

Partner fidelity and asymmetric specialization in ecological networks

Supplementary material

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Dataset

Here's a summary of the full dataset we used in our analyses (table 1).

Table 1: Random sample of 10 rows from the full dataset.

| connected | type | subtype | r_ND | c_ND | resource_sp | consumer_sp | id_pair | network_id |
|-----------|------|-----------------|------|------|--------------------------------|--------------------------------|---------|------------|
| 0 | A | HostParasite | 0.35 | 0.07 | <i>Cricetulus migratorius</i> | <i>Frontopsylla protera</i> | 3206 | A_HP_029 |
| 0 | A | HostParasite | 0.47 | 0.25 | <i>Alticola argentatus</i> | <i>Frontopsylla elata</i> | 2710 | A_HP_011 |
| 0 | M | PlantPollinator | 0.02 | 0.11 | <i>Hieracium pilosella</i> | <i>Formica fusca</i> | 839 | M_PL_047 |
| 1 | A | HostParasite | 0.86 | 0.58 | <i>Microtus arvalis</i> | <i>Megabothris turbidus</i> | 3486 | A_HP_048 |
| 1 | A | PlantHerbivore | 0.25 | 0.43 | <i>Xanthocephalum texanum</i> | <i>Melanoplus desultorius</i> | 2201 | A_PH_005 |
| 1 | A | PlantHerbivore | 0.42 | 0.19 | <i>Croton pottsii</i> | <i>Melanoplus gladstoni</i> | 2159 | A_PH_005 |
| 1 | M | PlantPollinator | 0.05 | 0.06 | <i>Ranunculus japonicus</i> | <i>Melanostoma scalare</i> | 1434 | M_PL_053 |
| 1 | M | PlantPollinator | 0.16 | 0.05 | <i>Tanacetum vulgare</i> | <i>Sphaerophoria scripta</i> | 1824 | M_PL_018 |
| 1 | A | HostParasite | 0.71 | 0.13 | <i>Clethrionomys glareolus</i> | <i>Rhadinopsylla integella</i> | 3008 | A_HP_018 |
| 0 | M | PlantPollinator | 0.02 | 0.59 | <i>Cirsium arvense</i> | <i>Bombus pascuorum</i> | 331 | M_PL_006 |

- **connected:** observed species interaction (0 = no interaction observed, 1 = interaction observed)
- **type:** type of interaction (A = antagonistic; M = mutualistic)
- **subtype:** specific type of interaction (PlantPollinator, PlantHerbivore, PlantSeedDisperser, HostParasite)
- **r_ND:** normalized degree of resource species (mean = 0.28, SD = 0.24)
- **c_ND:** normalized degree of consumer species (mean = 0.28, SD = 0.23)
- **resource_sp:** resource species ID (n = 444)
- **consumer_sp:** consumer species ID (n = 803)
- **id_pair:** consumer-resource interaction ID (n = 4075)
- **network_id:** ecological network ID (n = 133; labels match those on the Web of Life)

We also analyze a subset of this data that only consists of weighted networks (table 2).

- **connected:** 0 = no interaction observed, 1 = interaction observed
- **type:** A = antagonistic, M = mutualistic

Table 2: Random sample of 10 rows from the subset of weighted networks.

| connected | type | subtype | r_ND | c_ND | log.sum_r | log.sum_c | resource_sp | consumer_sp | id_pair | network_id |
|-----------|------|--------------------|------|------|-----------|-----------|------------------------|------------------------------|---------|------------|
| 0 | M | PlantPollinator | 0.01 | 0.02 | 2.40 | 1.95 | Reynoutria japonica | Eristalis tenax | 1570 | M_PL_044 |
| 0 | A | HostParasite | 0.16 | 0.40 | 2.40 | 4.91 | Apodemus peninsulae | Ctenophthalmus congeneroides | 2793 | A_HP_049 |
| 1 | A | HostParasite | 0.47 | 0.69 | 4.66 | 6.93 | Apodemus uralensis | Corrodopsylla birulai | 2837 | A_HP_020 |
| 0 | M | PlantSeedDisperser | 0.23 | 0.08 | 1.39 | 1.39 | Cecropia schreberiana | Tyrannus dominicensis | 2441 | M_SD_005 |
| 0 | A | HostParasite | 0.54 | 0.15 | 5.98 | 2.77 | Microtus arvalis | Neopsylla pleskei | 3510 | A_HP_044 |
| 0 | M | PlantPollinator | 0.06 | 0.09 | 3.87 | 2.83 | Deutzia crenata | Episyrphus balteatus | 561 | M_PL_054 |
| 0 | M | PlantSeedDisperser | 0.15 | 0.44 | 2.56 | 4.14 | Miconia affinis | Loxigilla portoricensis | 2569 | M_SD_004 |
| 1 | A | HostParasite | 0.65 | 0.56 | 7.30 | 4.63 | Clethrionomys rutilus | Frontopsylla elata | 3048 | A_HP_020 |
| 1 | A | HostParasite | 0.12 | 1.00 | 2.56 | 5.24 | Cricetus cricetus | Rhadinopsylla li | 3358 | A_HP_044 |
| 0 | A | HostParasite | 0.43 | 0.06 | 7.94 | 0.69 | Cricetulus migratorius | Rhadinopsylla ucrainica | 3249 | A_HP_006 |

- **subtype:** HostParasite, PlantPollinator, PlantSeedDisperser
- **r_ND:** mean = 0.35, SD = 0.2
- **c_ND:** mean = 0.34, SD = 0.2
- **log.sum_r:** mean = 4.5, SD = 2.2
- **log.sum_c:** mean = 4, SD = 2.1
- **resource_sp:** n = 167
- **consumer_sp:** n = 291
- **id_pair:** n = 1813
- **network_id:** n = 68

Note that the general structure of the subset of data is the same as the full dataset, except we have added two new variables. These variables correspond to the logarithm of observed interactions (sum of interaction frequency) for a resource (**log.sum_r**) and consumer (**log.sum_c**) in a network. These variables give information on sampling effort. Note also that we only have three interaction **subtypes** now (no weighted networks for PlantHerbivore).

Prior to our analyses, we scaled normalized degree (mean = 0, SD = 1) for both consumers and resources. This allowed us to interpret both main effects and statistical interactions within the same model, and also allowed us to easily compare their effect sizes (Schielzeth, 2010). We also scaled the logarithm of observed interactions for both consumers and resources.

```

full.df <- full.df %>%
  mutate(sc.r_ND = scale(r_ND),
         sc.c_ND = scale(c_ND))

weighted_subset.df <- weighted_subset.df %>%
  mutate(sc.r_ND = scale(r_ND),
         sc.c_ND = scale(c_ND),
         sc.log.sum_r = scale(log.sum_r),
         sc.log.sum_c = scale(log.sum_c))

```

For **type**, we created a contrast so that the intercept term represents the average probability of an interaction across mutualistic and antagonistic interactions, and this coefficient represents the effect of mutualistic (relative to antagonistic) interactions (table 3).

Table 3: Contrasts for **type**.

| | A | M |
|---------|------|-----|
| Ave | 0.5 | 0.5 |
| _M.vs.A | -1.0 | 1.0 |

To test for the effect of network **subtype** within each **type**, we create two new variables:

```

full.df <- full.df %>%
  mutate(subtype_Herb.vs.Para = ifelse(type == "M", 0,
                                       ifelse(subtype == "PlantHerbivore", 1/2, -1/2)),
         subtype_Poll.vs.Disp = ifelse(type == "A", 0,
                                       ifelse(subtype == "PlantPollinator", 1/2, -1/2)))

```

Now, **subtype_Herb.vs.Para** tests for an effect of herbivory (relative to parasitism), and **subtype_Poll.vs.Disp** tests for an effect of pollination (relative to seed dispersal).

Since we do not have multiple **subtypes** for antagonistic interactions in the data subset, we only fit a **subtype** contrast for mutualistic interactions.

```
weighted_subset.df <- weighted_subset.df %>%  
  mutate(subtype_Poll.vs.Disp = ifelse(type == "A", 0,  
                                       ifelse(subtype == "PlantPollinator", 1/2, -1/2)))
```

Statistical Models

We fit the following statistical model to our full dataset:

```
interaction.formula <- brmsformula(  
  connected ~ type + subtype_Herb.vs.Para + subtype_Poll.vs.Disp + sc.r_ND + sc.c_ND +  
    type:sc.r_ND + type:sc.c_ND + sc.r_ND:sc.c_ND +  
    type:sc.r_ND:sc.c_ND +  
    (1 | resource_sp) + (1 | consumer_sp) + (1 | id_pair) + (1 | network_id),  
  family = bernoulli(link = "logit")  
)
```

and a similar model to the data subset:

```
interaction_subset.formula <- brmsformula(  
  connected ~ type + subtype_Poll.vs.Disp + sc.r_ND + sc.c_ND +  
    type:sc.r_ND + type:sc.c_ND + sc.r_ND:sc.c_ND +  
    type:sc.r_ND:sc.c_ND +  
    (1 | resource_sp) + (1 | consumer_sp) + (1 | id_pair) + (1 | network_id),  
  family = bernoulli(link = "logit")
```

```
) # note that we do not include subtype_Herb.vs.Para, since we do not have
# PlantHerbivore interactions in the weighted subset.
```

These models analyze the probability of a species interaction as a function of all main effects, as well as two- and three-way interactions between the type of interaction (**type**) and scaled normalized degree of resources (**sc.r_ND**) and consumers (**sc.c_ND**)(fixed effects). Note that we only test for main effects of network subtypes within the type of interaction. This models also allows the probability of interactions to vary among resource and consumer species, the unique consumer-resource pair, as well as among unique ecological networks (random effects). Note that by including the unique consumer-resource pair as a random effect, we are testing how the different factors in our model influence partner fidelity (probability of an interaction when two species co-occur). Note also that specifying a Bernoulli distribution on the logit scale for the error distribution in our model makes it so that the fixed and random effects in our statistical model represent effects on the log odds of partner fidelity.

For the subset of data, we also fit the following model:

```
sampling_effects.formula <- brmsformula(
  connected ~ type + subtype_Poll.vs.Disp + sc.log.sum_r + sc.log.sum_c +
    type:sc.log.sum_r + type:sc.log.sum_c + sc.log.sum_r:sc.log.sum_c +
    type:sc.log.sum_r:sc.log.sum_c +
    (1 | resource_sp) + (1 | consumer_sp) + (1 | id_pair) + (1 | network_id),
  family = bernoulli(link = "logit")
) # again, we do not include subtype_Herb.vs.Para, since we do not have
# PlantHerbivore interactions in the weighted subset.
```

This model is similar to the previous models except that we substitute the logarithm of observed interactions for the normalized degree. The logic behind this model is that, if we observe the same patterns as we do when using normalized degree, then our results could simply be due to variation in sampling effort.

Choosing Priors

Given the number of random effects in our model, we used a Bayesian approach to estimate our model's parameters (as advised by Bolker et al. 2008). This required us to choose prior distributions for the fixed and random effects in our model.

We specified the following priors in our models:

```
interaction.priors <- c(
  set_prior("normal(0,2)", class = "b", coef = "type_M.vs.A"),
  set_prior("normal(0,2)", class = "b", coef = "subtype_Herb.vs.Para"),
  set_prior("normal(0,2)", class = "b", coef = "subtype_Poll.vs.Disp"),
  set_prior("normal(1,2)", class = "b", coef = "sc.r_ND"),
  set_prior("normal(1,2)", class = "b", coef = "sc.c_ND"),
  set_prior("normal(0,2)", class = "b", coef = "sc.r_ND:sc.c_ND"),
  set_prior("normal(0,2)", class = "b", coef = "type_M.vs.A:sc.r_ND"),
  set_prior("normal(0,2)", class = "b", coef = "type_M.vs.A:sc.c_ND"),
  set_prior("normal(0,2)", class = "b", coef = "type_M.vs.A:sc.r_ND:sc.c_ND"),
  set_prior("normal(0,2)", class = "sd"))

interaction_subset.priors <- c(
  set_prior("normal(0,2)", class = "b", coef = "type_M.vs.A"),
  set_prior("normal(0,2)", class = "b", coef = "subtype_Poll.vs.Disp"),
  set_prior("normal(1,2)", class = "b", coef = "sc.r_ND"),
  set_prior("normal(1,2)", class = "b", coef = "sc.c_ND"),
  set_prior("normal(0,2)", class = "b", coef = "sc.r_ND:sc.c_ND"),
  set_prior("normal(0,2)", class = "b", coef = "type_M.vs.A:sc.r_ND"),
```

```

set_prior("normal(0,2)", class = "b", coef = "type_M.vs.A:sc.c_ND"),
set_prior("normal(0,2)", class = "b", coef = "type_M.vs.A:sc.r_ND:sc.c_ND"),
set_prior("normal(0,2)", class = "sd"))

```

```

sampling_effect.priors <- c(
  set_prior("normal(0,2)", class = "b", coef = "type_M.vs.A"),
  set_prior("normal(0,2)", class = "b", coef = "subtype_Poll.vs.Disp"),
  set_prior("normal(1,2)", class = "b", coef = "sc.log.sum_r"),
  set_prior("normal(1,2)", class = "b", coef = "sc.log.sum_c"),
  set_prior("normal(0,2)", class = "b", coef = "sc.log.sum_r:sc.log.sum_c"),
  set_prior("normal(0,2)", class = "b", coef = "type_M.vs.A:sc.log.sum_r"),
  set_prior("normal(0,2)", class = "b", coef = "type_M.vs.A:sc.log.sum_c"),
  set_prior("normal(0,2)", class = "b", coef = "type_M.vs.A:sc.log.sum_r:sc.log.sum_c"),
  set_prior("normal(0,2)", class = "sd"))

```

Choosing priors requires thinking on the scale of the model. Therefore, we first give a description of what each term quantifies in these models before justifying our choices. Note that all of these fixed effects (except for **Intercept**) can be interpreted as an effect on the log-odds of partner fidelity:

- **Intercept** = log-odds of partner fidelity across interaction types at the mean normalized degree of resources and consumers.
- **type_M.vs.A** = effect of a mutualistic interaction (relative to antagonistic).
- **subtype_Herb.vs.Para** = effect of herbivory relative to parasitism.
- **subtype_Poll.vs.Disp** = effect of pollination relative to seed disperser.
- **sc.r_ND** = effect of 1 SD increase in resource normalized degree across interaction types.
- **sc.c_ND** = effect of 1 SD increase in consumer normalized degree across interaction types.
- **type_M.vs.A:sc.r_ND** = effect of a mutualistic interaction (relative to antagonistic) on a 1 SD increase in resource normalized degree.

- **type_M.vs.A:sc.c_ND** = effect of a mutualistic interaction (relative to antagonistic) on a 1 SD increase in consumer normalized degree.
- **sc.r_ND:sc.c_ND** = nonadditive effect of 1 SD increase in resource and consumer normalized degree across interaction types. A positive value indicates that symmetry in partners normalized degree increases partner fidelity, whereas a negative value indicates that *asymmetry* in partners normalized degree increases partner fidelity (see justification for this in section **Asymmetry effect**).
- **type_M.vs.A:sc.r_ND:sc.c_ND** = nonadditive effect of a mutualistic interaction (relative to antagonistic) on a 1 SD increase in resource and consumer normalized degree. A positive value indicates that mutualistic interactions enhance the effects of symmetry on partner fidelity, whereas a negative value indicates that mutualistic interactions enhance the effects of *asymmetry*.

For each of our random effects (**resource_sp**, **consumer_sp**, **id_pair**, and **network_id**), our model estimates the SD that describes the assumed normal distribution in their effect sizes.

For the sampling effects model, the fixed and random effects are the same as before except the baseline is the average logarithm of observed interactions instead of normalized degree. We also replace normalized degree with the following terms:

- **sc.log.sum_r** = effect of 1 SD increase in the log of observed interactions for a resource.
- **sc.log.sum_c** = effect of 1 SD increase in the log of observed interactions for a consumer.
- **type_M.vs.A:sc.log.sum_r** = effect of a mutualistic interaction (relative to antagonistic) on a 1 SD increase in the log of observed interactions for a resource.
- **type_M.vs.A:sc.log.sum_c** = effect of a mutualistic interaction (relative to antagonistic) on a 1 SD increase in the log of observed interactions for a consumer.
- **sc.log.sum_r:sc.log.sum_c** = nonadditive effect of 1 SD increase in the log of observed interactions for a resource and consumer across interaction types. A positive value indicates that symmetry in partner observations increases partner fidelity, whereas a negative value

indicates that *asymmetry* in partner observations increases partner fidelity.

- **type_M.vs.A:sc.r_ND:sc.c_ND** = nonadditive effect of a mutualistic interaction (relative to antagonistic) on a 1 SD increase in the logarithm of resource and consumer observed interaction. A positive value indicates that mutualistic interactions enhance the effects of symmetry on partner fidelity, whereas a negative value indicates that mutualistic interactions enhance the effects of *asymmetry*.

Below, we give a justification for each of the prior distributions we chose for these parameters.

Type of interaction: type_M.vs.A

Let's take a hypothetical example, where the effect of **type_M.vs.A** on partner fidelity is really large, ranging from a probability of 0.25 to 0.75. The example below shows that this corresponds to a logistic regression coefficient of ~2.2.

```
# probability of a mutualistic interaction when two species co-occur
pM <- 0.75

# probability of an antagonistic interaction when two species co-occur
pA <- 0.25

# logistic regression coefficient, which is the difference in log-odds
# for 1 unit increase in the predictor
(mu_mutualist <- log(pM / (1-pM)) - log(pA / (1-pA)))

## [1] 2.197225
```

We would expect such a large effect to be unlikely though. Also, we have no strong prior expectation as to whether mutualistic or antagonistic interactions will have a positive or negative effect on partner fidelity. So let's explore what a normal distribution looks like where the coefficient is

centered on zero, but the variance is large enough to allow for a large effect (**type_M.vs.A** = 2.2, denoted by dotted line below) if there is enough evidence to support it.

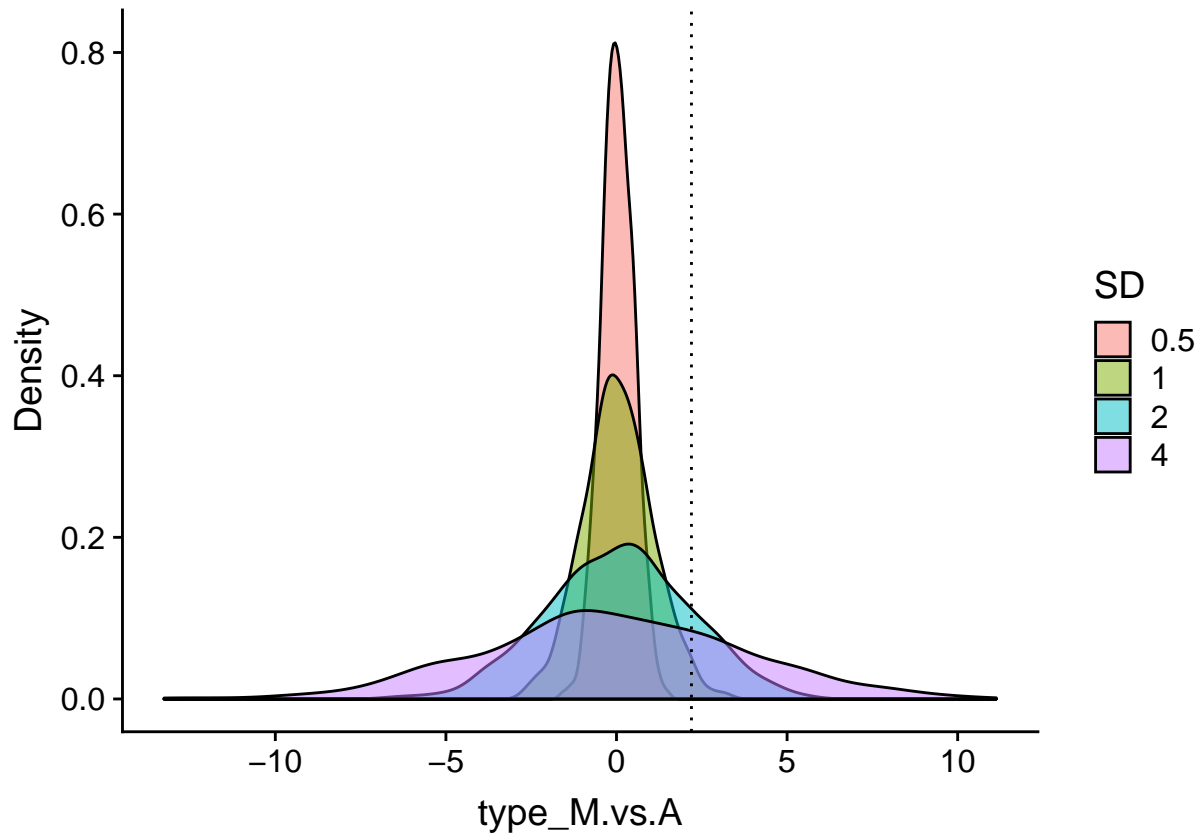


Figure 1: Simulating prior distributions for the effect of interaction type.

Based on these distributions, we think a normal prior with mean=0 and SD=2 would be appropriate. This creates a regularizing prior where the mass of the distribution is centered on zero (i.e., no effect), but allows for the model to detect large effects if the data supports it.

Subtype of interaction: subtype_Herb.vs.Para and subtype_Poll.vs.Disp

We expect similar effects for different subtypes of interaction as we would for different interaction types. Therefore, we choose to use the same prior: `normal(mean=0, SD=2)`.

Scaled normalized degree: `sc.r_ND` and `sc.c_ND`

Since the normalized degree of a species defines its probability of interacting with a co-occurring partner, regardless of its identity, our prior expectation is that there is a 1:1 relationship between the normalized degree of a species and its probability of interacting with another species. In other words, the probability of observing an interaction is the same as the normalized degree.

Let's get some intuition as to what this prior looks like when normalized degree is on a standardized scale (1 SD above the mean) and the response is in terms of log odds, which matches the assumptions of our model. Note that we chose to only look 1 SD above the mean because this reflects how the coefficient is estimated in the model (effect of 1 unit increase in predictor variable). We do this first for resources:

```
# probability of average species interacting
pMean_r <- mean(full.df$r_ND)

# probability of a relatively generalized species interacting
pGen_r <- mean(full.df$r_ND) + sd(full.df$r_ND)

# logistic regression coefficient, which is the difference in log-odds
# for a 1 SD unit increase in a species normalized degree.
(mu_sc.r_ND <- log(pGen_r / (1-pGen_r)) - log(pMean_r / (1-pMean_r)))

## [1] 1.040268
```

and then for consumers:

```
## Consumer species

# probability of average species interacting
pMean_c <- mean(full.df$c_ND)
```

```

# probability of a relatively generalized species interacting
pGen_c <- mean(full.df$c_ND) + sd(full.df$c_ND)

# logistic regression coefficient, which is the difference in log-odds
# for a 1 SD increase in a species normalized degree.
(mu_sc.c_ND <- log(pGen_c / (1-pGen_c)) - log(pMean_c / (1-pMean_c)))

## [1] 0.9944917

```

These examples indicate that we should have a prior expectation for the mean estimate of these coefficients to be ~1. How much variance around this coefficient might we expect though? Let's simulate a normal distribution with mean=1 (dotted line below), but different variances:

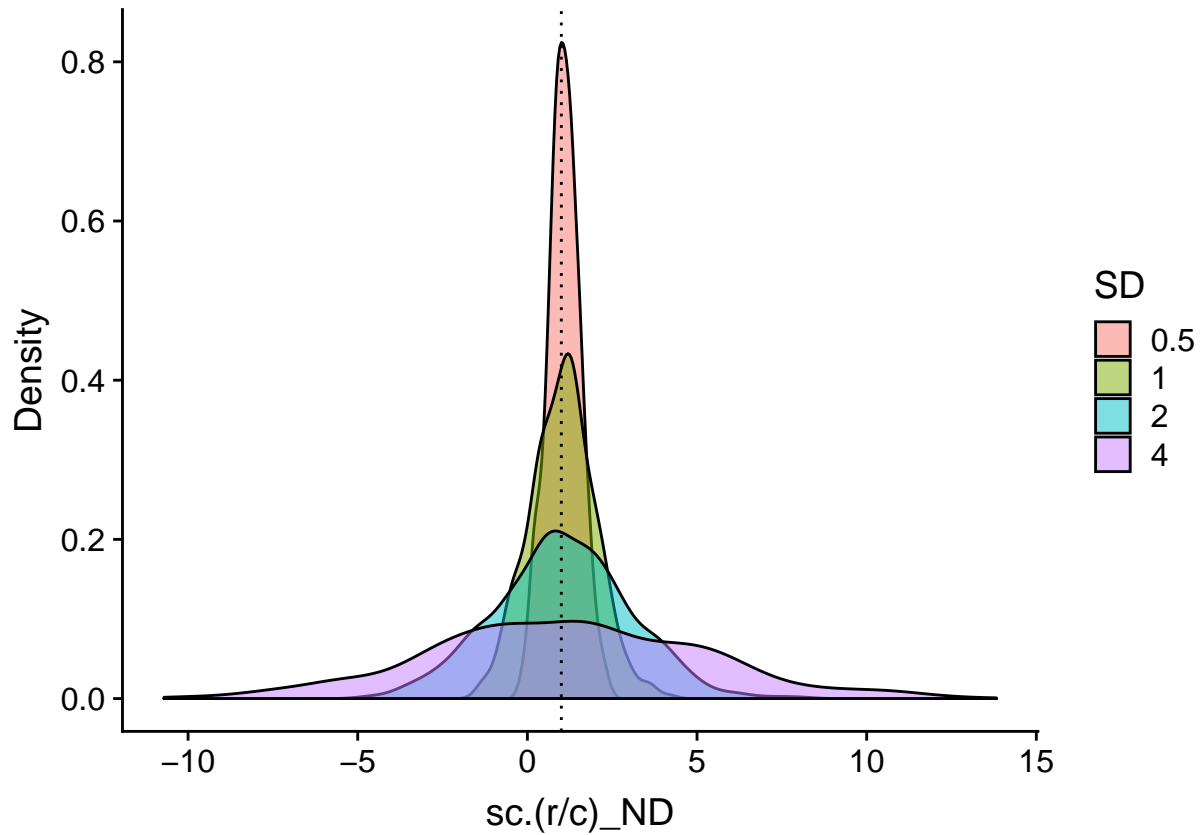


Figure 2: Simulating prior distributions for the effect of scaled normalized degree.

Most standardized logistic regression coefficients are less than 5 (Gelman et al., 2008), so we feel that specifying a standard deviation of 2 is reasonable since it more than covers the range from 0 to 5. It will also make the data “work” for larger values, since the mass of the distribution is centered on 1.

Statistical interactions between interaction type and normalized degree: `type_M.vs.A:sc.r_ND`, `type_M.vs.A:sc.c_ND`

We specified the same regularizing prior as for **`type_M.vs.A`** (i.e., `normal(mean=0, SD=2)`), because we have no strong prior expectation for whether interaction type will have a positive or negative effect on these relationships, and we want to make the data “work” for any strong effects.

Partner (a)symmetry effect: sc.r_ND:sc.c_ND

Although it is not intuitive, the sign of the statistical interaction between consumer and resource normalized degree indicates whether partner symmetry or asymmetry increases partner fidelity. To illustrate this, let's first assume that the main effects of scaled normalized degree for both resources and consumers equals 1 (also our prior expectation). For simplicity, let's assume that the statistical interaction is either -1 or +1. With these coefficients, we can now calculate how a change in scaled normalized degree for both resources and consumers affects the log-odds of an interaction. Below, we explore these effects ± 1 SD for the scaled normalized degree of both resources and consumers.

```
sim.log.odds <- expand.grid(
  b_sc.r_ND = 1,
  b_sc.c_ND = 1,
  `b_sc.r_ND:sc.c_ND` = c(-1, 1),
  delta.sc.r_ND = seq(-1, 1, 0.01),
  delta.sc.c_ND = seq(-1, 1, 0.01)) %>%
  mutate(log.odds.connected =
    b_sc.r_ND * delta.sc.r_ND + # main effect of sc.r_ND
    b_sc.c_ND * delta.sc.c_ND + # main effect of sc.c_ND
    `b_sc.r_ND:sc.c_ND` * delta.sc.r_ND * delta.sc.c_ND, # statistical interaction
    main.log.odds = b_sc.r_ND * delta.sc.r_ND + b_sc.c_ND * delta.sc.c_ND,
    diff.log.odds = log.odds.connected - main.log.odds)
```

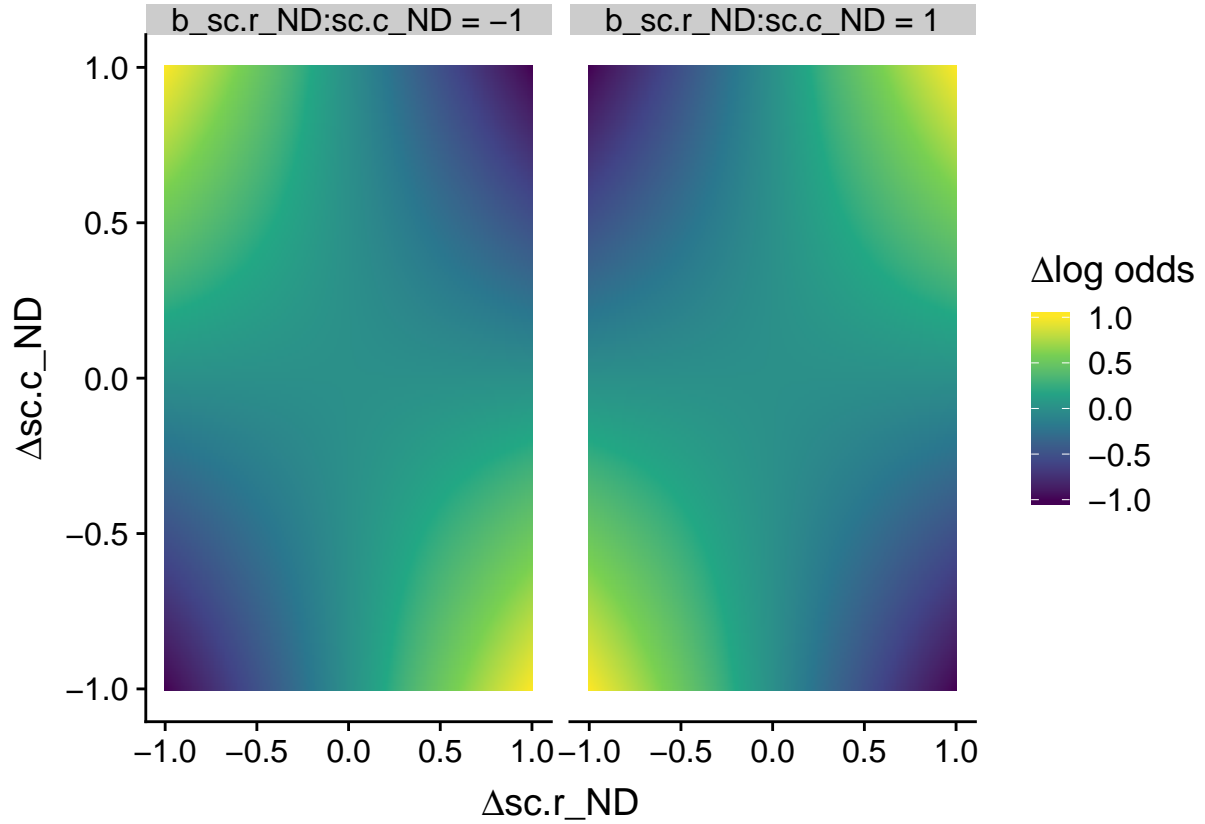


Figure 3: Plot of how the sign of $b_{sc.r_ND:sc.c_ND}$ determines how symmetry (right panel) or asymmetry (left panel) in partners normalized degree affects partner fidelity.

By inspecting figure 3, you can see how the sign of the statistical interaction between resource and consumer normalized degree affects the log odds of an interaction. When the sign is positive (right panel), symmetric normalized degrees increase the probability of an interaction (relative to main effects). In contrast, when the sign is negative (left panel), asymmetric normalized degrees increase the probability of an interaction. For example, if a relatively specialized consumer ($\Delta sc.c_ND = -1$) interacts with a relatively generalist resource ($\Delta sc.r_ND = +1$), there is an increase in the log-odds of an interaction (yellow spot in lower right corner of left panel in fig. 3).

Since we had no prior expectation as to how symmetry or asymmetry would affect partner fidelity, we set a normal prior with mean=0 and SD=2 to cover the range of most logistic regression

coefficients (Gelman et al., 2008).

Effect of mutualism on partner (a)symmetry in normalized degrees: type_M.vs.A:sc.r_ND:sc.c_ND

We again set a normal prior with mean=0 and SD=2, because we had no strong prior expectation for how interaction type would modify the effect of (a)symmetry in normalized degree on partner fidelity.

Main effects and statistical interactions with observed interactions (sc.log.sum_)

As with normalized degree, we expect the log of observed interactions for a resource or consumer to increase the probability of observing an interaction between co-occurring species. Therefore, we specified the same priors as we did for normalized degree for both main effects (normal(mean=1, SD=2) for `sc.log.sum_r`, `sc.log.sum_c`) and statistical interactions (normal(mean=0, SD=2) for `sc.log.sum_r:sc.log.sum_c`, `type_M.vs.A:sc.log.sum_r`, `type_M.vs.A:sc.log.sum_c`, `type_M.vs.A:sc.log.sum_r:sc.log.sum_c`).

Random effects: resource_sp, consumer_sp, id_pair, network_id

We specified a half-normal prior with mean=0 and SD=2 for each of the random effects in our model. This prior assumes that the variance in these effect sizes is small, but with sufficient evidence, the model can still estimate larger effects. Note that we specify this as a normal distribution in the code, but the R package we use constrains this prior to only positive values since standard deviations cannot be less than zero.

Model Analyses

We used the *brms* package (Bürkner, 2017) and its default sampling behavior (four sampling chains for 2000 iterations each, discarding the first 1000 iterations as burn-in) to fit these statistical models. To mitigate bias in the posterior sampling distribution, we set **adapt_delta = 0.99** and **max_treedepth = 20**.

For the majority of our inferences below, we keep coefficients on the log odds scale. This is because effect sizes are invariant on this scale. For intercept terms, we make inferences on the probability scale, and note the specific values at which this effect is measured. To calculate probabilities, we applied the inverse logit, $\frac{\exp(\beta)}{\exp(\beta)+1}$, to estimates reported in each table.

Full model

```
full.brm <- brm(  
  formula = interaction.formula, data = full.df,  
  prior = interaction.priors, algorithm = "sampling",  
  chains = 4, iter = 2000, warmup = 1000,  
  control = list(adapt_delta = 0.99, max_treedepth = 20))
```

Below, we give a biological interpretation of each term in this model (table 4):

- On the probability scale, the average level of partner fidelity across interaction types equals 0.65($= \frac{\exp(\beta)}{\exp(\beta)+1}$, where $\beta = 0.63$) for the average level of normalized degree for a resource and consumer.
- Mutualistic interactions increase the log odds of partner fidelity by 1.4 relative to antagonistic interactions.

Table 4: Mean and 95% credible intervals of fixed effects from our full model.

| Term | Estimate | 2.5% | 97.5% |
|-----------------------------|----------|-------|-------|
| Intercept | 0.63 | 0.17 | 1.05 |
| type_M.vs.A | 1.40 | 0.55 | 2.26 |
| subtype_Herb.vs.Para | 1.30 | -0.22 | 2.75 |
| subtype_Poll.vs.Disp | 2.60 | 1.73 | 3.50 |
| sc.r_ND | 2.00 | 1.85 | 2.16 |
| sc.c_ND | 1.51 | 1.39 | 1.64 |
| type_M.vs.A:sc.r_ND | 0.57 | 0.31 | 0.84 |
| type_M.vs.A:sc.c_ND | -0.15 | -0.36 | 0.07 |
| sc.r_ND:sc.c_ND | 0.16 | 0.04 | 0.28 |
| type_M.vs.A:sc.r_ND:sc.c_ND | -0.78 | -1.01 | -0.52 |

- There is no clear difference between herbivory and parasitism on partner fidelity (95% credible intervals overlap with zero).
- Pollination increases the log odds of partner fidelity by 2.6 relative to seed dispersers.
- A 1 SD increase in resource normalized degree increases the log odds of partner fidelity by 2 across interaction types.
- A 1 SD increase in consumer normalized degree increases the log odds of partner fidelity by 1.51 across interaction types.
- Mutualistic interactions increase the positive effect of resource normalized degree on the log odds of partner fidelity by 0.57 relative to antagonistic interactions.
- There is no clear evidence that mutualistic interactions (relative to antagonistic) modify the positive effect of consumer normalized degree on partner fidelity (95% credible intervals overlap with zero).

- Across interaction types, symmetry between partners in their normalized degree increases the log odds of partner fidelity by 0.16.
- Mutualistic interactions (relative to antagonistic) decrease the effects of symmetry on the log odds of partner fidelity by -0.78. Put another way, mutualistic interactions increase the effects of *asymmetry* on the log odds of partner fidelity by 0.78.

In addition to these fixed effects, there is considerable variation in partner fidelity explained by our random effects. In particular, **network_id** has a strong effect compared to the other sources of variation (table 5).

Table 5: Mean and 95% credible intervals of random effects from our full model.

| Term | Estimate | 2.5% | 97.5% |
|---------------------------|----------|------|-------|
| sd_consumer_sp__Intercept | 0.22 | 0.12 | 0.32 |
| sd_id_pair__Intercept | 0.48 | 0.38 | 0.58 |
| sd_network_id__Intercept | 1.47 | 1.24 | 1.74 |
| sd_resource_sp__Intercept | 0.48 | 0.37 | 0.60 |

While the model above is useful for determining the effects of mutualistic relative to antagonistic interactions on partner fidelity, it is also useful to separately estimate relationships for mutualistic and antagonistic interactions. We can do this by removing the intercept term from the model, and estimating unique relationships for normalized degree for both mutualistic and antagonistic interactions.

```
no.intercept_formula <- brmsformula(
  connected ~ -1 + type + subtype_Herb.vs.Para + subtype_Poll.vs.Disp +
  type:sc.r_ND + type:sc.c_ND +
  type:sc.r_ND:sc.c_ND +
```

```

      (1 | resource_sp) + (1 | consumer_sp) + (1 | id_pair) + (1 | network_id),
family = bernoulli(link = "logit"))

no.intercept_priors <- c(
  set_prior("normal(0,2)", class = "b", coef = "typeA"), # corresponds to probability of 0.5
  set_prior("normal(0,2)", class = "b", coef = "typeM"), # corresponds to probability of 0.5
  set_prior("normal(0,2)", class = "b", coef = "subtype_Herb.vs.Para"),
  set_prior("normal(0,2)", class = "b", coef = "subtype_Poll.vs.Disp"),
  set_prior("normal(1,2)", class = "b", coef = "typeA:sc.r_ND"),
  set_prior("normal(1,2)", class = "b", coef = "typeM:sc.r_ND"),
  set_prior("normal(1,2)", class = "b", coef = "typeA:sc.c_ND"),
  set_prior("normal(1,2)", class = "b", coef = "typeM:sc.c_ND"),
  set_prior("normal(0,2)", class = "b", coef = "typeA:sc.r_ND:sc.c_ND"),
  set_prior("normal(0,2)", class = "b", coef = "typeM:sc.r_ND:sc.c_ND"),
  set_prior("normal(0,2)", class = "sd"))

no.intercept_brm <- brm(
  formula = no.intercept_formula, data = full.df,
  prior = no.intercept_priors, algorithm = "sampling",
  chains = 4, iter = 2000, warmup = 1000,
  control = list(adapt_delta = 0.99, max_treedepth = 20))

```

The results from this model (table 6) can be interpreted as follows:

- The average level of partner fidelity for antagonistic interactions is 0.47 ($= \frac{\exp(\beta)}{\exp(\beta)+1}$, where $\beta = -0.12$) at the average level of normalized degree for a resource and consumer.

Table 6: Mean and 95% credible intervals of fixed effects from model without intercepts.

| Term | Estimate | 2.5% | 97.5% |
|-----------------------|----------|-------|-------|
| typeA | -0.12 | -0.83 | 0.62 |
| typeM | 1.35 | 0.90 | 1.78 |
| subtype_Herb.vs.Para | 1.22 | -0.25 | 2.61 |
| subtype_Poll.vs.Disp | 2.58 | 1.65 | 3.46 |
| typeA:sc.r_ND | 1.72 | 1.60 | 1.84 |
| typeM:sc.r_ND | 2.29 | 2.05 | 2.55 |
| typeA:sc.c_ND | 1.59 | 1.49 | 1.70 |
| typeM:sc.c_ND | 1.44 | 1.24 | 1.64 |
| typeA:sc.r_ND:sc.c_ND | 0.55 | 0.43 | 0.67 |
| typeM:sc.r_ND:sc.c_ND | -0.23 | -0.44 | -0.01 |

- The average probability of partner fidelity for mutualistic interactions is 0.79 ($= \frac{\exp(\beta)}{\exp(\beta)+1}$, where $\beta = 1.35$) at the average level of normalized degree for a resource and consumer.
- A 1 SD increase in resource normalized degree in antagonistic interactions increases the log odds of an interaction by 1.72.
- A 1 SD increase in resource normalized degree in mutualistic interactions increases the log odds of an interaction by 2.29.
- A 1 SD increase in consumer normalized degree in antagonistic interactions increases the log odds of an interaction by 1.59.
- A 1 SD increase in consumer normalized degree in mutualistic interactions increases the log odds of an interaction by 1.44.
- Symmetry in partner normalized degrees increases the log odds of partner fidelity by 0.55 for antagonistic interactions.

- Asymmetry in partner normalized degrees increases the log odds of partner fidelity by 0.23 for mutualistic interactions.

Analysis of data subset

Before testing for potential biases due to sampling effort, we test whether we observe the same results for the data subset.

```
weighted_subset.brm <- brm(
  formula = interaction_subset.formula, data = weighted_subset.df,
  prior = interaction_subset.priors, algorithm = "sampling",
  chains = 4, iter = 2000, warmup = 1000,
  control = list(adapt_delta = 0.99, max_treedepth = 20))
```

Table 7: Mean and 95% credible intervals of fixed effects from our weighted subset model.

| Term | Estimate | 2.5% | 97.5% |
|-----------------------------|----------|-------|-------|
| Intercept | 1.53 | 1.09 | 2.00 |
| type_M.vs.A | 2.85 | 2.03 | 3.70 |
| subtype_Poll.vs.Disp | 1.57 | 0.31 | 2.81 |
| sc.r_ND | 2.04 | 1.74 | 2.35 |
| sc.c_ND | 1.79 | 1.52 | 2.09 |
| type_M.vs.A:sc.r_ND | 0.33 | -0.21 | 0.94 |
| type_M.vs.A:sc.c_ND | -0.17 | -0.71 | 0.40 |
| sc.r_ND:sc.c_ND | 0.26 | -0.02 | 0.55 |
| type_M.vs.A:sc.r_ND:sc.c_ND | -0.68 | -1.22 | -0.09 |

Note that the **Intercept** and effect of **type_M.vs.A** is higher in this subset of data (table 7). This is likely due to the fact that herbivory had a tendency to increase partner fidelity

(**subtype_Herb.vs.Para** in table 4); therefore, its absence from the data subset enhances the average estimate of partner fidelity as well as the apparent effect of mutualistic interactions. Other terms are similar, except that there is less clear evidence of mutualistic interactions enhancing the effect of resource normalized degree (**type_M.vs.A:sc.r_ND** in table 7), and less clear evidence of symmetry in partner normalized degrees to positively affect partner fidelity (**sc.r_ND:sc.c_ND** in table 7). Importantly, there is still clear evidence that mutualistic interactions generally enhance partner fidelity (**type_M.vs.A** in table 7) and also enhance the effects of *asymmetry* in partner normalized degrees on partner fidelity (**type_M.vs.A:sc.r_ND:sc.c_ND** in table 7).

As with the full model, we observe a particularly strong effect of **network_id** compared to the other sources of variation (table 8).

Table 8: Mean and 95% credible intervals of random effects from our weighted subset model.

| Term | Estimate | 2.5% | 97.5% |
|---------------------------|----------|------|-------|
| sd_consumer_sp__Intercept | 0.10 | 0.01 | 0.25 |
| sd_id_pair__Intercept | 0.84 | 0.72 | 0.97 |
| sd_network_id__Intercept | 1.11 | 0.89 | 1.37 |
| sd_resource_sp__Intercept | 0.41 | 0.23 | 0.58 |

Testing for bias due to sampling effort

Our goal here is to test whether sampling effort can explain the results we observed in the previous models, in particular, the effect of interaction type and its three-way statistical interaction with resource and consumer normalized degree. As a reminder, we replaced normalized degree with the log of observed interactions for both resources and consumers.

```
sampling_effects.brm <- brm(
  formula = sampling_effects.formula, data = weighted_subset.df,
  prior = sampling_effect.priors, algorithm = "sampling",
```



```
chains = 4, iter = 2000, warmup = 1000,
control = list(adapt_delta = 0.99, max_treedepth = 20))
```

Table 9: Mean and 95% credible intervals of fixed effects from our sampling effects model.

| Term | Estimate | 2.5% | 97.5% |
|---------------------------------------|----------|-------|-------|
| Intercept | 1.75 | 1.44 | 2.09 |
| type_M.vs.A | 2.89 | 2.27 | 3.52 |
| subtype_Poll.vs.Disp | -1.06 | -1.91 | -0.18 |
| sc.log.sum_r | 1.50 | 1.31 | 1.69 |
| sc.log.sum_c | 1.36 | 1.20 | 1.53 |
| type_M.vs.A:sc.log.sum_r | 0.72 | 0.37 | 1.09 |
| type_M.vs.A:sc.log.sum_c | 0.66 | 0.33 | 1.00 |
| sc.log.sum_r:sc.log.sum_c | 0.26 | 0.10 | 0.42 |
| type_M.vs.A:sc.log.sum_r:sc.log.sum_c | -0.08 | -0.39 | 0.24 |

Inspecting the table of fixed effects (table 9), there are a few results worth noting. First, the effect of pollination (relative to seed dispersal) on partner fidelity has reversed; in other words, it now has a negative effect (*what exactly does this mean?*, **subtype_Poll.vs.Disp** in table 9). Second, mutualistic interactions increase the positive effect of observed consumer interactions on partner fidelity (*what exactly does this mean?*, **type_M.vs.A:sc.log.sum_c** in table 9). Third, we do not see evidence of a three-way interaction between the observed interactions of resources and consumers and interaction type (**type_M.vs.A:sc.log.sum_r:sc.log.sum_c** in table 9). This indicates that sampling effects cannot explain the effect of mutualistic interactions on partner fidelity (**type_M.vs.A** in tables 4, 7) or the three-way interaction between normalized degree of resources and consumers and interaction type that we observed in previous models (**type_M.vs.A:sc.r_ND:sc.c_ND** in tables 4, 7).

The results for the random effects are similar to the other models (tables 5, 8), except that the most important random effect has changed to **id_pair**, although **network_id** is a close second (table 10).

Table 10: Mean and 95% credible intervals of random effects from our sampling effects model.

| Term | Estimate | 2.5% | 97.5% |
|---------------------------|----------|------|-------|
| sd_consumer_sp__Intercept | 0.31 | 0.17 | 0.47 |
| sd_id_pair__Intercept | 0.71 | 0.60 | 0.82 |
| sd_network_id__Intercept | 0.66 | 0.52 | 0.83 |
| sd_resource_sp__Intercept | 0.40 | 0.25 | 0.57 |

Alternative models to account for sampling effort

There are alternative ways we can account for sampling effort. For example, we could fit a model where resource and consumer observed interactions are simply covariates in a model that includes main effects and statistical interactions for resource and consumer normalized degree:

```
subset.sampling_formula <- brmsformula(
  connected ~ sc.log.sum_r + sc.log.sum_c + # add covariates
  type + subtype_Poll.vs.Disp + sc.r_ND + sc.c_ND +
  type:sc.r_ND + type:sc.c_ND + sc.r_ND:sc.c_ND +
  type:sc.r_ND:sc.c_ND +
  (1 | resource_sp) + (1 | consumer_sp) + (1 | id_pair) + (1 | network_id),
  family = bernoulli(link = "logit"))

subset.sampling_priors <- c(
  set_prior("normal(1,2)", class = "b", coef = "sc.log.sum_r"),
  set_prior("normal(1,2)", class = "b", coef = "sc.log.sum_c"),
  set_prior("normal(0,2)", class = "b", coef = "type_M.vs.A"),
```

```

set_prior("normal(0,2)", class = "b", coef = "subtype_Poll.vs.Disp"),
set_prior("normal(1,2)", class = "b", coef = "sc.r_ND"),
set_prior("normal(1,2)", class = "b", coef = "sc.c_ND"),
set_prior("normal(0,2)", class = "b", coef = "sc.r_ND:sc.c_ND"),
set_prior("normal(0,2)", class = "b", coef = "type_M.vs.A:sc.r_ND"),
set_prior("normal(0,2)", class = "b", coef = "type_M.vs.A:sc.c_ND"),
set_prior("normal(0,2)", class = "b", coef = "type_M.vs.A:sc.r_ND:sc.c_ND"),
set_prior("normal(0,2)", class = "sd"))

```

```

subset.sampling_brm <- brm(
  formula = subset.sampling_formula, data = weighted_subset.df,
  prior = subset.sampling_priors, algorithm = "sampling",
  chains = 4, iter = 2000, warmup = 1000,
  control = list(adapt_delta = 0.99, max_treedepth = 20))

```

Or alternatively, we can include an additional term that accounts for (a)symmetric effects of observed interactions (i.e., **sc.log.sum_r:sc.log.sum_c**):

```

subset.sampling.v2_formula <- brmsformula(
  connected ~ sc.log.sum_r + sc.log.sum_c + sc.log.sum_r:sc.log.sum_c +
    type + subtype_Poll.vs.Disp + sc.r_ND + sc.c_ND +
    type:sc.r_ND + type:sc.c_ND + sc.r_ND:sc.c_ND +
    type:sc.r_ND:sc.c_ND +
    (1 | resource_sp) + (1 | consumer_sp) + (1 | id_pair) + (1 | network_id),
  family = bernoulli(link = "logit"))

```

```

subset.sampling.v2_priors <- c(
  set_prior("normal(1,2)", class = "b", coef = "sc.log.sum_r"),

```

Table 11: Mean and 95% credible intervals of fixed effects from model with main effects for sampling effort.

| Term | Estimate | 2.5% | 97.5% |
|-----------------------------|----------|-------|-------|
| Intercept | 1.54 | 1.16 | 1.95 |
| sc.log.sum_r | 0.52 | 0.38 | 0.68 |
| sc.log.sum_c | 0.19 | 0.07 | 0.32 |
| type_M.vs.A | 2.94 | 2.19 | 3.72 |
| subtype_Poll.vs.Disp | 0.96 | -0.07 | 2.04 |
| sc.r_ND | 1.51 | 1.19 | 1.86 |
| sc.c_ND | 1.62 | 1.33 | 1.92 |
| type_M.vs.A:sc.r_ND | 0.26 | -0.29 | 0.82 |
| type_M.vs.A:sc.c_ND | -0.19 | -0.71 | 0.35 |
| sc.r_ND:sc.c_ND | 0.30 | 0.03 | 0.58 |
| type_M.vs.A:sc.r_ND:sc.c_ND | -0.56 | -1.10 | 0.00 |

```

set_prior("normal(1,2)", class = "b", coef = "sc.log.sum_c"),
set_prior("normal(0,2)", class = "b", coef = "sc.log.sum_r:sc.log.sum_c"),
set_prior("normal(0,2)", class = "b", coef = "type_M.vs.A"),
set_prior("normal(0,2)", class = "b", coef = "subtype_Poll.vs.Disp"),
set_prior("normal(1,2)", class = "b", coef = "sc.r_ND"),
set_prior("normal(1,2)", class = "b", coef = "sc.c_ND"),
set_prior("normal(0,2)", class = "b", coef = "sc.r_ND:sc.c_ND"),
set_prior("normal(0,2)", class = "b", coef = "type_M.vs.A:sc.r_ND"),
set_prior("normal(0,2)", class = "b", coef = "type_M.vs.A:sc.c_ND"),
set_prior("normal(0,2)", class = "b", coef = "type_M.vs.A:sc.r_ND:sc.c_ND"),
set_prior("normal(0,2)", class = "sd"))

```

```
subset.sampling.v2_brm <- brm(
  formula = subset.sampling.v2_formula, data = weighted_subset.df,
  prior = subset.sampling.v2_priors, algorithm = "sampling",
  chains = 4, iter = 2000, warmup = 1000,
  control = list(adapt_delta = 0.99, max_treedepth = 20))
```

Table 12: Mean and 95% credible intervals of fixed effects from model that includes covariates for observed interactions of resources and consumers and their statistical interaction.

| Term | Estimate | 2.5% | 97.5% |
|-----------------------------|----------|-------|-------|
| Intercept | 1.53 | 1.13 | 1.94 |
| sc.log.sum_r | 0.52 | 0.37 | 0.67 |
| sc.log.sum_c | 0.16 | 0.03 | 0.28 |
| type_M.vs.A | 2.96 | 2.20 | 3.77 |
| subtype_Poll.vs.Disp | 1.22 | 0.19 | 2.28 |
| sc.r_ND | 1.53 | 1.21 | 1.86 |
| sc.c_ND | 1.67 | 1.37 | 1.97 |
| sc.log.sum_r:sc.log.sum_c | 0.21 | 0.10 | 0.31 |
| type_M.vs.A:sc.r_ND | 0.30 | -0.26 | 0.89 |
| type_M.vs.A:sc.c_ND | -0.12 | -0.66 | 0.43 |
| sc.r_ND:sc.c_ND | 0.15 | -0.13 | 0.43 |
| type_M.vs.A:sc.r_ND:sc.c_ND | -0.62 | -1.16 | -0.08 |

Inspecting table 11 and table 12, we see that our key results are robust. Specifically, mutualistic interactions generally enhance partner fidelity and also enhance the effects of *asymmetry* in partner normalized degrees on partner fidelity.

Robustness to Different Priors

To test how robust our results were to a different choice of priors, we re-analyzed the full model with the default priors from the *brms* package, which are designed to be non or very weakly informative. Note that we had to increase **adapt_delta = 0.999** to avoid bias in the posterior sampling of this model.

```
nopriors.brm <- brm(  
  formula = interaction.formula, data = full.df,  
  # prior = interaction.priors, # remove and use default priors  
  algorithm = "sampling", chains = 4, iter = 2000, warmup = 1000,  
  control = list(adapt_delta = 0.999, max_treedepth = 20))
```

Table 13: Mean and 95% credible intervals of fixed effects from the no priors model.

| Term | Estimate | 2.5% | 97.5% |
|-----------------------------|----------|-------|-------|
| Intercept | 0.65 | 0.16 | 1.12 |
| type_M.vs.A | 1.40 | 0.46 | 2.29 |
| subtype_Herb.vs.Para | 1.40 | -0.18 | 3.01 |
| subtype_Poll.vs.Disp | 2.72 | 1.83 | 3.64 |
| sc.r_ND | 2.01 | 1.86 | 2.18 |
| sc.c_ND | 1.52 | 1.41 | 1.64 |
| type_M.vs.A:sc.r_ND | 0.59 | 0.32 | 0.87 |
| type_M.vs.A:sc.c_ND | -0.14 | -0.35 | 0.07 |
| sc.r_ND:sc.c_ND | 0.16 | 0.04 | 0.28 |
| type_M.vs.A:sc.r_ND:sc.c_ND | -0.78 | -1.01 | -0.52 |

There is an incredibly close correspondence between these results (tables 13, 14) and the one where we specified the priors (tables 4, 5), indicating that our results are robust.

Table 14: Mean and 95% credible intervals of random effects from the no priors model.

| Term | Estimate | 2.5% | 97.5% |
|---------------------------|----------|------|-------|
| sd_consumer_sp__Intercept | 0.22 | 0.12 | 0.31 |
| sd_id_pair__Intercept | 0.49 | 0.39 | 0.58 |
| sd_network_id__Intercept | 1.49 | 1.25 | 1.76 |
| sd_resource_sp__Intercept | 0.49 | 0.38 | 0.61 |

References

- Bürkner, P.-C. 2017. brms: An R package for bayesian multilevel models using Stan. *Journal of Statistical Software* 80:1–28.
- Gelman, A., A. Jakulin, M. G. Pittau, and Y.-S. Su. 2008. A weakly informative default prior distribution for logistic and other regression models. *Annals of Applied Statistics* 2:1360–1383.
- Schielzeth, H. 2010. Simple means to improve the interpretability of regression coefficients. *Methods in Ecology and Evolution* 1:103–113.