

Distinguishable Dyads: Model Specification and Output

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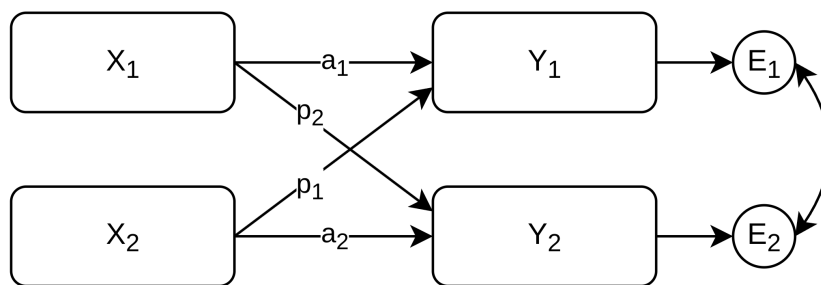
Full GitHub repository: The full repository contains the tutorial source files, reusable helper functions, model code, rendered PDFs, and additional information: <https://github.com/Pascal-Kueng/05DyadicDataAnalysis>

1 Background

Distinguishable dyads have partner roles that are meaningful for the model. In this tutorial example, the partners are distinguished by gender and represented with `is_male` and `is_female`.

For intensive longitudinal data, a distinguishable APIM needs to model:

- role-specific fixed effects, because the two partners have meaningful labels;
- role-specific average time trends and actor/partner effects;
- stable between-dyad differences in each role's average level and slopes;
- correlations among the role-specific random effects;
- role-specific residual variances, when the two roles may differ in unexplained variability;
- same-day residual interdependence between partners after fixed and random effects have been accounted for.



2 Data structure

```
dist_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),  
  gender = rep(c("female", "male", "female", "male"), each = 3),
```

```

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_apim <- prepare_interdep_data(
  data = dist_raw,
  group = coupleID,
  member = userID,
  role = gender,
  time = diaryday,
  predictors = provided_support,
  model_type = "apim"
) |>
  rename_interdep_for_tutorial(
    predictor = "provided_support"
  ) |>
  mutate(
    diaryday_c = diaryday - mean(diaryday)
  )

```

Table 1: Example person-day structure for a distinguishable dyad

coupleID	userID	diaryday	gender	is_female	is_male	provided_support	provided_support_cbp_actor	provided_support_cbp_partner	provided_support_cbp_partner
31	31_1	0	female	1	0	-0.2000000	-0.2666667	0.0000000	-0.1333333
31	31_1	1	female	1	0	0.2000000	0.0333333	0.0000000	-0.1333333
31	31_1	2	female	1	0	0.0000000	0.2333333	0.0000000	-0.1333333
31	31_2	0	male	0	1	-0.2666667	-0.2000000	-0.1333333	0.0000000
31	31_2	1	male	0	1	0.0333333	0.2000000	-0.1333333	0.0000000
31	31_2	2	male	0	1	0.2333333	0.0000000	-0.1333333	0.0000000
32	32_1	0	female	1	0	-0.1333333	0.0000000	-0.1666667	0.3000000
32	32_1	1	female	1	0	0.1666667	-0.1000000	-0.1666667	0.3000000
32	32_1	2	female	1	0	-0.0333333	0.1000000	-0.1666667	0.3000000
32	32_2	0	male	0	1	0.0000000	-0.1333333	0.3000000	-0.1666667
32	32_2	1	male	0	1	-0.1000000	0.1666667	0.3000000	-0.1666667
32	32_2	2	male	0	1	0.1000000	-0.0333333	0.3000000	-0.1666667

`prepare_interdep_data()` creates the role indicators and the within-person and between-person actor-partner predictors. The tutorial helper drops the `.i_` prefix while retaining names such as `cwp_actor` and `cbp_partner`.

3 glmmTMB model

```

model_dist_apim_long_glmmTMB <- glmmTMB(
  closeness ~ 0 + is_male + is_female +

  # Role-specific time slopes.
  is_male:diaryday_c +
  is_female:diaryday_c +

  # Between-person APIM effects.
  is_male:provided_support_cbp_actor +
  is_male:provided_support_cbp_partner +
  is_female:provided_support_cbp_actor +
  is_female:provided_support_cbp_partner +

```

```

# Within-person APIM effects.
is_male:provided_support_cwp_actor +
is_male:provided_support_cwp_partner +
is_female:provided_support_cwp_actor +
is_female:provided_support_cwp_partner +

# Dyad-level random intercepts and time slopes.
(0 + is_male + is_female +
  is_male:diaryday_c +
  is_female:diaryday_c | coupleID) +

# Same-day residual covariance between partners.
# us() estimates partner-specific residual variances and their covariance.
us(0 + is_male + is_female | coupleID:diaryday),

# The Gaussian residual variance is represented by the us() 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_apim
)

```

4 brms model

```

formula_dist_apim_long_simple <- bf(
  closeness ~ 0 + is_male + is_female +

  # Role-specific time slopes.
  is_male:diaryday_c +
  is_female:diaryday_c +

  # Between-person APIM effects.
  is_male:provided_support_cbp_actor +
  is_male:provided_support_cbp_partner +
  is_female:provided_support_cbp_actor +
  is_female:provided_support_cbp_partner +

  # Within-person APIM effects.
  is_male:provided_support_cwp_actor +
  is_male:provided_support_cwp_partner +
  is_female:provided_support_cwp_actor +
  is_female:provided_support_cwp_partner +

  # Dyad-level random intercepts and time slopes.
  (0 + is_male + is_female +
    is_male:diaryday_c +
    is_female:diaryday_c | coupleID) +

  # Native same-day residual correlation between partners.
  unstr(time = gender, gr = coupleID:diaryday),

  # Role-specific residual SDs.
  # brms estimates sigma coefficients on the log scale, so b_sigma_* draws
  # must be exponentiated before reporting residual SDs.
  sigma ~ 0 + is_male + is_female
)

priors_dist_apim_long_simple <- c(
  prior(normal(4, 2), class = "b", coef = "is_male"),
  prior(normal(4, 2), class = "b", coef = "is_female"),
  prior(normal(0, 2), class = "b"),
  prior(exponential(1), class = "sd"),
  prior(lkj(2), class = "cor"),
  prior(normal(0, 0.7), class = "b", dpar = "sigma"),
  prior(lkj(2), class = "cortime")
)

```

```

model_dist_apim_long_simple <- brm(
  formula = formula_dist_apim_long_simple,
  data = df_long_apim,
  family = gaussian(link = identity),
  prior = priors_dist_apim_long_simple,
  chains = 4,
  cores = 4,
  iter = 2000,
  warmup = 1000,
  seed = 123,
  file = file.path("brms_cache", "example1_dist_apim_long_simple")
)

```

5 Output helper

The helper function `summarize_distinguishable_apim_brms()` used below is defined in `00_R_Functions/ReportModels.R` on GitHub. It summarizes fixed effects, random-effect SDs/correlations, and residual quantities. For `brms`, sigma coefficients are stored on the log scale, so the helper exponentiates `b_sigma_*` draws before computing residual SDs, variances, and same-day residual covariance.

For `glmmTMB`, the same residual quantities are available from the fitted variance-covariance output, but interval estimation is less direct because there are no posterior draws. One would usually transform parametric bootstrap draws or asymptotic draws from the fitted parameter covariance matrix.

```

dist_results <- summarize_distinguishable_apim_brms(
  model_dist_apim_long_simple,
  gr = "coupleID"
)

```

6 Random-effect SDs

```

kable(
  dist_results$random_sd_summary,
  digits = 3,
  caption = "Random-effect standard deviations with 95% credible intervals"
)

```

Table 2: Random-effect standard deviations with 95% credible intervals

parameter	estimate	est_error	q_low	q_high
is_female	0.920	0.067	0.798	1.064
is_female:diaryday_c	0.016	0.001	0.014	0.019
is_male	0.845	0.062	0.730	0.972
is_male:diaryday_c	0.017	0.002	0.014	0.020

7 Random-effect correlations

```
kable(
  dist_results$random_cor_summary,
  digits = 3,
  caption = "Random-effect correlations with credible intervals",
  booktabs = TRUE
) |>
kable_styling(latex_options = "scale_down", font_size = 7)
```

Table 3: Random-effect correlations with credible intervals

parameter	estimate	est_error	q_low	q_high
is_female with is_female:diaryday_c	0.502	0.082	0.328	0.651
is_female with is_male:diaryday_c	0.024	0.113	-0.207	0.244
is_male with is_female	0.171	0.101	-0.046	0.348
is_male with is_female:diaryday_c	0.185	0.101	-0.015	0.378
is_male with is_male:diaryday_c	0.504	0.090	0.320	0.668
is_male:diaryday_c with is_female:diaryday_c	-0.016	0.120	-0.249	0.224

8 Residual structure

```
kable(
  dist_results$residual_summary,
  digits = 3,
  caption = "Residual SDs, variances, and same-day residual association"
)
```

Table 4: Residual SDs, variances, and same-day residual association

section	parameter	estimate	est_error	q_low	q_high
Residual structure	residual_variance_is_female	0.521	0.010	0.502	0.542
Residual structure	residual_variance_is_male	1.260	0.025	1.211	1.309
Residual structure	sigma_is_female	0.722	0.007	0.708	0.736
Residual structure	sigma_is_male	1.122	0.011	1.101	1.144

9 Compact reporting summary

Table 5: Compact distinguishable-dyad reporting summary

section	parameter	estimate	est_error	q_low	q_high
Fixed effects	is_male	4.487	0.086	4.318	4.649
Fixed effects	is_female	5.739	0.090	5.557	5.911
Fixed effects	is_male:diaryday_c	-0.003	0.002	-0.007	0.000
Fixed effects	is_female:diaryday_c	0.011	0.002	0.007	0.014
Fixed effects	is_male:provided_support_cbp_actor	1.132	0.109	0.911	1.339
Fixed effects	is_male:provided_support_cbp_partner	0.302	0.103	0.100	0.506
Fixed effects	is_female:provided_support_cbp_actor	1.376	0.105	1.176	1.578
Fixed effects	is_female:provided_support_cbp_partner	0.592	0.113	0.363	0.811
Fixed effects	is_male:provided_support_cwp_actor	0.185	0.021	0.143	0.227
Fixed effects	is_male:provided_support_cwp_partner	0.125	0.021	0.084	0.165
Fixed effects	is_female:provided_support_cwp_actor	0.419	0.013	0.393	0.446
Fixed effects	is_female:provided_support_cwp_partner	0.170	0.013	0.144	0.196
Random-effect SDs	is_female	0.920	0.067	0.798	1.064
Random-effect SDs	is_female:diaryday_c	0.016	0.001	0.014	0.019

Table 5: Compact distinguishable-dyad reporting summary (*continued*)

section	parameter	estimate	est_error	q_low	q_high
Random-effect SDs	is_male	0.845	0.062	0.730	0.972
Random-effect SDs	is_male:diaryday_c	0.017	0.002	0.014	0.020
Random-effect correlations	is_female with is_female:diaryday_c	0.502	0.082	0.328	0.651
Random-effect correlations	is_female with is_male:diaryday_c	0.024	0.113	-0.207	0.244
Random-effect correlations	is_male with is_female	0.171	0.101	-0.046	0.348
Random-effect correlations	is_male with is_female:diaryday_c	0.185	0.101	-0.015	0.378
Random-effect correlations	is_male with is_male:diaryday_c	0.504	0.090	0.320	0.668
Random-effect correlations	is_male:diaryday_c with is_female:diaryday_c	-0.016	0.120	-0.249	0.224
Residual structure	residual_variance_is_female	0.521	0.010	0.502	0.542
Residual structure	residual_variance_is_male	1.260	0.025	1.211	1.309
Residual structure	sigma_is_female	0.722	0.007	0.708	0.736
Residual structure	sigma_is_male	1.122	0.011	1.101	1.144