on GitHub. It reconstructs the common/couple-mean and `idiff` covariance matrices for every posterior draw, rotates each draw into the full APIM partner-level matrix, and then summarizes the transformed covariance, SD, correlation, fixed-effect, and residual quantities.

For `glmmTMB`, the same back-transformation is algebraically just as straightforward, but interval estimation (CI) is less direct because there are no posterior draws. A helper function implementing the delta-method is also available on GitHub.

```

idiff_term <- if (
  "sd_coupleID__idiff" %in% posterior::variables(model_exch_long_apim)
) "idiff" else "Idiff"

apim_results <- summarize_exchangeable_apim_brms(
  model_exch_long_apim,
  gr = "coupleID",
  idiff = idiff_term,
  term_labels = c("int", "day", "actor_wp", "partner_wp"),
  partner_labels = c("A", "B")
)

```

6 Variance-covariance matrix

```

kable(
  round(apim_results$full_covariance_matrix, 3),
  caption = "Back-transformed full APIM random-effects variance-covariance matrix",
  booktabs = TRUE
) |>
  kable_styling(latex_options = "scale_down", font_size = 7)

```

Table 2: Back-transformed full APIM random-effects variance-covariance matrix

	A_int	A_day	A_actor_wp	A_partner_wp	B_int	B_day	B_actor_wp	B_partner_wp
A_int	1.180	0.011	0.096	0.018	-0.264	-0.002	-0.063	0.005
A_day	0.011	0.000	0.001	0.000	-0.002	0.000	-0.001	0.000
A_actor_wp	0.096	0.001	0.024	0.004	-0.063	-0.001	-0.018	-0.002
A_partner_wp	0.018	0.000	0.004	0.012	0.005	0.000	-0.002	0.002
B_int	-0.264	-0.002	-0.063	0.005	1.180	0.011	0.096	0.018
B_day	-0.002	0.000	-0.001	0.000	0.011	0.000	0.001	0.000
B_actor_wp	-0.063	-0.001	-0.018	-0.002	0.096	0.001	0.024	0.004
B_partner_wp	0.005	0.000	-0.002	0.002	0.018	0.000	0.004	0.012

7 SD table

```

kable(
  apim_results$sd_summary,
  digits = 3,
  caption = "Back-transformed APIM random-effect standard deviations with 95% credible intervals"
)

```

Table 3: Back-transformed APIM random-effect standard deviations with 95% credible intervals

parameter	estimate	est_error	q_low	q_high
A_actor_wp	0.153	0.018	0.119	0.191
A_day	0.018	0.001	0.016	0.020
A_int	1.085	0.056	0.987	1.206
A_partner_wp	0.107	0.020	0.066	0.144
B_actor_wp	0.153	0.018	0.119	0.191
B_day	0.018	0.001	0.016	0.020
B_int	1.085	0.056	0.987	1.206
B_partner_wp	0.107	0.020	0.066	0.144

8 Correlation matrix

```
kable(
  round(apim_results$full_correlation_matrix, 3),
  caption = "Back-transformed APIM random-effect correlation matrix",
  booktabs = TRUE
) |>
  kable_styling(latex_options = "scale_down", font_size = 7)
```

Table 4: Back-transformed APIM random-effect correlation matrix

	A_int	A_day	A_actor_wp	A_partner_wp	B_int	B_day	B_actor_wp	B_partner_wp
A_int	1.000	0.582	0.570	0.152	-0.223	-0.125	-0.376	0.041
A_day	0.582	1.000	0.367	0.141	-0.125	-0.137	-0.210	0.044
A_actor_wp	0.570	0.367	1.000	0.253	-0.376	-0.210	-0.754	-0.091
A_partner_wp	0.152	0.141	0.253	1.000	0.041	0.044	-0.091	0.211
B_int	-0.223	-0.125	-0.376	0.041	1.000	0.582	0.570	0.152
B_day	-0.125	-0.137	-0.210	0.044	0.582	1.000	0.367	0.141
B_actor_wp	-0.376	-0.210	-0.754	-0.091	0.570	0.367	1.000	0.253
B_partner_wp	0.041	0.044	-0.091	0.211	0.152	0.141	0.253	1.000

9 Final reporting summary

Table 5: Compact reporting summary

section	parameter	estimate	est_error	q_low	q_high
Fixed effects	Intercept	5.102	0.070	4.966	5.240
Fixed effects	diaryday_c	0.004	0.001	0.001	0.006
Fixed effects	provided_support_cwp_actor	0.300	0.014	0.273	0.328
Fixed effects	provided_support_cwp_partner	0.149	0.015	0.120	0.177
Fixed effects	provided_support_cbp_actor	1.316	0.088	1.140	1.483
Fixed effects	provided_support_cbp_partner	0.382	0.086	0.212	0.557
Back-transformed random-effect SDs	A_actor_wp	0.153	0.018	0.119	0.191
Back-transformed random-effect SDs	A_day	0.018	0.001	0.016	0.020
Back-transformed random-effect SDs	A_int	1.085	0.056	0.987	1.206
Back-transformed random-effect SDs	A_partner_wp	0.107	0.020	0.066	0.144
Back-transformed random-effect SDs	B_actor_wp	0.153	0.018	0.119	0.191
Back-transformed random-effect SDs	B_day	0.018	0.001	0.016	0.020
Back-transformed random-effect SDs	B_int	1.085	0.056	0.987	1.206
Back-transformed random-effect SDs	B_partner_wp	0.107	0.020	0.066	0.144
Back-transformed random-effect correlations	A_actor_wp with A_day	0.369	0.101	0.169	0.558
Back-transformed random-effect correlations	A_actor_wp with A_int	0.572	0.083	0.403	0.723
Back-transformed random-effect correlations	A_day with A_int	0.581	0.056	0.470	0.681
Back-transformed random-effect correlations	A_partner_wp with A_actor_wp	0.266	0.152	-0.028	0.558
Back-transformed random-effect correlations	A_partner_wp with A_day	0.146	0.129	-0.114	0.400
Back-transformed random-effect correlations	A_partner_wp with A_int	0.157	0.117	-0.069	0.382
Back-transformed random-effect correlations	B_actor_wp with A_actor_wp	-0.755	0.151	-0.983	-0.412
Back-transformed random-effect correlations	B_actor_wp with A_day	-0.211	0.111	-0.415	0.019
Back-transformed random-effect correlations	B_actor_wp with A_int	-0.377	0.103	-0.572	-0.163
Back-transformed random-effect correlations	B_actor_wp with A_partner_wp	-0.096	0.160	-0.412	0.215
Back-transformed random-effect correlations	B_actor_wp with B_day	0.369	0.101	0.169	0.558
Back-transformed random-effect correlations	B_actor_wp with B_int	0.572	0.083	0.403	0.723
Back-transformed random-effect correlations	B_day with A_actor_wp	-0.211	0.111	-0.415	0.019
Back-transformed random-effect correlations	B_day with A_day	-0.136	0.118	-0.362	0.094
Back-transformed random-effect correlations	B_day with A_int	-0.124	0.084	-0.288	0.040
Back-transformed random-effect correlations	B_day with A_partner_wp	0.046	0.138	-0.231	0.310
Back-transformed random-effect correlations	B_day with B_int	0.581	0.056	0.470	0.681
Back-transformed random-effect correlations	B_int with A_actor_wp	-0.377	0.103	-0.572	-0.163
Back-transformed random-effect correlations	B_int with A_day	-0.124	0.084	-0.288	0.040
Back-transformed random-effect correlations	B_int with A_int	-0.221	0.095	-0.402	-0.039
Back-transformed random-effect correlations	B_int with A_partner_wp	0.043	0.125	-0.199	0.281

Table 5: Compact reporting summary (*continued*)

section	parameter	estimate	est_error	q_low	q_high
Back-transformed random-effect correlations	B_partner_wp with A_actor_wp	-0.096	0.160	-0.412	0.215
Back-transformed random-effect correlations	B_partner_wp with A_day	0.046	0.138	-0.231	0.310
Back-transformed random-effect correlations	B_partner_wp with A_int	0.043	0.125	-0.199	0.281
Back-transformed random-effect correlations	B_partner_wp with A_partner_wp	0.230	0.394	-0.570	0.960
Back-transformed random-effect correlations	B_partner_wp with B_actor_wp	0.266	0.152	-0.028	0.558
Back-transformed random-effect correlations	B_partner_wp with B_day	0.146	0.129	-0.114	0.400
Back-transformed random-effect correlations	B_partner_wp with B_int	0.157	0.117	-0.069	0.382
Residual structure	residual_variance	0.878	0.012	0.854	0.903
Residual structure	sigma	0.937	0.007	0.924	0.950