



Koster, J., Leckie, G., Miller, A., & Hames, R. (2015). Multilevel modeling analysis of dyadic network data with an application to Ye'kwana food sharing. *American Journal of Physical Anthropology*, 157(3), 507-512. 10.1002/ajpa.22721

Peer reviewed version

Link to published version (if available):
[10.1002/ajpa.22721](https://doi.org/10.1002/ajpa.22721)

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Multilevel Modeling Analysis of Dyadic Network Data
With an Application to Ye'kwana Food Sharing

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Page count (including bibliography): 18

Word count (including bibliography): ~4,404

Abbreviated title: Multilevel Modeling Analysis of Dyadic Networks

Key words: food sharing, social network analysis, cooperation, association index, Social Relations Model

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Abstract

Behavioral ecologists have recently begun using multilevel modeling for the analysis of social behavior. We present a multilevel modeling formulation of the “Social Relations Model” that is well suited for the analysis of dyadic network data. This model, which we adapt for count data and small datasets, can be fitted using standard multilevel modeling software packages. We illustrate this model with an analysis of meal sharing among Ye’kwana horticulturalists in Venezuela. In this setting, meal sharing among households is predicted by an association index, which reflects the amount of time that members of the households are interacting. This result replicates recent findings that inter-household food sharing is especially prevalent among households that interact and cooperate in multiple ways. We discuss opportunities for human behavioral ecologists to expand their focus to the multiple currencies and cooperative behaviors that characterize interpersonal relationships in preindustrial societies. We discuss possible extensions to this statistical modeling approach and applications to research by human behavioral ecologists and primatologists.

Social behavior has long attracted attention from both human and primate behavioral ecologists (Gurven, 2004; Sussman et al., 2005; Boyd and Richerson, 2009; Silk et al., 2013b). For the statistical analysis of dyadic social behavior, Hemelrijk (1990) developed and promoted the use of matrix permutation methods, which continue to be used by both human behavioral ecologists (Alvard, 2009; Koster, 2011; Nolin, 2011) and primatologists (Adiseshan et al., 2011; Massen et al., 2012, Wakefield, 2013). Matrix permutation methods have limitations, however. Most notably, matrix permutation methods account for the structure of network data only when determining statistical significance, but otherwise assume the independence of observations when estimating coefficients and model fit. Also, while it is possible to adapt such methods to accommodate response variables other than continuous outcomes, such as dichotomous network ties (e.g., Nolin, 2011), most applications have either assumed normally distributed outcomes or have applied non-parametric transformations that reduce the information available from the original data.

Owing to these limitations, behavioral ecologists have increasingly turned to multilevel modeling, also known as generalized linear mixed models (GLMM) or hierarchical linear modeling (Allen-Arave et al., 2008; Gomes et al., 2009; Gomes and Boesch, 2009; Cheney et al., 2010; Gomes and Boesch, 2011; Hooper et al., 2013; Silk et al., 2013a). Compared to matrix permutation methods, multilevel models easily accommodate different response types, including binomial proportion data (Jaeggi et al., 2010) and count data (Silk et al., 2013a). They also advantageously allow multiple smaller networks to be pooled into a broader dataset for a single analysis (e.g., Silk et al., 2013a) rather than analyzing each group discretely with matrix permutation methods (e.g., Watts, 1997).

Despite the advances afforded by the use of multilevel modeling, the analysis of dyadic reciprocity has remained problematic. In several analyses, researchers have modeled the bidirectional flows within a dyad by regressing the flow in one direction on the flow in the other direction (e.g., Jaeggi et al., 2010; Silk et al., 2013a). However, this creates a fundamental problem as the flow entered as the covariate will be correlated with the model's error term, leading to endogeneity bias (Kenny et al., 2006). More complex versions of this approach might allow additional covariates or include various random effects, but this fundamental endogeneity problem will remain (Supplemental File 1). The multilevel formulation of the Social Relations Model (SRM) presented by Snijders and Kenny (1999) circumvents this problem of endogeneity by effectively modeling the two flows as two separate response variables. Dyadic reciprocity is then captured by including correlated random effects.

The primary goal of this paper is methodological, as we demonstrate the application of the multilevel SRM to the kinds of dyadic network data that are common to research by behavioral ecologists. Another goal of the paper is to replicate the analysis of Koster and Leckie (2014), who show that an association index of behavioral interactions is a significant predictor of food sharing among indigenous Nicaraguan horticulturalists. Whereas primatologists frequently control for dyadic association (e.g., Gomes et al., 2009), the use of such association indices is rare in food sharing research by human behavioral ecologists, seemingly because these latter studies examine inter-household food sharing via methods that do not necessarily permit the simultaneous collection of data on affiliative behavior (Gurven et al., 2000; Ziker and Schnegg, 2005; Allen-Arave et al., 2008; Nolin, 2010).

Our response variable is the number of meals shared among eight Ye'kwana households in Venezuela. Similar count data are quite common in studies of dyads by primate behavioral ecologists, whether the sum of food exchanges, grooming bouts, greetings, or agonistic interventions (Watts, 1997; Range and Noë, 2002; Whitham and Maestriperi, 2003; Ferreira et al., 2006; Mitani, 2006). We therefore present a multilevel formulation of the SRM that is adapted for count outcomes and small samples, and we show how this model can be estimated as a standard cross-classified (i.e., crossed random effects) Poisson model using the MLwiN multilevel modeling software (Rasbash et al., 2009). Finally, we discuss possible extensions to our modeling approach and the opportunity for human behavioral ecologists to expand their focus to currencies and cooperative activities other than food sharing.

Methods

Data collection took place in Toki, a village of indigenous Ye'kwana horticulturalists in Venezuela (for ethnographic background on the study site and observational methods, see Hames and McCabe, 2007). During a 10-month period in 1975–1976, the village was comprised of 81 residents, divided among 8 households. Throughout the study period, one of us (RH) used instantaneous scan observations (or the “spot check” method) to document the behavior of these residents at randomized times during daylight hours (Borgerhoff Mulder and Caro, 1985). Both the behavior and the location of the observed individuals were recorded. Approximately 1.5% of the 18,947 observations documented the consumption of meals by individuals at others' households. These observations of meal sharing comprise our outcome variable, aggregated to reflect the total number of meals

provided from one household to another. Hames and McCabe (2007) likewise present an analysis of these data using OLS regression, evaluating meal sharing as a function of kinship, distance, and reciprocity. That analysis, however, does not consider the association index that we develop in this paper.

After removing observations of meal sharing and large communal gatherings, we use the remainder of the behavioral observation database to construct an inter-household association index.¹ Following Koster and Leckie's (2014) method, we added all of the times in which a member of Household A was observed interacting with Household B, which produces a valued, symmetric 8×8 sociomatrix.² We then normalized the matrix using an iterative process in UCINET (Borgatti et al., 2002), which reweights the values until the marginal sums of all rows and columns are approximately equal to one. The resulting association index provides a measure of interactions among members of the respective households. When members of different households spend time together, the most common behaviors were either idleness or leisure, which comprise approximately half of such observations. Other common behaviors during inter-household affiliations include routine housework and childcare (16%), hunting or fishing (8%), horticultural work (6%), and food processing or cooking (3%).

Other covariates include the geographic distance between the households, measured in meters, and the purported genetic relatedness between households, as derived from genealogical interviews. Subsequently described as “kinship,” this latter measure is

¹ Although some scan observations occurred on the same day, the briefest interval between scans was two hours. It is therefore rare for two individuals to be recorded as interacting in the observation immediately before or after an observation of meal sharing that involves one of those two individuals.

² Interactions were inferred from location codes in the observational data. When individuals were simultaneously in the same location, they were considered to be interacting unless their behavior at the time precluded meaningful interaction (e.g., sleeping).

operationalized as the average coefficient of relatedness between all members of the respective households (Hames, 1987; Allen-Arave et al., 2008). The association index is moderately correlated with distance, as closer neighbors spend more time together, but the association index is evidently uncorrelated with kinship (Supplemental Table 1).

Analysis

Following Koster and Leckie (2014), we treat meal sharing as a Poisson distributed response (y) in a multilevel formulation of the social relations model (SRM) for count data. Ideally suited for dyadic network data, the standard SRM decomposes the response variance into separate giving (σ_g^2), receiving (σ_r^2), and relationship (σ_a^2) variance components (Kenny, 1994; Snijders and Kenny, 1999; Kenny et al., 2006). Furthermore, by estimating the correlation of the respective relationship random effects, we obtain a measure of “dyadic reciprocity” (ρ_{da}), the degree to which transfers are reciprocated within a dyad beyond the reciprocity expected from the households’ respective propensities as givers and receivers. Analogously, estimation of the correlation of the household-level giver and receiver random effects provides a measure of “generalized reciprocity” (ρ_{gr}), the degree to which households who are net givers to the community are also net receivers. Because Hames and McCabe (2007) found evidence for reciprocity in Ye’kwana meal sharing, we expect dyadic reciprocity to be positive. There are no clear evolutionary predictions for the estimate of generalized reciprocity, but we note that the giver-level variance tends to exceed the receiver-level variance, suggesting a redistributive pattern (Gurven, 2004; Koster and Leckie, 2014).

We also include three relationship-level “fixed effects” covariates in our model: the association index (x_1), distance (x_2), and kinship (x_3). The association index and kinship are predicted to have positive effects on meal sharing while distance is expected to exhibit a negative effect, with greater sharing among closer neighbors.

Using the notation of Koster and Leckie (2014), we specify the following model for y_{ij} , the observed number of meals given from household i to household j ($i, j = 1, \dots, 8$):

$$y_{ij} \sim \text{Poisson}(\mu_{ij})$$

$$\log(\mu_{ij}) = \beta_0 + \beta_1 x_{1|ij|} + \beta_2 x_{2|ij|} + \beta_3 x_{3|ij|} + g_i + r_j + d_{ij}$$

$$\begin{pmatrix} g_i \\ r_i \end{pmatrix} \sim N \left\{ \begin{pmatrix} 0 \\ 0 \end{pmatrix}, \begin{pmatrix} \sigma_g^2 & \\ \sigma_{gr} & \sigma_r^2 \end{pmatrix} \right\}$$

$$\begin{pmatrix} d_{ij} \\ d_{ji} \end{pmatrix} \sim N \left\{ \begin{pmatrix} 0 \\ 0 \end{pmatrix}, \begin{pmatrix} \sigma_d^2 & \\ \sigma_{dd} & \sigma_d^2 \end{pmatrix} \right\}$$

where μ_{ij} denotes the expected number of shared meals, and g_i , r_j , and d_{ij} are the giver, receiver, and relationship random effects. We distinguish between asymmetric (directed) and symmetric (undirected) relationship variables by using the ij and $|ij|$ subscripts, respectively. We derive the generalized and dyadic correlations in the usual way:

$$\rho_{gr} = \frac{\sigma_{gr}}{\sigma_g \sigma_r}, \quad \rho_{dd} = \frac{\sigma_{dd}}{\sigma_d^2}$$

A limitation of the study is that with only eight households, we are not able to estimate ρ_{gr} with any degree of precision.³ We therefore constrain this correlation to zero by imposing $\sigma_{gr} = 0$.

The above model cannot be fitted in standard multilevel modelling software (Koster and Leckie 2014 use the WinBUGS software). However, because we choose to impose $\rho_{gr} = 0$ and are willing to assume $0 \leq \rho_{ad} \leq 1$, we can reformulate the model as a cross-classified Poisson multilevel model, which can be estimated in the multilevel modeling software, MLwiN. The reformulated model can be written as:

$$y_{ij} \sim \text{Poisson}(\mu_{ij})$$

$$\log(\mu_{ij}) = \beta_0 + \beta_1 x_{1|ij|} + \beta_2 x_{2|ij|} + \beta_3 x_{3|ij|} + g_i + r_j + \underbrace{u_{|ij|} + e_{ij}}_{d_{ij}}$$

$$g_i \sim N(0, \sigma_g^2)$$

$$r_j \sim N(0, \sigma_r^2)$$

$$u_{|ij|} \sim N(0, \sigma_u^2)$$

$$e_{ij} \sim N(0, \sigma_e^2)$$

where $u_{|ij|}$ and e_{ij} are intermediate random effects with associated parameters σ_u^2 and σ_e^2 .⁴

We can recover the remaining parameters of interest as follows:

³ Given the lack of a significant correlation (Pearson's $r = 0.36$; $p = 0.38$; $n = 8$) between the households' sum of meals provided and the sum of meals received (i.e., the corresponding marginal sums of the meal sharing sociomatrix), there is little reason to expect a more noteworthy estimate for the generalized reciprocity correlation of the SRM.

⁴ Note that whereas $u_{|ij|}$ is a symmetric (undirected) relationship-level random effect, e_{ij} is an asymmetric (directed) relationship-level random effect. The former takes one value per dyad, the latter takes one value

$$\sigma_d^2 = \sigma_u^2 + \sigma_e^2$$

$$\sigma_{dd} = \sigma_u^2$$

$$\rho_{dd} = \frac{\sigma_{dd}}{\sigma_d^2}$$

The formulation imposes $\rho_{gr} = 0$ by specifying g_i and r_j as independent random effects, while it implicitly assumes $0 \leq \rho_{dd} \leq 1$ since $\sigma_u^2 \geq 0$ and $\sigma_e^2 \geq 0$.

Estimation

We fit our models using Markov chain Monte Carlo (MCMC) methods, as implemented in MLwiN. We specify “diffuse” prior distributions for all parameters. We run a burn-in of 50,000 iterations to allow the chains to converge to their stationary distributions, relying on conventional MCMC diagnostics to confirm that the chains achieve stationarity. We then sample 200,000 additional “monitoring” iterations as the basis for inference. We call MLwiN from within Stata using the `runmlwin` command (Leckie and Charlton, 2013). In Supplemental Folder 1, we present the code for these commands and the equivalent code for fitting these models using the R2MLwiN package within the R Project for Statistical Computing (Zhang et al., 2014). We also include the data for replicative purposes.

Results

We present multiple models. The first model is an “intercept-only” model with no covariates. We use this model to calculate variance partition coefficients (VPC) to quantify

per observation within the dyad. A unique random effect is therefore fitted for every observation in the dataset ($n = 56$).

the relative importance of givers, receivers, and unique relationships as sources of variation in meal sharing between households. Each VPC is calculated by dividing the corresponding variance component by the total of the variance components.

We then present models with the three relationship-level covariates, first as independent predictors and finally in a multivariate model that includes all of the effects. Table 1 presents the results.

The intercept-only model

The giver, receiver, and relationship variances, σ_g^2 , σ_r^2 , and σ_d^2 , are estimated to be 3.44, 0.18, and 1.76, respectively. The relationship-level VPC, $\sigma_d^2 / (\sigma_g^2 + \sigma_r^2 + \sigma_d^2)$, is therefore estimated as $1.76 / (3.44 + 0.18 + 1.76) = 0.33$ and so 33% of the variance in meal sharing is attributed to unique household-level relationships. The giver and receiver variances are estimated to account for 64% and 3% of the variance in meal sharing, respectively. In other words, while relational effects account for a modest proportion of the total variation in meal sharing, most of the variance pertains to household-level variation in providing meals, which dwarfs the variation as receivers. This pattern is reflected in the raw data, which show that 3 of the 8 households together provide 86% of the given meals (Supplemental Figure 1).

Dyadic reciprocity $\rho_{dd} = \sigma_{dd} / \sigma_d^2$ is estimated to be strong and significant (0.80), and so when one household gives an especially high number of meals to another household, that behavior is very often reciprocated.

The models with fixed effect covariates

As predicted, the association index exhibits a significant positive effect on meal sharing, as seen in the estimated coefficient ($\beta_1 = 16.14$) in Model 2. In other words, households whose members regularly spend time together also show a greater propensity for sharing meals. Similarly, distance ($\beta_2 = -0.007$) exhibits a significant effect in Model 3, as closer neighbors share more meals. In contrast, kinship ($\beta_3 = -2.55$) seemingly has little effect on meal sharing, as seen in Model 4.

In the full model, Model 5, the association index ($\beta_1 = 11.13$) remains a strong and significant predictor of food sharing whereas we no longer find a significant effect of distance ($\beta_2 = -0.006$). Kinship remains uninformative ($\beta_3 = -3.41$).

The dyadic reciprocity correlation is substantially attenuated in models that include the association index, but the correlation is stronger and significant in all other models.

In the full model, the giver, receiver, and relationship variances, σ_g^2 , σ_r^2 , and σ_d^2 , are now estimated to be 3.29, 0.26, and 0.84, respectively. Comparing these results to the intercept-only model shows that the inclusion of the covariates explains $(1.76 - 0.84)/1.76 = 0.52$, or 52% of the relationship-level variation in inter-household meal sharing. In contrast, the estimates for the giver and receiver variance are largely unchanged by the inclusion of the covariates. The VPCs indicate that 75% of the remaining unexplained variance in meal sharing is attributable to households in their role as givers.

Discussion

The Multilevel Social Relations Model for Dyadic Network Data

We have illustrated a multilevel modeling approach to dyadic data that would be well suited for analyses by behavioral ecologists. The model is appropriate for count data, but

we note that the model can be easily adapted to accommodate other response types, including continuous and dichotomous outcomes. Whatever the response type, the multilevel SRM exhibits the advantages of other multilevel modeling methods used recently by behavioral ecologists while avoiding the aforementioned endogeneity problem of estimating dyadic reciprocity via entering reciprocal flows as a fixed effects covariate. The inclusion of dyadic random effects further allows for the partitioning of variance, which provides information on the sources of variation in the data and insight about the extent to which covariates account for the variance. Instead of treating the estimated variances as unreported nuisance parameters, this application illustrates the insight that can be gained from considering the variances and VPCs.

The second formulation of the SRM presented here assumes zero generalized reciprocity and positive dyadic reciprocity, which permits the model to be estimated as a cross-classified model in MLwiN and other standard multilevel modeling packages. For behavioral interactions such as food sharing, positive dyadic reciprocity may be a safe assumption. For other behaviors, however, negative dyadic reciprocity might be expected. When individuals vary in status and dominance, for example, agonistic interactions could exhibit negative dyadic reciprocity (Scott and Lockard, 2006). In such cases, we encourage researchers to use the first formulation of the SRM, which permits the correlation to be either negative or positive and can be fitted in specialized software packages, such as the Bayesian statistical modeling WinBUGS software (see Koster and Leckie, 2014). Similarly, although the generalized reciprocity correlation typically lacks a clear theoretical interpretation for behavioral ecologists, researchers who wish to estimate this correlation will again need to specify the first formulation of the model.

Further extensions of the multilevel SRM are possible. For instance, behavioral ecologists are interested in the extent to which reciprocal food transfers are contingent on other variables, such as kinship or begging frequency (Allen-Arave et al., 2008; Silk et al., 2013a). In principal, one can specify a model that allows the magnitude of the dyadic reciprocity correlation to vary as a function of the covariates (Leckie et al., 2014) where an inverse-tanh link function (or some other suitable function) can be used to ensure the resulting correlation lies between -1 and $+1$. Typically one would then also model the dyadic variance-component as heterogeneous, for example, by specifying it as a log-linear function of the same set of covariates. A second extension would be to model two currencies (e.g., food sharing and non-food gifts) simultaneously. This could be achieved by specifying a bivariate response version of the multilevel SRM (Card et al., 2008). The resulting model would have a four-by-four generalized reciprocity matrix and a four-by-four dyadic reciprocity matrix allowing one to estimate cross-currency generalized and dyadic reciprocity correlations as well as the usual same-currency correlations. A third potential extension relates to the response variable in dyadic network data often being “zero-inflated” (Gomes and Boesch, 2011; MacFarlan et al., 2012), and there being no convenient link function or transformation for such data. Multilevel models can accommodate mixture distributions, however, and it would be worthwhile to develop a formulation of the SRM that does not require either dichotomization of the response variable or the removal of data from the analysis.⁵

The correlates of food sharing in human societies

⁵ See McElreath and Koster (2014) for an example of a multilevel mixture model.

Behavioral ecologists have long acknowledged the possibility that shared food might be repaid in another currency, such as childcare, political support, or contributed labor (Winterhalder, 1996; Patton, 2005; Nolin, 2010). Partly owing to the challenges of multifaceted data collection and the conversion of all goods and services into a common currency, however, the subject of trade has received little empirical attention from human behavioral ecologists (Gurven, 2004). By contrast, primatologists have explored the extent to which altruistic behaviors among non-human primates are reciprocated in other currencies, finding that chimpanzees provide political support in exchange for meat and grooming, for example (Mitani, 2006; Gomes and Boesch, 2011). It is unclear whether such trades serve to smooth imbalances in the exchange of other commodities, but at this early stage of research, it would be beneficial for human behavioral ecologists to begin by testing for correlations between the exchanges of different resources and services that typify interpersonal relationships in small-scale societies.

This article advances that research agenda by showing that the residents of Toki more commonly share meals when they have multidimensional inter-household relationships, as reflected by the predictive effect of the association index. A previous analysis of these data showed that meal sharing is significantly predicted by dyadic reciprocity and inter-household distance (Hames and McCabe, 2007). Our reanalysis suggests that close neighbors and members of reciprocating households interact in a variety of ways, and in the full model, the association index is the most informative predictor of meal sharing.

Whereas this study replicates the significance of the association index as a predictor of food sharing, what distinguishes the Ye'kwana from the indigenous Nicaraguans described by Koster and Leckie (2014) is the apparent unimportance of kinship. Among the

Mayangna and Miskito of Nicaragua, close kin spend considerable time together, leading to high correlations between kinship, the association index, residential proximity, and food sharing. Such results are consistent with the view that genetic kinship is the principle basis of social organization in small-scale societies (Alvard, 2009). In Toki, by contrast, kinship predicts none of the other covariates, which is surprising given that the average inter-household relatedness (0.06) exceeds the average in two other Neotropical settings where kinship is highly predictive of food sharing and other cooperative interactions, namely an Ache community in Paraguay (average inter-household relatedness = 0.02; Allen-Arave et al., 2008) and a Mayangna community in Nicaragua (average = 0.03; Koster, 2011). In other words, despite exhibiting greater relatedness than comparable indigenous communities, the residents of Toki generally share time and meals with people other than close kin.

The relative unimportance of kinship in this study is surprising because prior research in this community shows that cooperative garden labor is predicted by inter-household relatedness (Hames, 1987). Alloparental care in Toki is also predicted by genetic relatedness (Hames, 1988). As noted, however, the association index aggregates these behaviors and many other kinds of activities, including routine interactions in the community, which are abundantly represented in the aggregated dataset. As in other studies, these considerations suggest a pattern in which kin collaborate on high cost or high benefit activities whereas cooperative activities with reduced costs or benefits are transacted through friends (Hames, in press). Meal sharing seems to emerge from this

latter context, perhaps indicating that sharing food at meals serves to bolster casual, amicable relationships among non-kin.⁶

Because of the small size of this dataset, we hesitate to draw extensive conclusions about the results of the analysis. The estimated positive relationship between meal sharing and the association index is a noteworthy finding that should spur further research into the multidimensional relationships that characterize household dyads. The estimated variance components, however, indicate that the unexplained variation lies primarily in household-level propensities for sharing meals. The SRM can accommodate household-level variables, and it would be preferable to replicate this study with a larger sample of households to assess the robustness of these results and to include household-level characteristics that could explain variation in meal sharing at this level of analysis.

⁶ Distance and proximity have sometimes been considered indicators of tolerated scrounging (e.g., Patton 2005). Our analysis does not preclude the possibility that meal sharing in Toki could stem from tolerated scrounging, particularly given the prominence of idleness and leisure as the basis of the association index.

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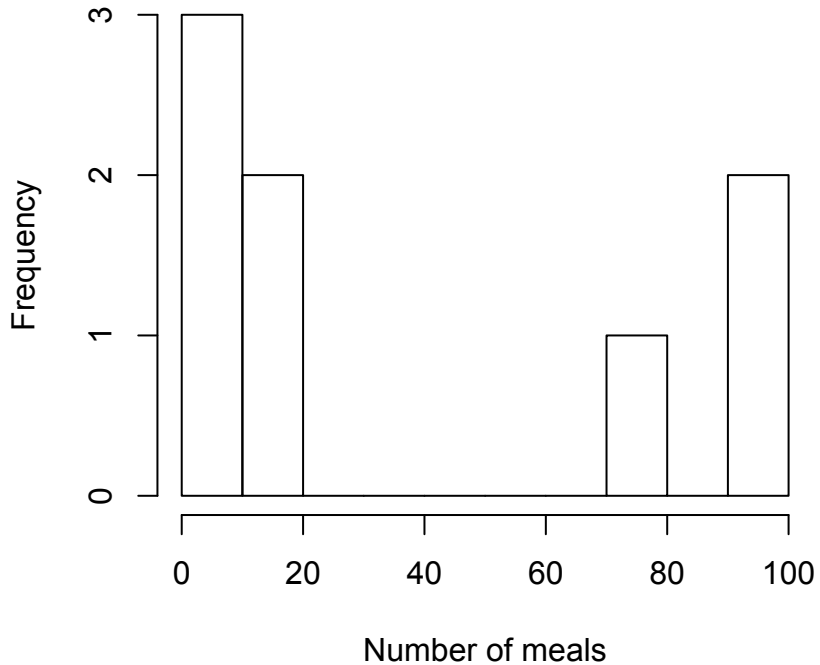
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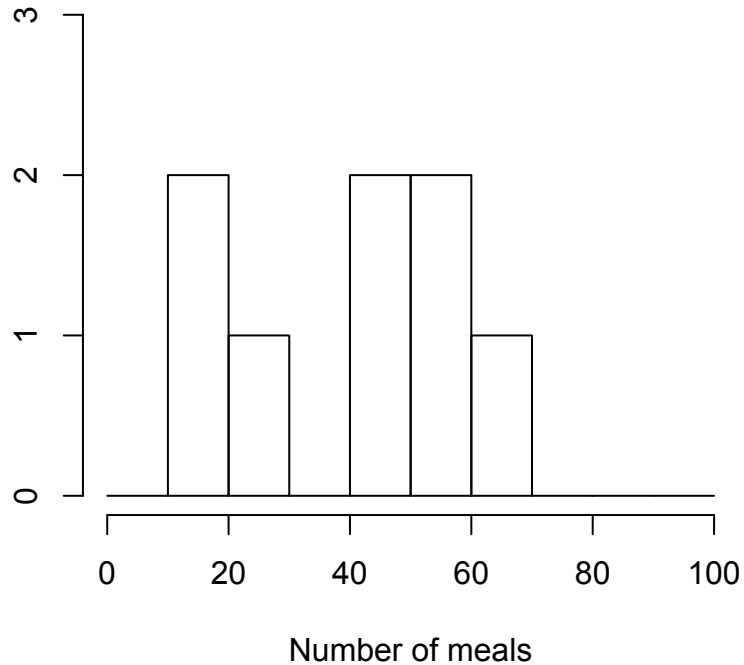
FIGURE CAPTION

Supplemental Figure 1. Histograms of the household-level centrality measures of the empirical data. Out-degree centrality measures the total number of meals that each of the eight households provided to other households. In-degree centrality measures the total number of meals that the households received from other households.

Out-degree



In-degree



The Endogeneity Problem

Consider a simpler linear regression model for y_{ij} the flow from individual i to individual j ($i, j = 1, \dots, n$)

$$y_{ij} = \beta_0 + \beta_1 y_{ji} + e_{ij} \quad (1)$$

where y_{ji} is the reciprocal flow from individual j to individual i and e_{ij} is the error term capturing all other factors.

Equally we have

$$y_{ji} = \beta_0 + \beta_1 y_{ij} + e_{ji} \quad (2)$$

Substituting (1) into (2) gives

$$\begin{aligned} y_{ji} &= \beta_0 + \beta_1(\beta_0 + \beta_1 y_{ji} + e_{ij}) + e_{ji} \\ &= \frac{\beta_0 + \beta_1 \beta_0 + \beta_1 e_{ij} + e_{ji}}{(1 - \beta_1^2)} \end{aligned}$$

And so y_{ji} is a function of e_{ij} . Thus y_{ji} and e_{ij} in (1) are positively correlated and so y_{ji} is endogenous. The regression coefficients in (1) will therefore suffer from endogeneity bias.

Table 1. Results for Model 1 (the intercept-only model), Models 2, 3 and 4 (which each contain one predictor), and Model 5 (the full model)

Parameter	Model 1		Model 2		Model 3		Model 4		Model 5	
	Mean	SD	Mean	SD	Mean	SD	Mean	SD	Mean	SD
β_0 Intercept	0.24	0.80	-1.85	0.97	1.24	0.91	0.36	0.78	-0.19	1.45
β_1 Association Index	-	-	16.14	4.08	-	-	-	-	11.13	5.14
β_2 Distance	-	-	-	-	-0.007	0.003	-	-	-0.006	0.004
β_3 Kinship	-	-	-	-	-	-	-2.55	5.06	-3.41	3.97
σ_g^2 Giver variance	3.44	3.03	3.84	3.74	3.40	3.70	3.45	2.97	3.29	3.00
σ_r^2 Receiver variance	0.18	0.33	0.49	0.57	0.12	0.26	0.26	0.46	0.26	0.45
σ_d^2 Relationship variance	1.76	0.80	0.67	0.49	1.33	0.64	1.86	0.86	0.84	0.49
ρ_{gr} Generalized reciprocity	0	0	0	0	0	0	0	0	0	0
ρ_{dd} Dyadic reciprocity	0.80	0.23	0.59	0.35	0.68	0.32	0.83	0.20	0.46	0.35
Giver VPC	0.64		0.77		0.70		0.62		0.75	
Receiver VPC	0.03		0.10		0.02		0.05		0.06	
Relationship VPC	0.33		0.13		0.27		0.33		0.19	

Note: Reported means and SDs are the means and standard deviations of the parameter chains, analogous to the point estimates and standard errors typically presented in frequentist analyses. Fixed effect parameters in bold represent estimates whose 95% credible intervals do not include zero and are therefore viewed as statistically significantly different from zero. Because the present formulation of the model constrains the dyadic reciprocity correlation to be positive (see text for details), dyadic reciprocity is considered significant when the z-score exceeds 1.96. Generalized reciprocity is constrained to be zero.

Supplemental Table 1. Models that estimate the association index as a function of the other covariates, kinship and distance.

Parameter	Model 1	Model 2
Intercept	0.1495 (0.0187)	0.1778 (0.0271)
Kinship	-0.0999 (0.16154)	
Distance		-0.0002 (0.0001)
Household-level variance	0.0013 (0.0014)	0.0022 (0.0027)
Residual variance	0.0025 (0.0008)	0.0021 (0.0007)

Note: Because all of these variables are symmetric, there is only one value for each of the 28 dyads. To account for the replication of households across dyads, we employ multiple membership models, assigning a weight of 0.5 to each household in the dyad. We stipulate a normal response variable, and we fit our models using MCMC estimation, as implemented in MLwiN. We run a burn-in of 5,000 iterations, then sample an additional 10,000 monitoring iterations for inference. During a diagnostic review of Model 2, it was apparent that one of the household-level random effects deviated from the assumption that higher-level random effects should be normally distributed around the mean. Following methods described in Koster and Leckie (2014), we generated a binary “fixed” effect to account for all dyads in which this household appeared. In the model that includes this binary effect for the outlier (full model results not presented here), the effect of distance on the association index is stronger and significant (posterior mean = -0.0005; posterior standard deviation = 0.0002).