



A Tale of Two Datasets: Representativeness and Generalisability of Inference for Samples of Networks

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A Tale of Two Datasets: Representativeness and Generalisability of Inference for Samples of Networks

Abstract

The last two decades have seen considerable progress in foundational aspects of statistical network analysis, but the path from theory to application is not straightforward. Two large, heterogeneous samples of small networks of within-household contacts in Belgium were collected using two different but complementary sampling designs: one smaller but with all contacts in each household observed, the other larger and more representative but recording contacts of only one person per household. We wish to combine their strengths to learn the social forces that shape household contact formation and facilitate simulation for prediction of disease spread, while generalising to the population of households in the region.

To accomplish this, we describe a flexible framework for specifying multi-network models in the exponential family class and identify the requirements for inference and prediction under this framework to be consistent, identifiable, and generalisable, even when data are incomplete; explore how these requirements may be violated in practice; and develop a suite of quantitative and graphical diagnostics for detecting violations and suggesting improvements to candidate models. We report on the effects of network size, geography, and household roles on household contact patterns (activity, heterogeneity in activity, and triadic closure).

Keywords: exponential-family random graph model, ERGM, missing data, network size, model-based inference, regression diagnostics

1 Introduction

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6 Networks of human interaction provide invaluable insights into epidemiology of directly
7 transmitted infectious disease, and there is a great deal of interest in translating network
8 data into epidemic models (Keeling and Eames 2005, for a review). It is common to focus on
9 epidemiologically important settings such as households (Goeyvaerts et al. 2018; Grijalva
10 et al. 2015) and schools (Mastrandrea et al. 2015, for example), and such data are often
11 used as they are for simulating disease spread and evaluating the impact of intervention
12 strategies (Cencetti et al. 2021, for example). However, observation of larger and broader
13 epidemiologically relevant networks is limited by time, resources, and considerations such as
14 privacy, so it is often indirect or incomplete in a variety of ways, therefore requiring statistical
15 models to learn network structure from the available data and reconstruct (simulate)
16 networks consistent with it (Krivitsky and Morris 2017).

17 Exponential-Family Random Graph Models (ERGMs), also called p^* models (Wasserman
18 and Pattison 1996; Lusher et al. 2012; Schweinberger et al. 2020, among many), are
19 a popular framework for specifying probability models for networks, postulating an expo-
20 nential family on the sample space of graphs. Most applications of ERG modelling concern
21 a single, completely observed population network, but methods for incomplete or indirect
22 observation exist (Handcock and Gile 2010; Krivitsky and Morris 2017, among others). At
23 the same time, questions of ERGM asymptotics and inference—particularly under varying
24 network size—have been debated in the literature (Schweinberger et al. 2020).

25 Increasingly, networks are collected in samples, however. Examples include social net-
26 works, such as multiple classrooms (Lubbers 2003; Stewart et al. 2019), multiple households
27 (Goeyvaerts et al. 2018; Grijalva et al. 2015), and multiple persons' social support networks
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(Ersig et al. 2011); but also other types of networks such as connections among brain regions for multiple subjects (Schweinberger et al. 2020, Sec. 8).

Though simpler mathematically, inference from samples of independent, non-overlapping networks is no less substantively challenging. In practice, the straightforward “i.i.d.” inference scenario (e.g., brain networks) is relatively rare, and it is far more common—particularly for social and contact networks—to observe multiple non-overlapping settings, similar to each other in nature and with the same notion of a relationship, but varying in size, composition, and exogenous influences. This variation is important because size and composition of networks can have profound effects on their structure (Krivitsky et al. 2011). Furthermore, the selection of networks to be observed may itself be a complex process, and the selected networks themselves may be incompletely observed, requiring network model inference to be integrated with survey sampling inference.

Samples of networks also offer new opportunities. With just one network, methods to diagnose how well the model fits—and how well the inference generalises—are limited to working within that network: Hunter et al. (2008a) proposed a form of lack-of-fit testing that compares the observed network’s relational features not explicitly in the model to the distribution of those features simulated from the fitted model, and Koskinen et al. (2018) leveraged missing data techniques to compute an analogue of Cook’s distance for each actor (the effect of observing each actor’s observed relations on parameter estimates). On the other hand, models for independent (if heterogeneous) samples of networks can be diagnosed using familiar techniques developed for regression—provided those techniques can be adapted to networks, including partially observed networks.

A variety of techniques exist for ERG modelling of samples of networks. One popular approach is meta-analysis, pooling individual networks’ estimates (Lubbers 2003). This

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3 approach is impractical for large samples of small networks, because the model may be
4 nonidentifiable on each network individually (Vega Yon et al. 2021). More recent is multi-
5 level (hierarchical) modelling: Zijlstra et al. (2006) developed it for the related p^2 model,
6 and Slaughter and Koehly (2016) for a Bayesian ERGM with random effects. Vega Yon et
7 al. (2021) described exact maximum likelihood inference for samples of very small networks.
8 Also, when modelling a time series of networks, *transitions* between successive networks
9 are typically treated as conditionally independent (Leifeld et al. 2018, for example).

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12 However, assessing an ERGM's goodness-of-fit for a sample of networks has tended to
13 be limited to comparing distributions of observed network statistics to expected (Slaughter
14 and Koehly 2016; Stewart et al. 2019, for example) and replicating diagnostics of Hunter et
15 al. for each network (Vega Yon et al. 2021). Little attention has been paid to methods ap-
16 propriate for partially observed networks, for large samples of networks, and to identifying
17 precisely how the model is misspecified.

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19 Here, we consider two samples of within-household contact networks: one more complete
20 but restricted to households with a young child, the other larger and more representative
21 but with only one member's relations observed in each household, and both heterogeneous
22 in household sizes and compositions. We wish to fit a probability model to these samples
23 to pool their information and combine their strengths, which will allow us to learn about
24 the social forces affecting the formation of their contacts (i.e., inference) and predict their
25 unobserved relations or other households in the population (i.e., prediction and simulation).
26 More generally, we seek to answer three questions:

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41 1. What are we estimating when we jointly fit a model to multiple networks?
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44 2. What do we need to assume to combine information from multiple networks?
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3 3. How do we test these assumptions?
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7 In Section 2, we begin to address Question 1 by describing the household contact
8 datasets and applying the principles of model-based survey sampling inference to make
9 explicit assumptions associated with inference from samples of networks that were previ-
10 ously left implicit. In Section 3, we review ERGM inference for missing data, describe
11 a parametrisation for jointly modelling an ensemble of networks, and discuss its inferen-
12 tial properties—and the requirements for valid inference, addressing Question 2. We then
13 consider in Section 4 the different ways in which these requirements may be violated and
14 combine missing data theory with classic generalised linear model (GLM) diagnostics to
15 produce tools for diagnosing lack of fit in the proposed framework, addressing Question
16 3; and in addition propose fast model selection techniques for ERGMs for ensembles of
17 networks. Finally, in Section 5, we apply these techniques to select and diagnose models
18 for our data, and report our substantive findings.
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27 Additional information can be found in the appendices, referenced throughout. Refer-
28 ences to appendix figures and tables are prefixed: e.g., Figure B5 is in Appendix B.
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32 **2 Data and Inferential Questions**
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35 **2.1 Study Designs**
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37 Two paper-based surveys (Hoang et al. 2021; Goeyvaerts et al. 2018) were conducted in
38 Belgium in 2010–2011, using similar survey instruments but differing in sampling design. In
39 both surveys, recruited by random-digit dialling, respondents (or their guardians) reported
40 their and their household members’ demographic information and recorded their contacts
41 over the course of one day, including the contacts’ ages and genders. Approximate duration
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| Female, 40 | 1 | | 1 | 1 | 1 |
| Male, 41 | 2 | 1 | | 1 | 1 |
| Male, 13 | 3 | 1 | 1 | | 0 |
| Female, 11 | 4 | 1 | 1 | 0 | |

(a) H dataset: Contacts among household members for household #11.

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|------------|----------|----------|----------|----------|----------|
| Male, 26 | 1 | | 0 | 0 | 1 |
| Female, 54 | 2 | 0 | | ? | ? |
| Male, 57 | 3 | 0 | ? | | ? |
| Female, 23 | 4 | 1 | ? | ? | |

(b) E dataset: Report of within-household contacts by ego #8.

Figure 1: Example observation units from the two datasets. Household composition is observed for both, but whereas every contact in the H households is observed, in the E households contacts not involving the ego are missing by design.

and frequency of each contact was also recorded, but here, we focus our attention on presence or absence of contacts involving skin-to-skin touching.

The first major difference between the surveys is that whereas in the *egocentric* (E) survey (Hoang et al. 2021), only one member in each household (the *ego*) was enrolled; in the other (Goeyvaerts et al. 2018), the whole *household* (H) was. This within-household sampling design impacts profoundly the information available about the households: while all contacts are known for the networks in the H dataset (Figure 1a), only contacts incident on the one respondent in the household are known for the E dataset (Figure 1b), though, importantly (Krivitsky and Morris 2017), enough information (discussed in Appendix A.1) was collected to identify these contacts uniquely within the household.

The second major difference is that the H survey was restricted to households with a child aged at most 12, whereas the E survey was not. For convenience, we define E_{12} to be the set of households in E with at least one such child—that potentially *could have been* in the H dataset—and $E_{\bar{12}}$ to be those without any, that could not. (Throughout, we will

use “presence of a child” and similar wording to refer to this specific criterion.)

More incidentally, the surveys differed slightly in their geographical localisation: both surveys included households in the Flemish (Dutch-speaking) areas of Belgium, but only the H survey included households from the (majority-French-speaking) Brussels-Capital region. Also, both surveys’ designs called for fine-grained stratification by age, but the surveyor was not able to adhere to it exactly; and in the H survey, households for which any members’ contacts were not successfully recorded were dropped altogether.

2.2 Descriptive Statistics

Dataset H comprises 318 households of size 2–7 for a total of 1266 members/respondents. Requiring less effort per household to collect, E comprises 1463 respondents whose households (ranging in size 2–8) have a total of 4780 members with 52% of the households’ relationship states observed.

In H , individuals in their mid 20s are underrepresented; E is more representative in this respect, except for omitting individuals living alone or in shared housing (disproportionately young adults and seniors). Both datasets’ households are on average gender-balanced, but E ’s respondents have a different age and gender distribution from its household members in general, with women aged 25–55 overrepresented and adolescents of both genders underrepresented. Most households (H : 71%, E : 75%) were observed on a weekday; 11% of the H households are in Brussels. E_{12} constitutes 35% of E .

With respect to social structure, the networks are, on average, dense (H : 93%, E_{12} : 90%, $E_{\overline{12}}$: 67%), with H ’s networks being more dense on average (vs. E_{12} : $P = 0.02$; vs. $E_{\overline{12}}$: < 0.001), and those of E_{12} more dense than those of $E_{\overline{12}}$ ($P < 0.001$). H ’s networks exhibit high triadic closure (global clustering coefficient $\frac{3 \times \# \text{ triangles}}{\# \text{2-stars}}$ averaging 92%); it

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3 cannot be estimated on the partially observed E dataset.
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5 More information can be found in Appendix A.2.
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2.3 Implications for Inference

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 E dataset is representative but consists of egocentric, incomplete networks; H dataset is very selective but of complete networks. E generalises better to the population of Flanders. H allows higher-order (e.g., triadic) effects to be estimated, and includes Brussels. Combining information from multiple surveys with different strengths is not uncommon, and a variety of approaches can be taken (Elliott et al. 2018).

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19 These data and the substantive problem are particularly amenable to a model-based
20 approach: the ERGM framework seamlessly integrates exogenous (e.g., age) and endogenous (e.g., friend-of-a-friend) effects likely to be relevant. The model-based approach is
21 also feasible: unlike some egocentric data (Krivitsky and Morris 2017) each respondent's
22 contacts in E could be identified uniquely within the household, so model-based inference
23 of Handcock and Gile (2010) is possible.

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30 For the purposes of prediction (e.g., given the distribution of household compositions,
31 how would an infection brought home from school spread?) we require the analysis to gen-
32 eralise to the population of households in Flanders and Brussels. The missing information
33 principle (Orchard and Woodbury 1972; Breckling et al. 1994) suggests that if the model
34 is accurate enough, it can be generalised to the population despite the heterogeneous and
35 biased sample. More precisely, we require that the sampling process be *ignorable* or, if
36 viewed as a missing data process, *missing at random*: the unobserved relationship states
37 must be conditionally independent of the selection process given the model and what is
38 observed (Rubin 1976; Handcock and Gile 2010). In our case, this also means that the
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3 model must render the dataset from which the network had come ignorable, which entails
4 accounting for network size, composition, geography, and other relevant effects.
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7 For the purposes of inference (e.g., do mothers have more contact with their children
8 than fathers?), we in addition require consistency and a sampling distribution for our
9 model parameters' estimators. Fortunately, we can treat these networks as an independent
10 sample: the probability that any member of any of the households in either sample has
11 interacted with a member of one of the other households in either sample is low, and such
12 an interaction is unlikely to affect within-household information in a systematic way in the
13 first place. However, there are further nuances, discussed in Section 4.1.
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16 20 21 22 23 24 25 26 27 28 29 30 31 32 33 34 35 36 37 38 39 40 3 Model Specification and Inference

41 In modelling an independent sample of networks, we represent two levels of effects: 1)
42 the exogenous and endogenous social forces affecting each network's relations; and 2) the
43 effects of a network's exogenous properties such as size, composition, and sampling stratum
44 membership on those social forces. For example, does the presence of a child (a network
45 composition property) affect the contacts between adult men and women in the household
46 (an exogenous relation effect)? Is triadic closure (an endogenous relation effect) stronger
47 or weaker in due to household size (a network property)? We discuss these levels in turn.

48 49 50 51 52 53 54 55 56 57 58 59 60 3.1 Exponential-Family Random Graph Models for Completely and Partially Observed Networks

We refer the reader to the text book by Lusher et al. (2012) and a review by Schweinberger et al. (2020) for detailed discussions of ERGMs' formulation, interpretation, and inference. For our purposes, let $N = \{1, 2, \dots, n\}$, for $n \geq 2$, be the set of actors whose relations

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are of interest. Since physical contacts are inherently two-way, we will focus on undirected graphs: the set of potential relations of interest $\mathbb{Y} \subseteq \{\{i, j\} \in N \times N : i \neq j\}$ is a subset of the set of *dyads*—distinct unordered pairs of actors. Then, the set of possible graphs of interest $\mathcal{Y} \subseteq 2^{\mathbb{Y}}$ (the set of all possible subsets of \mathbb{Y}). We use $\mathbf{y} \in \mathcal{Y}$ for the graph data structure, and $y_{i,j} \in \{0, 1\}$ as indicator of i and j being connected in \mathbf{y} (with $y_{i,j} \equiv y_{j,i}$).

An ERGM is specified by its sample space \mathcal{Y} , a collection $\mathbf{x} \in \mathcal{X}$ of quantitative and categorical exogenous attributes of actors (e.g., age and gender) or dyads (e.g., distance) used as predictors, and a (sufficient by construction) statistic $\mathbf{g} : \mathcal{Y} \times \mathcal{X} \mapsto \mathbb{R}^p$. This statistic operationalises the hypothesised social forces affecting the network's relations. With free model parameters $\boldsymbol{\theta} \in \mathbb{R}^p$, a random graph $\mathbf{Y} \sim \text{ERGM}_{\mathcal{Y}, \mathbf{x}, \mathbf{g}}(\boldsymbol{\theta})$ if

$$\Pr_{\mathcal{Y}, \mathbf{x}, \mathbf{g}}(\mathbf{Y} = \mathbf{y}; \boldsymbol{\theta}) = \exp\{\boldsymbol{\theta} \cdot \mathbf{g}(\mathbf{y}, \mathbf{x})\} / \kappa_{\mathcal{Y}, \mathbf{x}, \mathbf{g}}(\boldsymbol{\theta}), \quad \mathbf{y} \in \mathcal{Y},$$

where $\kappa_{\mathcal{Y}, \mathbf{x}, \mathbf{g}}(\boldsymbol{\theta}) = \sum_{\mathbf{y}' \in \mathcal{Y}} \exp\{\boldsymbol{\theta} \cdot \mathbf{g}(\mathbf{y}', \mathbf{x})\}$ is the normalising constant. For the sake of brevity, we will omit specification elements “ \mathcal{Y} ”, “ \mathbf{x} ”, “ \mathbf{g} ”, and “ $\boldsymbol{\theta}$ ” where unambiguous.

Network statistics that we will use in this work include the edge count $|\mathbf{y}|$ to model propensity to have relations; edge counts within or between exogenous groups of actors to model homophily and other types of mixing; and endogenous effects: count of 2-stars $g_{2\text{-star}}(\mathbf{y}) = \sum_{i=1}^n \binom{|y_i|}{2}$ (where $|y_i|$ is the degree—number of ties incident on actor i) to model degree heterogeneity and count of triangles $g_{\text{triangles}}(\mathbf{y}) = \sum_{1 \leq i < j < k \leq n} y_{i,j} y_{j,k} y_{k,i}$ to model triadic closure. Ordinarily, we would not use the latter two because of their well-known tendency to induce badly behaved “degenerate” models in large networks and instead use less degeneracy-prone effects (Schweinberger et al. 2020, Sec. 3.1 for context and history). However, this application’s networks are very small and thus largely unaffected, so we use them for their simplicity.

With respect to this ERGM, we may take expectations $\mathbb{E}(\cdot)$ and variances $\text{Var}(\cdot)$, in-

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3 cluding those of the sufficient statistic: let $\boldsymbol{\mu}(\boldsymbol{\theta}) \stackrel{\text{def}}{=} \mathbb{E}\{\mathbf{g}(\mathbf{Y})\}$ and $\boldsymbol{\Sigma}(\boldsymbol{\theta}) \stackrel{\text{def}}{=} \text{Var}\{\mathbf{g}(\mathbf{Y})\}$.
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6 Given an observed network \mathbf{y} , an ERGM is typically estimated by maximum likelihood,
7 with $l(\boldsymbol{\theta}) \stackrel{\text{def}}{=} \log \Pr(\mathbf{Y} = \mathbf{y}; \boldsymbol{\theta})$ and Fisher information $\mathcal{I}(\boldsymbol{\theta}) = -l''(\boldsymbol{\theta}) = \boldsymbol{\Sigma}(\boldsymbol{\theta})$. For most
8 interesting models, the normalising constant $\kappa(\boldsymbol{\theta})$ is intractable, and estimation requires
9 MCMC-based techniques (Schweinberger et al. 2020, Sec. 1.2.1 for references).
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12 If the network is incompletely observed, likelihood estimation proceeds as follows (Hand-
13 cock and Gile 2010): to the unobserved true population network \mathbf{y} , an observation process
14 $\text{obs}(\cdot)$ (deterministic or conditioned-on) is applied, producing the observed data structure
15 $\mathbf{y}^{\text{obs}} \stackrel{\text{def}}{=} \text{obs}(\mathbf{y})$, with $y_{i,j}^{\text{obs}} \in \{0, 1, \text{NA}\}$ representing observed-absent, observed-present, and
16 unobserved potential relations, respectively. For the E dataset, $\text{obs}(\mathbf{y})$ is such that
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$$y_{i,j}^{\text{obs}} \equiv \begin{cases} y_{i,j} & \text{if } i = 1 \vee j = 1, \\ \text{NA} & \text{otherwise.} \end{cases}$$

19 Let $\mathcal{Y}(\mathbf{y}^{\text{obs}}) \stackrel{\text{def}}{=} \{\mathbf{y}' \in \mathcal{Y} : \text{obs}(\mathbf{y}') = \mathbf{y}^{\text{obs}}\}$: all complete networks that could have
20 produced \mathbf{y}^{obs} or, equivalently, all possible imputations of unobserved relations of \mathbf{y}^{obs} ; and
21 define conditional expectation
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$$\boldsymbol{\mu}(\boldsymbol{\theta} \mid \mathbf{y}^{\text{obs}}) \stackrel{\text{def}}{=} \mathbb{E}\{\mathbf{g}(\mathbf{Y}) \mid \mathbf{Y} \in \mathcal{Y}(\mathbf{y}^{\text{obs}})\}$$

24 and, analogously, conditional covariance $\boldsymbol{\Sigma}(\boldsymbol{\theta} \mid \mathbf{y}^{\text{obs}})$. Then, under noninformative sampling
25 and/or missingness at random, the face-value log-likelihood is $l(\boldsymbol{\theta}) = \log \sum_{\mathbf{Y} \in \mathcal{Y}(\mathbf{y}^{\text{obs}})} \Pr_g(\mathbf{Y} =$
26 $\mathbf{y}; \boldsymbol{\theta})$ and *observed* information is (Orchard and Woodbury 1972; Sundberg 1974; Handcock
27 and Gile 2010)
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$$\mathcal{I}^{\text{obs}}(\boldsymbol{\theta}) = \boldsymbol{\Sigma}(\boldsymbol{\theta}) - \boldsymbol{\Sigma}(\boldsymbol{\theta} \mid \mathbf{y}^{\text{obs}}). \quad (1)$$

Unlike the completely observed case, (1) is not the Fisher information, because it depends on the data \mathbf{y}^{obs} . The Fisher information, then, also takes the expectation over the possible values of \mathbf{y}^{obs} under the model:

$$\mathcal{I}(\boldsymbol{\theta}) = \boldsymbol{\Sigma}(\boldsymbol{\theta}) - \mathbb{E}_{\mathbf{Y}}[\boldsymbol{\Sigma}\{\boldsymbol{\theta} \mid \text{obs}(\mathbf{Y})\}] \quad (2a)$$

$$= \text{Var}_{\mathbf{Y}}[\boldsymbol{\mu}\{\boldsymbol{\theta} \mid \text{obs}(\mathbf{Y})\}]. \quad (2b)$$

3.2 Multivariate Linear Models for ERGM Parameters

Now, consider a sample of networks indexed $s = 1, \dots, S$, that we wish to model jointly, incorporating network-level effects. There is no unique way to do so; the following approach—drawing on multivariate linear regression models and on seemingly unrelated regression models—has the advantages of familiarity, interpretability, and good inferential properties.

Let \mathbf{z}_s be a row q -vector of network-level covariates of interest, and let $\boldsymbol{\beta}$ a $q \times p$ parameter matrix. Set network-level parameters $\boldsymbol{\theta}_s \stackrel{\text{def}}{=} (\mathbf{z}_s \boldsymbol{\beta})^\top$. Then, jointly,

$$(\mathbf{Y}_1, \mathbf{Y}_2, \dots, \mathbf{Y}_S) \sim \text{ERGM}_{\mathbf{z}, \vec{\mathcal{Y}}, \vec{\mathbf{x}}, \vec{\boldsymbol{g}}}(\boldsymbol{\beta})$$

if $\mathbf{Y}_s \stackrel{\text{ind}}{\sim} \text{ERGM}_{\mathcal{Y}_s, \mathbf{x}_s, \mathbf{g}_s}(\boldsymbol{\theta}_s)$. Thus, the components of the network model specification (sample space, sufficient statistic, and any covariates—respectively, \mathcal{Y}_s , \mathbf{g}_s , and \mathbf{x}_s , collected into S -vectors $\vec{\mathcal{Y}}$, $\vec{\mathbf{g}}$, $\vec{\mathbf{x}}$) may vary arbitrarily between networks, but its parameters are parametrised in turn, with elements of $\boldsymbol{\beta}$ determining, in a manner analogous to the linear predictor of a GLM, how network-level covariates affect the ERGM parameters.

Although here we treat q and p as the same for all networks, we show in Appendix D that there is no loss of generality as long as selected elements of $\boldsymbol{\beta}$ can be fixed at 0. Also, this framework can be viewed as a special case (for $\boldsymbol{\Sigma} = \mathbf{0}$) of the model of Slaughter and Koehly (2016), whose prior can be expressed $\boldsymbol{\theta}_s \stackrel{\text{i.i.d.}}{\sim} \text{MVN}\{(\mathbf{z}_s \boldsymbol{\beta})^\top, \boldsymbol{\Sigma}\}$.

Example: Network size effects For a given type of social setting (e.g., classroom, household), bigger networks will typically have lower density ($|\mathbf{y}|/\{n(n - 1)/2\}$ for undirected networks), with mean degree ($|\mathbf{y}|/\{n/2\}$) being close to invariant to size. This includes our data (e.g., Figure A2); but the “default” ERGM behaviour is to preserve network density (Krivitsky et al. 2011) so that mean degree grows in proportion to n . Krivitsky et al. proposed to adjust this behaviour by an offset term of the form $-\log(n)|\mathbf{y}|$: other things being equal, the odds of a relation in a network of size n would be scaled by n^{-1} , stabilising the mean degree. But, their result is asymptotic, reliant on sparsity, and only adjusts lower-order properties (density, mixing, and, fortuitously, degree distribution).

Butts and Almquist (2015) proposed that the effect of network size on density could be estimated from a sample of networks, with $\log(n)$ above multiplied by a free parameter γ , rather than by -1 , making the mean degree approximately proportional to $n^{\gamma+1}$. Here, we can accomplish this by setting $z_{s,k} = \log(n_s)$ and $g_{s,l}(\mathbf{y}_s) = |\mathbf{y}_s|$ for some indices k and l ; then $\gamma \equiv \beta_{k,l}$. Considering that our networks are small and dense, we can model a nonlinear network size effect by adding a quadratic covariate $z_{s,k+1} = \log^2(n_s)$, with $\beta_{k+1,l}$ then becoming its coefficient. (The resulting design matrix is given in Appendix D.) Alternatively, orthogonal polynomial contrasts, a spline, or dummy variables could be used.

3.3 Inference

We now describe this framework’s inferential properties. Let I_d be an identity matrix of dimension d ; let \otimes be the Kronecker product; and let $Z_s \stackrel{\text{def}}{=} I_p \otimes \mathbf{z}_s$. Then, we can reexpress $\theta_s = \mathbf{z}_s^\top \boldsymbol{\beta}^\top \equiv Z_s \text{vec}(\boldsymbol{\beta})$, for an exponential family with a complete-data likelihood

$$\mathcal{L}(\boldsymbol{\beta}) = \exp \left\{ \text{vec}(\boldsymbol{\beta}) \cdot \sum_{s=1}^S Z_s^\top \mathbf{g}_s(\mathbf{y}_s) \right\} / \prod_{s=1}^S \kappa_{\mathbf{y}_s, \mathbf{x}_s, \mathbf{g}_s} \{(\mathbf{z}_s \boldsymbol{\beta})^\top\}.$$

Let $\boldsymbol{\mu}_s(\boldsymbol{\beta} \mid \mathbf{y}_s^{\text{obs}}) \stackrel{\text{def}}{=} \mathbb{E}\{\mathbf{g}_s(\mathbf{Y}_s) \mid \mathbf{Y}_s \in \mathcal{Y}(\mathbf{y}_s^{\text{obs}}); (\mathbf{z}_s\boldsymbol{\beta})^\top\}$ and analogously for $\boldsymbol{\mu}_s(\boldsymbol{\beta})$, $\boldsymbol{\Sigma}_s(\boldsymbol{\beta} \mid \mathbf{y}_s^{\text{obs}})$, and $\boldsymbol{\Sigma}_s(\boldsymbol{\beta})$. Then, its partially observed Fisher information is

$$\mathcal{I}(\text{vec } \boldsymbol{\beta}) = \sum_{s=1}^S Z_s^\top \text{Var}_{\mathbf{Y}_s}[\boldsymbol{\mu}\{\boldsymbol{\beta} \mid \text{obs}(\mathbf{Y}_s)\}] Z_s.$$

For those networks in the sample that are completely observed, $\boldsymbol{\mu}_s(\boldsymbol{\beta} \mid \mathbf{y}_s^{\text{obs}}) \equiv \mathbf{g}_s(\mathbf{y}_s)$ and $\text{Var}_{\mathbf{Y}_s}[\boldsymbol{\mu}\{\boldsymbol{\beta} \mid \text{obs}(\mathbf{Y}_s)\}] \equiv \boldsymbol{\Sigma}_s(\boldsymbol{\beta})$. Since this is an independent sample of networks, consistency and asymptotic normality of $\hat{\boldsymbol{\beta}}$ in S can be shown (Sundberg 1974), provided the sampling process is noninformative and $\mathcal{I}(\text{vec } \boldsymbol{\beta})$ is nonsingular asymptotically, which requires the model to be identifiable.

4 Diagnosing Multivariate Linear ERGMs

Whether or not the estimation can be consistent and the inference be generalised to a broader population of households depends on the model being identifiable given available data and on its goodness-of-fit—both of which must take into account that at least some of the networks in the sample are partially observed. Here, we discuss likely causes and diagnostics for nonidentifiability, develop a generalisation to residual diagnostics for partially observed networks, and consider a variety of ways in which a model may fit the data poorly and how to diagnose this.

4.1 Causes and Diagnostics for Nonidentifiability

The key condition for consistency by Sundberg (1974) is that $\mathcal{I}(\text{vec } \boldsymbol{\beta})$ must be nonsingular. Substantively, there is a number of reasons this condition might not be satisfied.

Nonidentifiable model specification A model may erroneously contain a relationship type or other network feature that is not possible in any potentially sampled network.

1
2
3 For a trivial example, counting the number of connections between adults and children
4 is not meaningful in a survey of households without children, nor is counting 2-stars in
5 households of size 2. Similarly, given the large selection of potential network features, and
6 a large selection of potential network-level covariates, it is easy to inadvertently specify a
7 model that is not full-rank. An example of this is network size as a covariate in a sampling
8 process that observes networks of only one distinct size; or a quadratic network size effect
9 if only two distinct sizes are observed. Then the minuend of (2a) (i.e., $\Sigma(\beta)$), respectively,
10 has zeros on the diagonal or linear dependence, and the model is not identified even under
11 complete observation.

12 This form of nonidentifiability can usually be detected during estimation by examining
13 the variance–covariance matrices of simulated sufficient statistics.
14

15 **Network observation process not informative of the model** If the sampling process
16 entails partially observed networks, some combinations of observation process and model
17 specification may make an otherwise identifiable model nonidentifiable.
18

19 **Example 1** Consider an undirected network with actors partitioned into groups A and
20 B . A 3-parameter model whose statistic comprises the counts of all edges, of edges within
21 group A , and of edges between members of A and members of B is identifiable, and its $\Sigma(\theta)$
22 is full-rank. But, if only relationships incident on members of group A ($A-A$ and $A-B$) are
23 observed, while $B-B$ relations are missing by design, then the elements of $\mu(\theta | \mathbf{y}^{\text{obs}})$ are
24 affinely dependent, making $\mathcal{I}(\theta)$ singular. (See Appendix B.1.)
25

26 **Example 2** For an i.i.d. sample of S 3-node undirected networks, it is possible to
27 estimate a 3-parameter model with edges, 2-stars, and triangles sufficient statistic; but not
28 if any one of the 3 possible relations is unobserved in each network: a direct enumeration
29 of the sample space in Appendix B.2 shows that (2b) is singular.
30

This form of nonidentifiability is more insidious. Its main symptom is that intermediate estimates of the difference in (2a) are not positive definite; but the algorithm of Handcock and Gile (2010) obtains this difference by subtracting the two simulated variance–covariance matrices, and for data with high missingness fraction and models with many parameters in particular, a false positive can result from Monte Carlo error.

4.2 Residual Diagnostics for Partially Observed Networks

Traditional model diagnostics—whether for linear regression or for ERGMs (Hunter et al. 2008a)—work by comparing the observed data points to those predicted by the fitted model. The approach of Hunter et al. in particular is to simulate networks from the fitted model, and compare the statistics of the simulated networks—particularly those statistics *not* in the original model—to their observed values. If the observed value falls outside of the range of the simulated, lack of fit is indicated. However, most of the networks in E are partially observed, and this means that there is no “true” observed value for a network feature. We therefore derive equivalent diagnostics for partially observed networks.

For notational convenience, let $\vec{y} = [\mathbf{y}_s]_{s=1}^S$ refer to a vector of completely observed networks. Consider a real-valued function $t(\vec{y})$ that evaluates a particular network feature of interest, either cumulatively over all of the networks or for a specific network. Analogously to $\mu(\cdot)$ and $\Sigma(\cdot)$ in Section 3.1, let $\tau(\beta) \stackrel{\text{def}}{=} \mathbb{E}\{t(\vec{Y}); \beta\}$ and $\Psi(\beta) \stackrel{\text{def}}{=} \text{Var}\{t(\vec{Y}); \beta\}$, and likewise for the conditional expectations.

We can form a standardised (Pearson) residual for $t(\vec{y})$ by evaluating

$$R_t = \{t(\vec{y}) - \tau(\hat{\beta})\} / \sqrt{\Psi(\hat{\beta})}, \quad (3a)$$

with the expectation and the variance estimated by simulating from the fitted model. Under the true model, this residual would, by construction, have mean 0 and variance close to 1;

1
2
3 this also facilitates outlier detection.
4

5 If the networks are not completely observed, $t(\vec{y})$ cannot be evaluated directly, it is
6 natural to replace it with its empirical best predictor (Hunter et al. 2008b; Stewart et
7 al. 2019; Krivitsky et al. 2023),
8

9

$$10 \quad \tau(\hat{\beta} | \vec{y}^{\text{obs}}) \stackrel{\text{def}}{=} \mathbb{E}\{t(\vec{Y}) | \vec{Y} \in \mathcal{Y}(\vec{y}^{\text{obs}})\},$$

11

12
13 where \vec{y}^{obs} is defined analogously to \vec{y} . Then,
14

15

$$16 \quad R_t = \{\tau(\hat{\beta} | \vec{y}^{\text{obs}}) - \tau(\hat{\beta})\} / \sqrt{\text{Var}_{\vec{Y}}[\tau(\hat{\beta} | \text{obs}(\vec{Y}))]}, \quad (3b)$$

17

18 Estimating the variance in the divisor in (3b) is not trivial. We discuss it in Appendix C.1.
19

20 4.3 Causes and Diagnostics for Lack-of-Fit

21 **Within-network** It may be the case that the within-network model fits poorly. Network
22 statistics used for diagnostics by Hunter et al. (2008a) include the full degree distribution,
23 counts of shared partners (i.e., for a given pair of connected actors, how many common
24 connections do they have?), and the distribution of geodesic distances. All of these can be
25 used as $t(\cdot)$, but it may be impractical for two reasons. Firstly, family networks are rela-
26 tively small and very dense. This makes the statistics typically used less than informative.
27 Secondly, the sheer number of networks in the dataset means that diagnosing each network
28 individually is infeasible, but, at the same time, pooling their within-network diagnostics
29 is likely to wash out any effects because of their heterogeneity.
30

31 Nonetheless, even if a statistic is suboptimal and difficult to interpret, for a model that
32 fits well, R_t will still have mean 0 and variance close to 1.
33

34 **Between-network** It may be the case that the model for the network-level parameters
35 (θ_s) as a function of global parameters (β) fits poorly: in particular, it may fail to account
36 for heterogeneity across networks.
37

for network size and composition effects. At network level, the model has a form similar to that of a GLM. We can thus use the developments of Section 4.2 directly to make familiar diagnostic plots: for some statistic $t_s(\vec{y}) \stackrel{\text{def}}{=} t(\mathbf{y}_s)$ (e.g., density), we can plot residuals R_{t_s} for $s = 1, \dots, S$ against their respective $\tau_s(\hat{\beta}) \stackrel{\text{def}}{=} \mathbb{E}\{t_s(\vec{Y})\}$ (the fitted values) or against a candidate predictor $z_{s,\text{new}}$. Or, we can use $\sqrt{|R_{t_s}|}$ instead for a scale–location plot, analogously to the standard diagnostic plots in R (2023).

We can also use residuals to test lack-of-fit hypotheses and assess potential explanatory power of $z_{s,\text{new}}$ —without the computationally costly ERGM fitting—by regressing $t_s(\vec{y}) - \tau_s(\hat{\beta})$ on $z_{s,\text{new}}$, weighted by their inverse-variance ($\text{Var}^{-1}\{t_s(\vec{Y})\}$). Individual networks are independent, so the residuals should be nearly independent as well.

Between-dataset If we wish for the fitted model to generalise and render the sampling designs ignorable, the model must account for differences in datasets without incorporating dataset effects directly. This can be done via a hypothesis test, such as a simulation score test, along the lines of that described by Krivitsky (2012) in the context of valued ERGMs, by testing the significance of an explicit dataset effect without refitting the model. Details are given in Appendix C.2.

Non-systematic heterogeneity Lastly, even if there is no systematic bias in the model, there may be between-network heterogeneity due to unobserved factors. The above-described Pearson residuals incidentally provide us with a way to tell whether there is any heterogeneity left to explain: if there is none, R_{t_s} in (3) will, by construction, have mean 0 and variance around 1.

5 Application

We now return to the data we had introduced in Section 2, discuss model specification, and report model diagnostics and results. As one reads this section, it may be helpful to refer to Appendix D for how these effects are represented in the framework described.

We have implemented the methodology described in an extension to the `ergm` package (Hunter et al. 2008b; Krivitsky et al. 2023) for the R (2023) statistical environment. To make this methodology accessible to a broad audience, we have published our implementation in an R package, `ergm.multi`. Materials needed to reproduce the analysis are included in the supplementary file, and the most recent versions of the packages can be found on the Comprehensive R Archive Network (R 2023) or the Statnet Project software repository (<https://github.com/statnet/>).

5.1 Initial Model

A model used to join these two datasets must be substantively meaningful and interpretable. It must account for within-network conditional dependence among the relations. It must make the network size, composition, and dataset effects ignorable to enable generalisable inference. And, it must do so without requiring more information than is available in the data. We therefore dedicate a great deal of attention to formulating and justifying each of the model's elements.

Here, we develop the initial model, *Model 0*, which we will then refine using diagnostics.

Household roles Our data do not record family relations (e.g., who is married to whom and who is whose child), so we must infer household roles from age and gender. In doing so, there is a tension between interpretability and accuracy: family roles are most conveniently modelled with discrete age categories; but outside of a few critical ages defined exogenously (e.g., school attendance, legal adulthood, and retirement), age effects are likely to be con-

tinuous, best modelled semiparametrically (e.g., with splines). Our compromise is to use relatively fine-grained edge categories.

A first classification was done according to age: *young child* (under 6), *preadolescent* (6–12), *adolescent* (13–18), *young adult* (19–24), *older adult* (25–60), and *senior* (over 60). (The age cut at 12 was chosen specifically to account for the design boundary.) In order to investigate gender-specific interactions (Goevaerts et al. 2018) we subdivided older adults into *older female adults* and *older male adults*. A total of 7 categories results.

We then modelled mixing by counting the contacts between pairs of these categories—essentially cells of a symmetric 7×7 contingency table. Our data about some of these cells are limited, both because some age groups are underrepresented for design reasons discussed above and in Section 2.2, and because some age combinations, such as young children and seniors, are rarely found together in a household (Figure A3 for pairwise counts). Thus, guided by substantive interest, sample size, and design effects, some of the cells were combined for modelling. For example, in modelling contacts with seniors, we combine young children with preadolescents and adolescents with young adults because of their very small sample sizes; but we do not combine all four cells because the combined cell would then cross the age-12 boundary. Similarly, despite a small sample size, young adults with young children were retained as a separate count, because their chances of being parent and child are relatively high. The final parametrisation is visualised in Figure 4.

Endogenous effects To model actor heterogeneity and triadic closure, we use 2-star and triangle counts, defined in Section 3.1. An additional caveat is that the E dataset, by virtue of only containing relations incident on one individual per household, does not contain information about triadic closure. (See Section 4.1 Example 2 and Appendix B.2.) We thus assume that net of all other effects, the effect of triadic closure on a household

of a given size that does not have a child is the same as the effect of triadic closure on a household of that size that does have a child. It is not possible to test this assumption with the available data.

Network size effects The effects of network size on our networks is not trivial: for example, in the analysis of the H dataset by Goeyvaerts et al. (2018), three different density and two different triadic parameters were used, depending on household size. In *Model 0*, we use the polynomial effects of $\log n_s$ described in Section 3.2 on edge, 2-star, and triangle counts. This also further guards against ERGM degeneracy, by allowing 2-star and triangle coefficients to decrease with network size.

Other network-level effects Some of the surveys were conducted on a weekend and others on a weekday (Table A1). Past literature (Goeyvaerts et al. 2018, for example) suggests that contact patterns may differ depending on the day.

Contact patterns may differ systematically between families that live in detached housing and families that live in apartments. This potential effect has received limited attention in the literature to date. Our data do not include housing type but do include postal codes. The population densities in those postal codes can then be used as a proxy for housing type. We use this potential predictor to illustrate the technique proposed in Section 4.3 of regressing the network-level residuals on potential network-level predictors. Alternatively, we might ask whether or not the post code belongs to any of Belgium's larger cities.

These properties may be predictive of edge, 2-star, or triangle counts. For the sake of parsimony, *Model 0* initially incorporates only weekend effect on density, and diagnostics are used to suggest additional effects.

1
2
3 **Design effects** Last but not least, if we wish to generalise our inference to the popula-
4 tion of households, our model must make any design effects ignorable. The substantively
5 motivated effects described above already control for some of those. For example, recall
6 that households in H were omitted if there was nonresponse from even a single member.
7 To the extent that the nonresponse rate is a function of household size (i.e., the bigger the
8 household, the more likely there is at least one nonrespondent), a model that accurately
9 controls for network size will reduce the informativeness of this nonresponse. Similarly,
10 although both surveys' selection was strongly affected by household members' ages, partic-
11 ularly children, granular modelling of age mixing effects—particularly for young children
12 and preadolescents—already reduces this design effect's informativeness.
13
14

15 It is, however, also possible that interactions among adult household members, and
16 other structural features, are affected by a child's presence—something that Goeyvaerts
17 et al.'s data could not be used to test. We can adjust for this by including the presence of
18 a child in a household as a network-level covariate for density overall, for the endogenous
19 effects, or for mixing. Given the wide range of possibilities, we do not incorporate any such
20 effects into *Model 0*, instead using residual diagnostics on it to select them.
21
22

23 To account for only the H dataset containing Brussels households, we add an indicator
24 of a Brussels post code as a network-level covariate for density. This completes *Model 0*.
25
26

36 5.2 Diagnostics 37

38 We now apply the techniques from Section 4 to the proposed models. To validate our diag-
39 nostic techniques, we also fit a number of reduced models: in Appendix E, we demonstrate
40 how our techniques can identify their deficiencies. In the following, recall our partitioning
41 of E into E_{12} (at least one child at most 12, potentially in H) and $E_{\bar{12}}$ (no such children).
42
43

1
2
3 **Effects of a child in a household** As discussed, we use diagnostics for *Model 0* to
4 select which network features depend on the presence of a child: we calculate the Pearson
5 residuals for counts of edges, 2-stars, triangles, and every pair of actor categories (excluding
6 young children, preadolescents, and seniors), breaking them down by subset H , E_{12} , and
7 $E_{\overline{12}}$. Then, category pairs with extreme residuals that have the same sign for H and E_{12}
8 but the opposite sign for $E_{\overline{12}}$ may suggest a relevant child effect.
9
10
11
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13

14 Three mixing cells have residuals with this sign pattern (Table F30): contacts between
15 older female and male adults (H : 2.7, E_{12} : 1.7, $E_{\overline{12}}$: -1.9), two male adults (-1.1, -1.7,
16 0.6), and two female adults (0.8, 0.1, -0.2). The latter two are likely spurious and cannot
17 be used in any case due to small sample size (per Appendix A.3).
18
19
20

21 Adding the effect of absence of a child on the coefficient for contacts between older
22 female and male adults yields *Model 1*; none of its global or mixing residuals (Table F37)
23 exceed 2 in magnitude. We focus on *Model 1* going forward, but, for illustrative purposes,
24 we also report *Model 1a*, with the absence-of-child effect on edge count instead.
25
26
27

28 **Additional substantive models** As proposed in Section 5.1, we regressed (per Sec-
29 tion 4.3) edge, 2-star, and triangle count residuals of *Model 1* on a number of candidate
30 predictors, with full results given in Table F34. The linear effect of log-population-density
31 is the most promising ($P = 0.041$), yielding *Model 2*, and, for illustrative purposes, we also
32 report *Model 2a*, adding the effect of the household being in a major city ($P = 0.27$) in-
33 stead. Specifications for all models are summarised in Table F1, and their complete results
34 and diagnostics are provided in Appendix F.
35
36
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41 **Unaccounted-for between-dataset differences** Selected residual plots are provided
42 in Figure 2. We also provide smoothing curves for each subset individually: these curves
43 diverging would indicate that the model had failed to account for some systematic difference
44
45
46
47

1
2
3 between the datasets. Panel (d) (triangle counts) excludes E 's networks, because those
4 contain almost no triadic information.
5

6 The network residuals for both edges and triangles (Panels (a)–(d)) are skewed down-
7 ward and exhibit a striped pattern. This is to be expected regardless of model fit: the un-
8 derlying network statistics are small counts close to their exogenous upper bounds. There
9 do not appear to be any clear patterns beyond that, and the edge residuals for H , E_{12} , and
10 $E_{\bar{12}}$ coincide on average (Panel (a)). This suggests that the model fuses the two datasets
11 well. The scales of the residuals (Panel (b)) do not exhibit unambiguous patterns either,
12 except for the residuals of $E_{\bar{12}}$ having consistently higher variances than others—whereas
13 the more similar H and E_{12} networks have similar residual variances.
14
15

16 The dataset hypothesis tests described above and in Appendix C.2 yield P -values 0.084,
17 0.14, and 0.21 for the edge, the 2-star, and their omnibus test, respectively (with de-
18 tails given in Table F35). Thus, at the conventional significance level, we do not detect
19 unaccounted-for differences between datasets for these features. (In contrast, the respective
20 P -values for *Model 0* (Table F28) are 0.021, 0.062, and 0.064, which is more suggestive.)
21
22

23 **Outliers** Our residual plots reveal some households inconsistent with typical behaviour.
24 For example, the E households #947, #730, and #554 highlighted in Panels (a) and (c)
25 are families of three or four with two older adults (male and female) and a young child (the
26 “respondent”), but no within-household contacts with the child on the day of the survey.
27
28

29 **Network size effects** Edge residuals against the network size are shown in Panel (c).
30 A model that fails to account for network size would display a linear or curved pattern in
31 the residuals. We see no evidence of such a pattern.
32
33

34 We confirm this with lack-of-fit tests, regressing edge, 2-star, and triangle count residuals
35 on network size treated as categorical (i.e., a dummy variable for each size but one). Lack
36
37

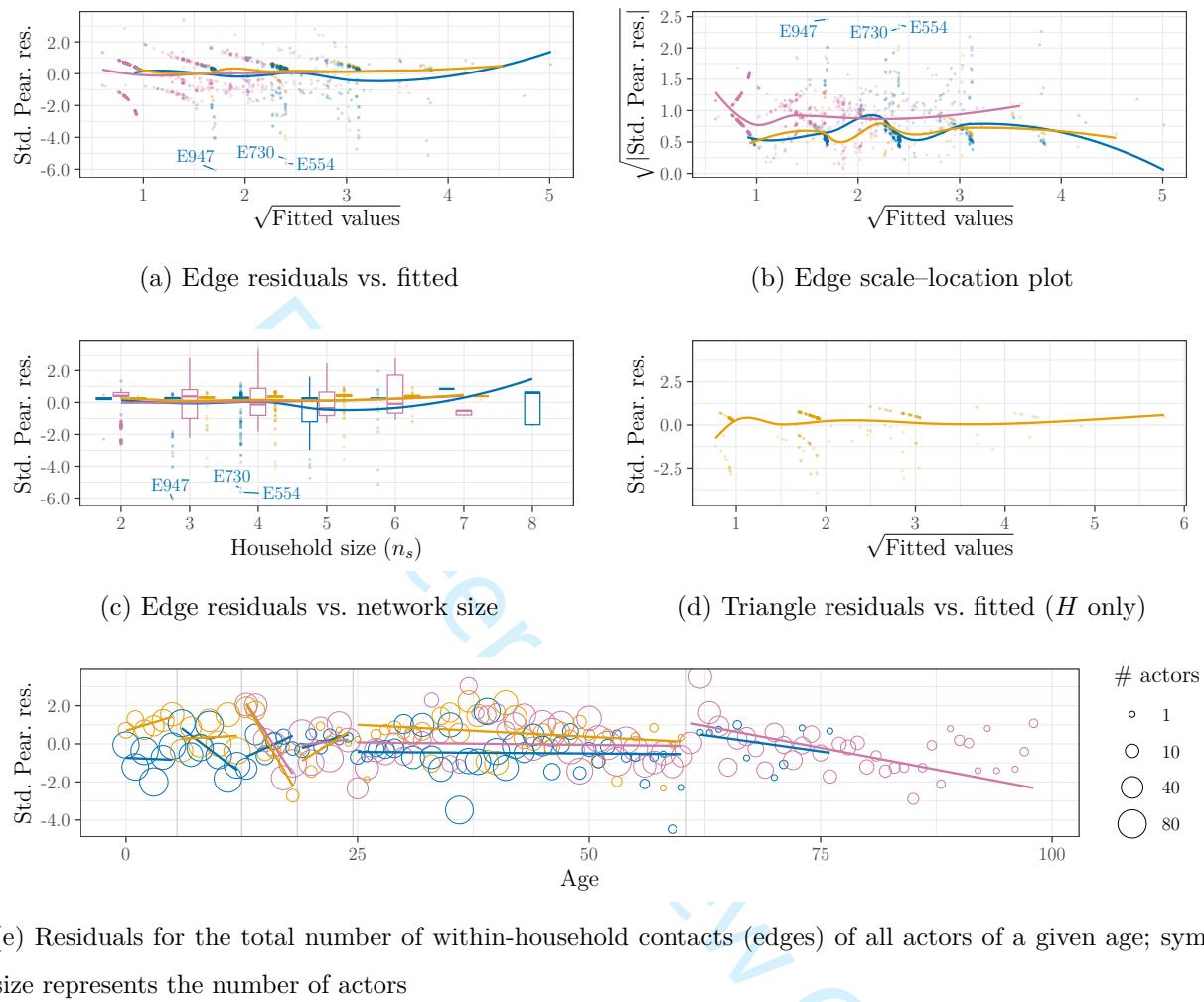


Figure 2: Selected Pearson residual plots of network statistics for *Model 1*, modelled after the diagnostic plots produced by R's (2023) built-in **stats** package for GLMs. Outliers are identified by their dataset and index within dataset. (Subsets: H E_{12} $E_{\bar{12}}$)

of fit would be indicated by statistical significance of these regressions; we do not find it for any of the three network statistics (weighted ANOVA omnibus P -vals. 0.22, 0.19, and 0.24, respectively, full results in Table F33).

Non-systematic heterogeneity The standard deviations of Pearson residuals for edges, 2-stars, and triangles are 1.00, 0.99, and 0.98, respectively, all close to 1 as hoped. (Breakdown by data subsets in Table F36.)

Continuous age effects Panel 2e shows the Pearson residuals of the total number of within-household contacts of individuals of each age. We see some indications that discretising ages into categories has an impact. For example, a senior's propensity to interact appears to drop off as they age, which the cutoff at 60 does not capture. The H household density tends to be slightly underpredicted relative to comparable households in E_{12} , though the differences do not appear to be particularly strong or consistent.

5.3 Results

Model comparison Table 1 gives the parameter estimates for *Model 1* and *Model 2*, suggested by our residual diagnostics. (Those for *Model 1a* and *Model 2a* are in Tables F38 and F52.) AIC (Table F2) is indifferent between *Model 1* ($AIC = 3697.1$) and *Model 2* (3696.9) within margin of MCMC error and prefers them over *Model 2a* (3698.2) and *Model 1a* (3714.3), the latter only slightly preferred over *Model 0* (3715.5). This is as predicted by the residual analyses discussed in Section 5.2.

A test of population density effect in *Model 2* is not significant at conventional level ($\hat{\beta} = 0.04$, $SE = 0.031$, $P = 0.18$), so we do not find evidence of housing type having an effect—or regional population density is a poor proxy; we leave these questions for future work, except to suggest that type of housing should be considered for future data collection.

Table 1: Parameter estimates for *Model 1* and *Model 2*.

| Relationship Effect × Network-Level Effect | Coefficient (S.E.) | |
|---|--------------------|------------------|
| | <i>Model 1</i> | <i>Model 2</i> |
| edges × log(n_s) | -14.35 (2.89)*** | -13.86 (2.97)*** |
| × log ² (n_s) | 5.72 (1.29)*** | 5.51 (1.33)*** |
| if Brussels post code | 0.08 (0.19) | -0.03 (0.20) |
| × log(pop. dens. in post code) | | 0.04 (0.03) |
| if on weekend | 0.14 (0.06)* | 0.13 (0.05)* |
| 2-stars | 1.98 (0.79)* | 1.12 (0.82) |
| × log(n_s) | -2.22 (0.41)*** | -1.18 (0.44)** |
| × log ² (n_s) | 0.36 (0.12)** | 0.05 (0.11) |
| triangles | 5.43 (0.96)*** | 7.43 (0.96)*** |
| × log(n_s) | -3.31 (1.40)* | -5.82 (1.47)*** |
| × log ² (n_s) | 0.89 (0.71) | 1.66 (0.74)* |
| Young Child with Young Child | 8.63 (1.50)*** | 8.70 (1.54)*** |
| Young Child with Preadolescent | 9.13 (1.49)*** | 9.19 (1.53)*** |
| Preadolescent with Preadolescent | 8.21 (1.46)*** | 8.27 (1.50)*** |
| Adolescent with Adolescent | 7.74 (1.44)*** | 7.79 (1.49)*** |
| Young Child with Young Adult | 9.67 (1.78)*** | 9.72 (1.83)*** |
| Preadolescent with Young Adult | 7.28 (1.46)*** | 7.32 (1.50)*** |
| Adolescent with Young Adult | 7.76 (1.45)*** | 7.86 (1.50)*** |
| Young Adult with Young Adult | 7.69 (1.45)*** | 7.74 (1.49)*** |
| Young Child with Older Female Adult | 10.29 (1.46)*** | 10.35 (1.50)*** |
| Preadolescent with Older Female Adult | 9.71 (1.44)*** | 9.78 (1.49)*** |
| Adolescent with Older Female Adult | 8.93 (1.44)*** | 9.00 (1.48)*** |
| Older Female Adult with Older Female Adult | 7.50 (1.47)*** | 7.55 (1.51)*** |
| Young Child with Older Male Adult | 9.13 (1.44)*** | 9.18 (1.49)*** |
| Preadolescent with Older Male Adult | 8.80 (1.43)*** | 8.87 (1.48)*** |
| Adolescent with Older Male Adult | 8.24 (1.43)*** | 8.30 (1.48)*** |
| Older Female Adult with Older Male Adult | 10.15 (1.45)*** | 10.21 (1.49)*** |
| if child absent | -1.22 (0.30)*** | -1.21 (0.30)*** |
| Older Male Adult with Older Male Adult | 6.62 (1.45)*** | 6.70 (1.49)*** |
| Older Female Adult with Senior | 8.16 (1.42)*** | 8.24 (1.47)*** |
| Older Male Adult with Senior | 7.55 (1.46)*** | 7.62 (1.50)*** |
| Senior with Senior | 7.86 (1.41)*** | 7.93 (1.46)*** |
| Adolescent with Young Child or Preadolescent | 8.11 (1.44)*** | 8.17 (1.48)*** |
| Young Adult with Older Adult | 8.06 (1.43)*** | 8.11 (1.48)*** |
| Young Child or Preadolescent with Senior | 8.32 (1.53)*** | 8.38 (1.57)*** |
| Adolescent or Young Adult with Senior | 9.96 (1.71)*** | 10.06 (1.77)*** |
| AIC | 3697.1 (0.2)† | 3696.9 (0.2) |
| BIC | 3927.5 (0.2) | 3933.8 (0.2) |
| log-likelihood | -1813.6 (0.1) | -1812.5 (0.1) |

Significance: *** ≤ 0.001 <** ≤ 0.01 <* ≤ 0.05

†Standard errors for AIC, BIC, and log-likelihood are due to MCMC error.

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3 **Substantive conclusions** We discuss results primarily from *Model 1*, though *Model 2*
4 yields the same conclusions. Only a few of the effects are interpretable in isolation. In
5 particular, we can conclude with some confidence ($\hat{\beta} = 0.14$, SE = 0.056, $P = 0.014$)
6 that weekends have a positive effect on the number of contacts that are observed in the
7 household, in line with prior literature (Grijalva et al. 2015). Presence of a child in a
8 household is associated with a higher propensity of older male adults and older female
9 adults (likely the parents) to interact with each other (if no child: $\hat{\beta} = -1.2$, SE = 0.30, $P <$
10 0.001). We do not detect an effect of being in Brussels on network density ($\hat{\beta} = 0.1$, SE =
11 0.19, $P = 0.68$).
12
13

14 The estimated polynomial log-network-size effects are shown in Figure 3. Though they
15 are difficult to interpret in isolation from each other, we observe that edge effect counterbal-
16 ances 2-star and triangle effects, which also decrease with network size, guarding against
17 ERGM degeneracy as hoped. Overall, there is strong evidence that network size effects
18 are present ($P < 0.001$), including quadratic ($P < 0.001$), and including those on 2-stars
19 and triangles ($P < 0.001$). Both 2-star ($P < 0.001$) and triangle ($P < 0.001$) effects are
20 significant in the presence of others. (Test details are given in Table F32.)
21
22

23 We report the parameter estimates for household member category mixing in a more
24 intuitive layout in Figure 4. Since, unlike Goeyvaerts et al. (2018), we do not use a baseline
25 category (“intercept”), they are not interpretable in isolation but only in contrast with
26 each other. Thus, we conclude that older female adults (i.e. mothers) tend to interact more
27 than older male adults (i.e. fathers) with young children ($\hat{\Delta} = 1.2$, SE = 0.47, $P = 0.013$),
28 preadolescents ($\hat{\Delta} = 0.9$, SE = 0.29, $P = 0.002$), and adolescents ($\hat{\Delta} = 0.7$, SE = 0.25, $P =$
29 0.006). We thus confirm and expand on similar findings by Goeyvaerts et al. (2018). We also
30 tested whether older female adults interacted with seniors more than older male adults did,
31
32

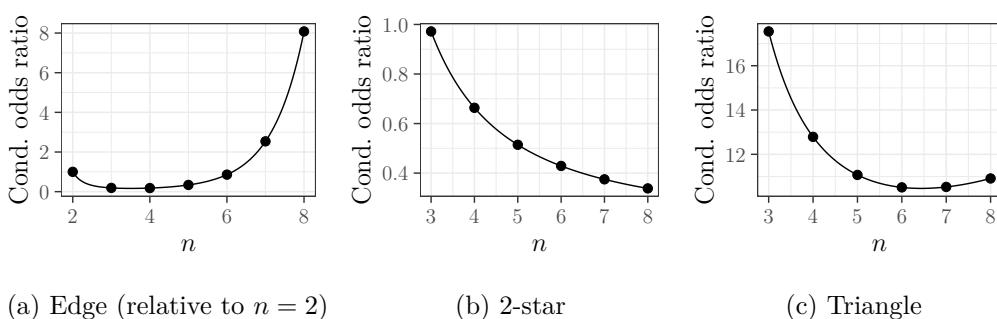


Figure 3: Estimated effects of network size on conditional odds of an instance of a graph feature. Two-stars and triangles are only possible for $n \geq 3$.

whether because they are more likely to care for elderly parents or because in a marriage, the female spouse is typically younger than the male spouse, and there is some evidence for this ($\hat{\Delta} = 0.6$, SE = 0.31, one-tailed $P = 0.026$). As with housing type, we recommend that future studies record specific familial relations for contacts.

6 Conclusion

Motivated by two collections of networks representing the same phenomena but collected using very different sampling designs, we combined their strengths, facilitating population-wide simulation of household networks. In the process, we identified the requirements of this procedure and developed generally applicable techniques for specifying and diagnosing models for large samples of networks, techniques that, through their relationship to GLMs, can be used by researchers from a wide variety of disciplines. The techniques we have developed do not rely on the networks being completely observed. To make this methodology accessible to a broad audience, we produced a user-friendly R package `ergm.multi`.

Our two surveys were conducted in Flanders and Brussels in 2010–2011. It is impor-

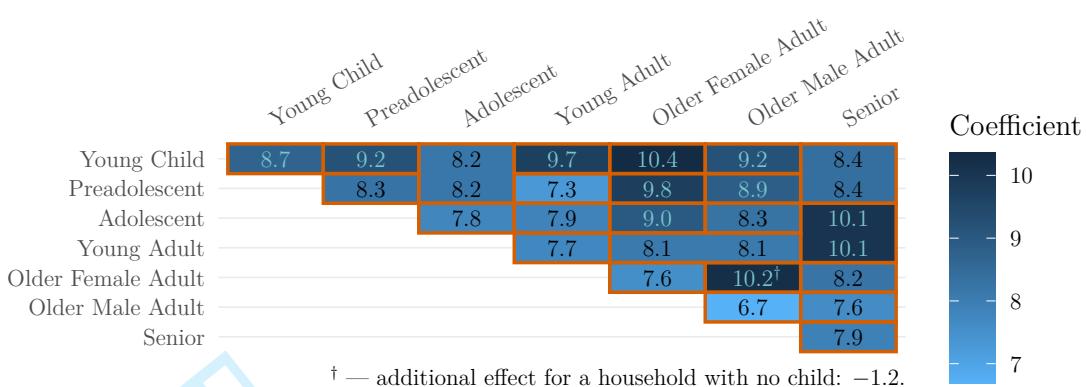


Figure 4: Parameter estimates for mixing by family role. Borders denote parametrisation. Because there is no “intercept” effect in the model, testing them against 0 is not meaningful.

tant to design and analyse household surveys in different settings with different inclusion criteria—but, ideally, compatible measurement instruments—to gain further insights on the contact patterns and the effects of endogenous factors such as triadic closure, exogenous individual attributes such as age, and exogenous household attributes such as size and type of residence. This work provides a foundation for identifying and testing these effects and for confirming the validity of the analysis—and opens the door to design of future cost-effective yet highly informative hybrid network studies.

A number of methodological research directions remain. In our work, we used Pearson residuals. Other types of residuals, such as deviance, tend to be better behaved and could, perhaps, be derived for this family of models. Similarly, Cook’s distance may be possible to compute inexpensively for each network using the approach of Koskinen et al. (2018).

We did not find evidence of non-systematic heterogeneity of networks. Where such is present, it can be accounted for in a mixed effects framework (Slaughter and Koehly 2016)

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3 at an additional computational cost, or perhaps by constructing ERGM sufficient statistics
4 to absorb the variation (Butts 2017; Krivitsky 2012). Alternatively, quasi-likelihood and
5 generalised estimating equation approaches may be extended to samples of networks.
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8 ERGM computational and diagnostic techniques are agnostic to the structure of the
9 sample space, so these approaches directly generalise to directed, temporal, valued, and
10 multilayer network scenarios. For our two surveys in particular, physical contact was not
11 the only relational measurement: the respondents were also asked about the approximate
12 duration of interaction (close proximity) on an ordinal scale (time ranges). Along similar
13 lines, the techniques for calculating standardised residuals under partially observed data
14 may be applicable to other domains that involve modelling independent samples of units
15 which are themselves partially observed.
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SUPPLEMENTARY MATERIAL

Appendices A–F: Further details, discussion, and results. (PDF file)

Code and data: Materials (including R packages) to reproduce the analysis. (ZIP file)

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8 **Supplement to**
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10 “**A Tale of Two Datasets:**
11 **Representativeness and**
12 **Generalisability of Inference for**
13 **Samples of Networks”:**
14 **Appendices A–F**

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| 8 | A Data | 3 |
| 9 | | |
| 10 | B Examples of Nonidentifiability due to Network Sampling | 10 |
| 11 | | |
| 12 | C Details of Diagnostic Methods | 14 |
| 13 | | |
| 14 | D Parametrisation and Network-Level Design Matrices | 18 |
| 15 | | |
| 16 | E Capacity to Detect Misspecification | 21 |
| 17 | | |
| 18 | F Additional Results and Diagnostics | 27 |
| 19 | | |
| 20 | | |
| 21 | | |
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| 23 | | |
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A Data

A.1 Data Collection and Pre-Processing

In both surveys, households were recruited via random-digit dialling on mobile phones and landlines and asked to record their social contacts on a diary during one quota-based assigned day (Hoang et al. 2021). For each contact the gender and the exact age or the estimated age interval of each contacted person were recorded, together with contacts' features including location, duration and frequency/intimacy level. Two types of contacts were recorded, one requiring a two-way conversation of at least three words and one requiring skin-to-skin contact. Participants also filled in a background survey, including information about age and gender of their household members. Contacts with a household member were identified requiring the contact was with a member of the household and checking that the age and gender of the contacted person matched the ones of a household member.

To account for potential errors in data entry from paper survey to digital form, we allowed for imperfect matching. If no exact match was found, we also considered the following contacts:

1. Exactly matched the age of a household member but not their gender.
2. Exactly matched the gender of a household member and but had a discrepancy in age, either off by 1 (to account for ageing between recruitment and survey completion) or a 1-digit discrepancy particularly when the digits were visually similar. For example, a report of a contact with a 43-year-old male would match a 48-year-old male household member if there were no better matches.

This error-correction was performed blindly with respect to the analysis. Its effect was to increase the number of matched contacts in E households from 2860 to 2925.

A.2 Additional Data Summaries

Data summaries most critical to the analysis are included in Section 2.2 in the body of the article. This appendix provides additional summaries and visualisations.

Figure A1 shows the distributions of household sizes and ages and genders of household members in the two datasets. Differences between the two are

due to design, with individuals aged around 25 years certainly underrepresented in the H dataset (Panel (a)), as they are unlikely to be either parents or children of parents of children 12 or under. The members of the households in the E dataset (Panel (b)) are more representative of the population (though not completely so, as individuals living alone ($n_s = 1$) are excluded); but survey respondents (Panel (b), bottom) have a different age and gender distribution from E household members in general, with females aged 25–55 years overrepresented and adolescents of both genders underrepresented.

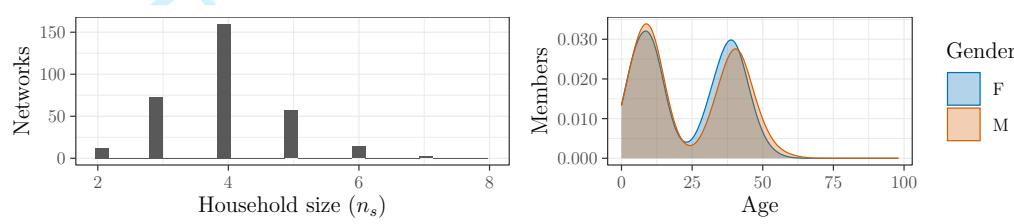
Densities of contacts in the households as a function of household size and subset (H , E_{12} , $E_{\bar{12}}$, respectively, H dataset, households in E dataset with a child at most 12, and E dataset households without) are shown in Figure A2, along with sample sizes of each combination. E households without a child differ systematically from those with a child (H or E), and tend to be concentrated among smaller household sizes, whereas those with a child tend to have a size of around 4. Overall, all subsets show a negative relationship between household size and its density of contacts. This is as expected (Krivitsky et al. 2011).

More household and structural summaries are provided in Table A1.

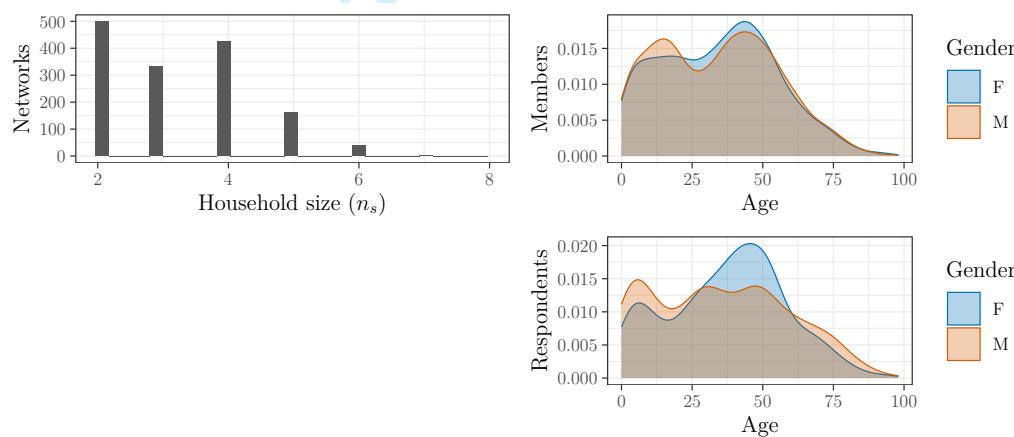
A.3 Sample Size Considerations

The number of relations whose state was observed was 2013 from the H and 3317 from the E datasets, for a total of 5330. This number would be our sample size under a model that assumed independence among the relations within each household, and is therefore an “optimistic” measure of the information available. In contrast, the number of households informative about at least one instance of a particular feature of the model is the “conservative” measure, since we do assume independence between households. Figure A3 shows these counts for the different combinations of household roles that we use in the model developed in Section 5.1.

We are modelling the impact of a child in a household on mixing patterns, both as a matter of substantive interest and as a design effect. However, we do not have sufficient information to model this effect for each category individually. The sample sizes for these effects are the total number of potential relations for a given category pair observed in subsets H and E_{12} (i.e., in the presence of a child) and this number for $E_{\bar{12}}$ (i.e., in the absence of a child). These are given in Figure A4. For example, we see that sample size is more than adequate for estimating a separate child effect for older female adult and older male adult contacts ($H + E_{12}$: 483, $E_{\bar{12}}$: 528) but not between two



(a) *H* dataset: 318 households with a total of 1266 members/respondents



(b) *E* dataset: 1463 households/respondents with a total of 4780 members

Figure A1: Household size distribution (left), household members' age and gender distribution (right), and respondents' age and gender distribution (bottom, *E* only).

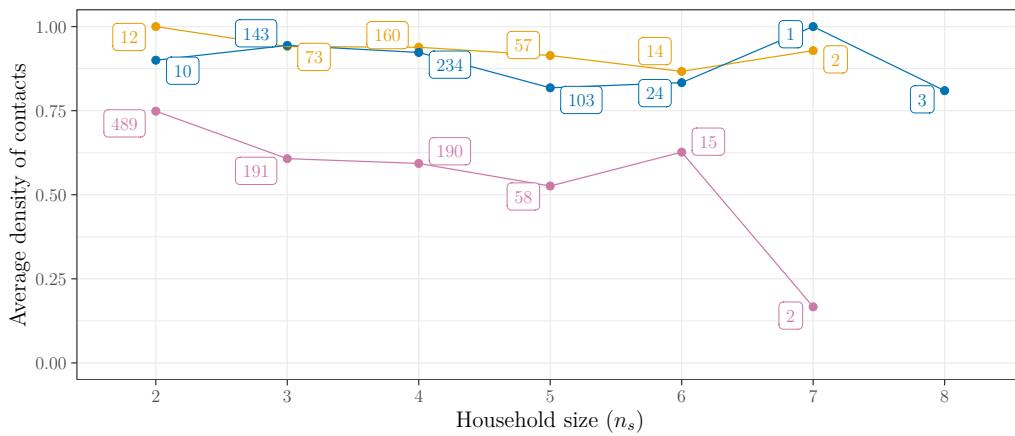
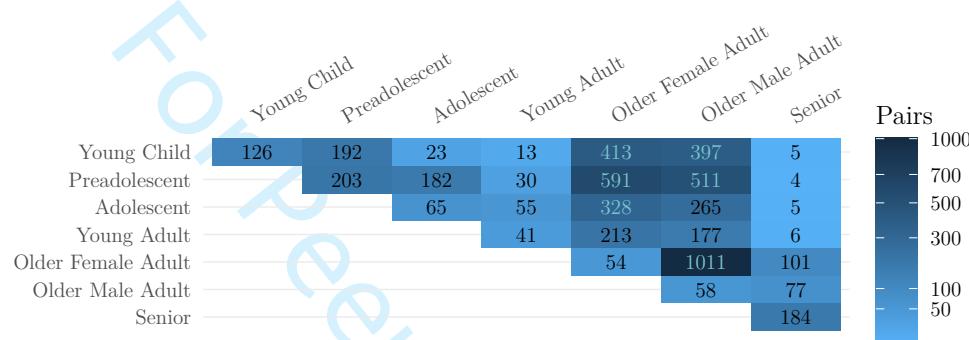


Figure A2: Mean household density of contacts (fraction of observable relations that are present) for each household size and data subset, and sample sizes for each household size and subset combination. (Subsets: H E_{12} $E_{\bar{12}}$)

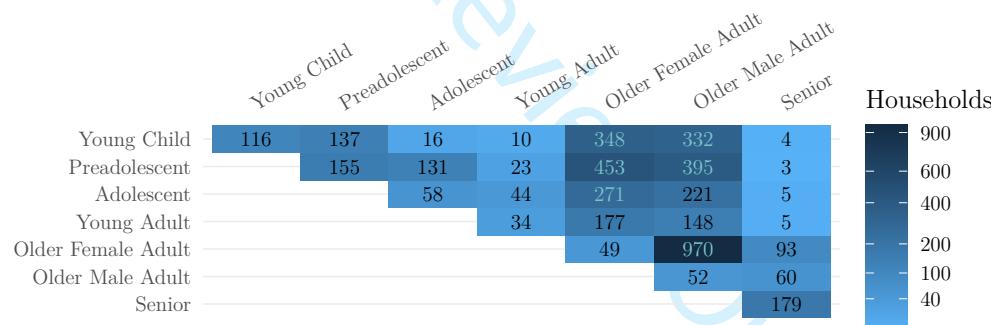
Table A1: Miscellaneous dataset composition information. In the H dataset, every household member is a “respondent”. Clustering coefficient is only meaningful for $n_s \geq 3$ and cannot be computed for the E dataset households.

| | H | E |
|--|-------------|-------------|
| Household members | 1266 (100%) | 4780 (100%) |
| Female | 636 (50%) | 2342 (49%) |
| Male | 630 (50%) | 2438 (51%) |
| Respondents | 1463 (100%) | |
| Female | | 768 (52%) |
| Male | | 695 (48%) |
| Dyads (observed) | 2013 (100%) | 6387 (52%) |
| Child present in household | 318 (100%) | 518 (35%) |
| Household observed on weekend | 91 (29%) | 364 (25%) |
| Household located in Brussels | 36 (11%) | 0 (0%) |
| Mean (std. dev.) net. density | 0.93 (0.15) | 0.75 (0.38) |
| Mean (std. dev.) net. clustering coef. | 0.92 (0.21) | |

older male adults ($H + E_{12}$: 2, $E_{\bar{12}}$: 56) or two older female adults ($H + E_{12}$: 6, $E_{\bar{12}}$: 48). This informs our modelling choices.



(a) Total pairs of individuals observed: the optimistic estimate



(b) Number of households with at least one pair observed: the conservative estimate

Figure A3: Each cell represents a measure of sample size for estimating the propensity of two individuals from those categories to interact. Unobserved relations (e.g., those not incident on a respondent in the *E* dataset) are not counted.

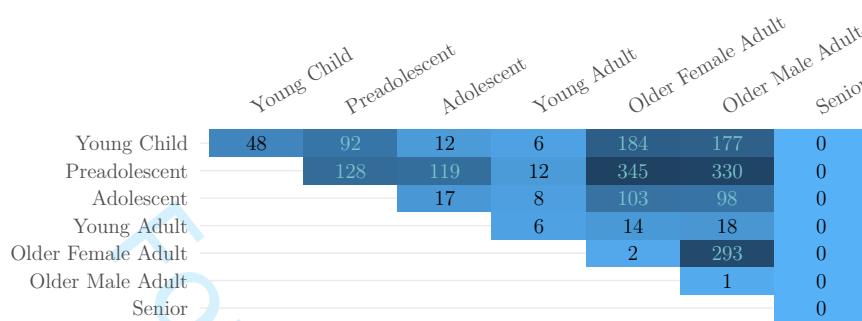
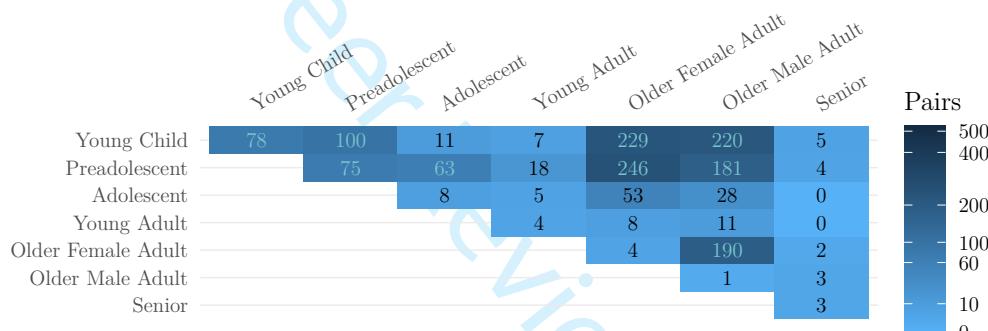
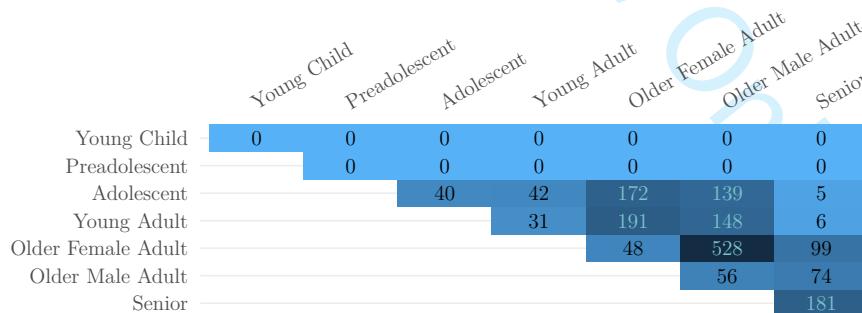
(a) H : Household dataset(b) E_{12} : Egocentric dataset, child at most 12 present(c) $E_{\bar{12}}$: Egocentric dataset, child at most 12 absent

Figure A4: Each cell gives the total number of pairs of individuals from those categories whose relationship state was observed (the “optimistic” sample size). Unobserved relations (e.g., those not incident on a respondent in the E dataset) are not counted.

B Examples of Nonidentifiability due to Network Sampling

B.1 Example 1: Exogenous Subgroups

Recall, an undirected network whose actor set N is partitioned into disjoint sets A and B . For actor sets $X \subseteq N$ and $Y \subseteq N$, let $|\mathbf{y}_{X,Y}|$ be the number of edges between actors in sets X and Y , and let $|\mathbf{y}|$ be the total edge count, and consider an ERGM with 3 parameters, whose sufficient statistic is

$$\mathbf{g}(\mathbf{y}) = [|\mathbf{y}|, |\mathbf{y}_{A,A}|, |\mathbf{y}_{A,B}|]^\top.$$

This statistic does not induce dependence among the dyads, and so under this model,

$$\begin{aligned} |\mathbf{Y}_{A,A}| &\sim \text{Binomial}\left(\binom{|A|}{2}, \text{logit}^{-1}(\theta_1 + \theta_2)\right) \\ |\mathbf{Y}_{A,B}| &\sim \text{Binomial}\left(|A||B|, \text{logit}^{-1}(\theta_1 + \theta_3)\right) \\ |\mathbf{Y}_{B,B}| &\sim \text{Binomial}\left(\binom{|B|}{2}, \text{logit}^{-1}(\theta_1)\right), \end{aligned}$$

all mutually independent. Call their variances $\sigma_{A,A}$, $\sigma_{A,B}$, and $\sigma_{B,B}$, respectively. Since $|\mathbf{y}| \equiv |\mathbf{y}_{A,A}| + |\mathbf{y}_{A,B}| + |\mathbf{y}_{B,B}|$,

$$\boldsymbol{\Sigma}(\boldsymbol{\theta}) = \begin{bmatrix} \sigma_{A,A} + \sigma_{A,B} + \sigma_{B,B} & \sigma_{A,A} & \sigma_{A,B} \\ \sigma_{A,A} & \sigma_{A,A} & 0 \\ \sigma_{A,B} & 0 & \sigma_{A,B} \end{bmatrix},$$

and $|\boldsymbol{\Sigma}(\boldsymbol{\theta})| = \sigma_{A,A}\sigma_{A,B}\sigma_{B,B}$, nonsingular as long as all elements of $\boldsymbol{\theta}$ are finite.

Now, consider an observation process in which only relationships incident on members of group A (A - A and A - B) are observed and B - B relations are missing by design. B - B relationships are not explicitly part of $\mathbf{g}(\mathbf{y})$, and, in fact, \mathbf{y}^{obs} contains all of the information needed to compute $g_2(\cdot)$ and $g_3(\cdot)$. Then,

$$\begin{aligned} \boldsymbol{\mu}(\boldsymbol{\theta} | \mathbf{y}^{\text{obs}}) &= [|\mathbf{y}_{A,A}| + |\mathbf{y}_{A,B}| + \mathbb{E}\{|\mathbf{Y}_{B,B}| \mid \mathbf{Y} \in \mathcal{Y}(\mathbf{y}^{\text{obs}})\}, |\mathbf{y}_{A,A}|, |\mathbf{y}_{A,B}|]^\top \\ &= [|\mathbf{y}_{A,A}| + |\mathbf{y}_{A,B}| + \binom{|B|}{2}p_{B,B}, |\mathbf{y}_{A,A}|, |\mathbf{y}_{A,B}|]^\top, \end{aligned}$$

because $|\mathbf{Y}_{B,B}|$ does not depend on \mathbf{y}^{obs} . Thus, $\mu_1(\boldsymbol{\theta} \mid \mathbf{y}^{\text{obs}})$ is an affine combination of $\mu_2(\boldsymbol{\theta} \mid \mathbf{y}^{\text{obs}})$ and $\mu_3(\boldsymbol{\theta} \mid \mathbf{y}^{\text{obs}})$ for all \mathbf{y}^{obs} , making $\mathcal{I}(\boldsymbol{\theta})$ singular. More explicitly, from (2b),

$$\begin{aligned}\mathcal{I}(\boldsymbol{\theta}) &= \text{Var}_{\mathbf{Y}}[\boldsymbol{\mu}\{\boldsymbol{\theta} \mid \text{obs}(\mathbf{Y})\}] \\ &= \text{Var}\left[|\mathbf{Y}_{A,A}| + |\mathbf{Y}_{A,B}| + \binom{|B|}{2} p_{B,B}, |\mathbf{Y}_{A,A}|, |\mathbf{Y}_{A,B}|\right]^{\top} \\ &= \begin{bmatrix} \sigma_{A,A} + \sigma_{A,B} + 0 & \sigma_{A,A} & \sigma_{A,B} \\ \sigma_{A,A} & \sigma_{A,A} & 0 \\ \sigma_{A,B} & 0 & \sigma_{A,B} \end{bmatrix}.\end{aligned}$$

Here, the first column of $\mathcal{I}(\boldsymbol{\theta})$ is the sum of its second and third.

B.2 Example 2: Triadic Effects

Now, consider an independent, identically distributed sample of S undirected networks of size $n = 3$ and an ERGM with the following sufficient statistic, counting edges, 2-stars, and triangles in network \mathbf{y} :

$$\mathbf{g}(\mathbf{y}) = \left[|\mathbf{y}|, \sum_{i=1}^n \binom{|y_i|}{2}, \sum_{1 \leq i < j < k \leq n} y_{i,j} y_{j,k} y_{k,i}\right],$$

where $|y_i|$ is the number of edges incident on actor i . Each network in the sample has a sample space of size $|\mathcal{Y}| = 2^{\binom{3}{2}} = 8$, enumerated in Table B1.

For simplicity, we will set $\boldsymbol{\theta} = \mathbf{0}$, making all networks equiprobable. Then, we can evaluate the population covariance matrix and obtain

$$\mathcal{I}(\mathbf{0}) = \frac{S}{64} \begin{bmatrix} 48 & 48 & 12 \\ 48 & 60 & 18 \\ 12 & 18 & 7 \end{bmatrix}$$

and $|\mathcal{I}(\mathbf{0})| = (9/4096)S^3$. For $S = 1$, the MLE for θ_3 will be infinite due to the sufficient statistic being at its highest or lowest possible value, but this is unrelated to nonidentifiability.

Now, consider an egocentric missing data regime in which relations between Actor 1 and the others are observed but the relationship between Actor 2 and Actor 3 ($y_{2,3}$) is missing. The conditional expectations $\boldsymbol{\mu}(\boldsymbol{\theta} \mid \mathbf{y}^{\text{obs}})$ and probabilities $\Pr(\mathbf{Y}^{\text{obs}} = \mathbf{y}^{\text{obs}})$ for every possible \mathbf{y}^{obs} are given in Table B2. Given those, the covariance matrix $\text{Var}_{\mathbf{Y}}[\boldsymbol{\mu}\{\boldsymbol{\theta} \mid \text{obs}(\mathbf{Y})\}]$ gives

$$\mathcal{I}(\mathbf{0}) = \frac{S}{64} \begin{bmatrix} 32 & 32 & 8 \\ 32 & 36 & 10 \\ 8 & 10 & 3 \end{bmatrix}$$

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8 and $|\mathcal{I}(\mathbf{0})| = 0$.
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13 Table B1: Possible undirected networks of size 3 and their edge, 2-star, and
14 triangle statistics.

| $y_{1,2}$ | $y_{1,3}$ | $y_{2,3}$ | edges | 2-stars | triangles |
|-----------|-----------|-----------|-------|---------|-----------|
| 0 | 0 | 0 | 0 | 0 | 0 |
| 0 | 0 | 1 | 1 | 0 | 0 |
| 0 | 1 | 0 | 1 | 0 | 0 |
| 1 | 0 | 0 | 1 | 0 | 0 |
| 0 | 1 | 1 | 2 | 1 | 0 |
| 1 | 0 | 1 | 2 | 1 | 0 |
| 1 | 1 | 0 | 2 | 1 | 0 |
| 1 | 1 | 1 | 3 | 3 | 1 |

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37 Table B2: Conditional expectations of edge, 2-star, and triangle statistics
38 for undirected networks of size 3 with $Y_{2,3}$ unobserved and their probabilities
39 under the null model.

| $\Pr(Y_{1,2} = y_{1,2}, Y_{1,3} = y_{1,3})$ | $y_{1,2}$ | $y_{1,3}$ | edges | 2-stars | triangles |
|---|-----------|-----------|-------|---------|-----------|
| 0.25 | 0 | 0 | 0.5 | 0.0 | 0.0 |
| 0.25 | 0 | 1 | 1.5 | 0.5 | 0.0 |
| 0.25 | 1 | 0 | 1.5 | 0.5 | 0.0 |
| 0.25 | 1 | 1 | 2.5 | 2.0 | 0.5 |

C Mathematical and Computational Details of Diagnostic Methods

C.1 Estimating the Variance of the Residuals for Partially Observed Networks

Here, we discuss estimation of $\text{Var}_{\vec{\mathbf{Y}}}[\tau\{\hat{\beta} \mid \text{obs}(\vec{\mathbf{Y}})\}]$ in (3b) in Section 4.2. This is a nested expectation, which calls for nested simulation of network statistics: first, we simulate a sample of complete networks $\vec{\mathbf{Y}}^{(1)}, \dots, \vec{\mathbf{Y}}^{(R_1)} \sim \text{ERGM}_{z, \vec{\mathcal{Y}}, \vec{x}, \vec{g}}(\beta)$, and then, for each $r_1 \in \{1, \dots, R_1\}$, simulate a sample $\vec{\mathbf{Y}}^{(r_1,1)}, \dots, \vec{\mathbf{Y}}^{(r_1,R_2)} \sim \text{ERGM}_{z, \vec{\mathcal{Y}}\{\text{obs}(\vec{\mathbf{Y}}^{(r_1)})\}, \vec{x}, \vec{g}}(\beta)$. We consider two ways to use these realisations to obtain the estimator.

Direct method Substituting simulated values into the expectation and the variance yields a consistent (as $R_1 \rightarrow \infty$ and $R_2 \rightarrow \infty$) estimator. This direct estimator for the variance of the conditional expectation in the divisor in (3b) has the following form:

$$\frac{1}{R_1 - 1} \sum_{r_1=1}^{R_1} \left\{ \overline{t(\vec{\mathbf{Y}}^{(r_1,:)})} - \overline{t(\vec{\mathbf{Y}}^{(:,,:)})} \right\}^2,$$

where $\overline{t(\vec{\mathbf{Y}}^{(r_1,:)})} \stackrel{\text{def}}{=} R_2^{-1} \sum_{r_2=1}^{R_2} t(\vec{\mathbf{Y}}^{(r_1,r_2)})$, an estimator of the inner expectation for a given $\text{obs}(\vec{\mathbf{Y}}^{(r_1)})$, and $\overline{t(\vec{\mathbf{Y}}^{(:,,:)})} \stackrel{\text{def}}{=} R_1^{-1} \sum_{r_1=1}^{R_1} \overline{t(\vec{\mathbf{Y}}^{(r_1,:)})}$, the grand mean. Here, we derive the approximate expression for its bias due to the variance capturing the additional variability (decreasing in R_2) in estimating the inner expectation by simulation.

Assuming that R_1 is sufficiently large that the variance of $\overline{t(\vec{\mathbf{Y}}^{(:,,:)})}$ is negligible, and since $\mathbb{E}\{t(\vec{\mathbf{Y}}^{(r_1,:)}) - t(\vec{\mathbf{Y}}^{(:,,:)})\} = 0$,

$$\begin{aligned} \mathbb{E}\{\overline{t(\vec{\mathbf{Y}}^{(r_1,:)})} - \overline{t(\vec{\mathbf{Y}}^{(:,,:)})}\}^2 &= \text{Var}\{\overline{t(\vec{\mathbf{Y}}^{(r_1,:)})} - \overline{t(\vec{\mathbf{Y}}^{(:,,:)})}\} \approx \text{Var}\{\overline{t(\vec{\mathbf{Y}}^{(r_1,:)})}\} \\ &\approx \text{Var}[\mathbb{E}\{\overline{\mathbf{g}(\vec{\mathbf{Y}}^{(r_1,:)})} \mid \vec{\mathbf{Y}}^{(r_1,1)}, \dots, \vec{\mathbf{Y}}^{(r_1,R_2)} \in \mathcal{Y}((\vec{\mathbf{Y}}^{(r_1)})^{\text{obs}})\}] \\ &\quad + \mathbb{E}[\text{Var}\{\overline{\mathbf{g}(\vec{\mathbf{Y}}^{(r_1,:)})} \mid \vec{\mathbf{Y}}^{(r_1,1)}, \dots, \vec{\mathbf{Y}}^{(r_1,R_2)} \in \mathcal{Y}((\vec{\mathbf{Y}}^{(r_1)})^{\text{obs}})\}] \\ &\approx \text{Var}[\mathbb{E}\{\mathbf{g}(\vec{\mathbf{Y}}') \mid \vec{\mathbf{Y}}' \in \mathcal{Y}((\vec{\mathbf{Y}})^{\text{obs}})\}] \\ &\quad + \frac{1}{R_2} \mathbb{E}[\text{Var}\{\mathbf{g}(\vec{\mathbf{Y}}') \mid \vec{\mathbf{Y}}' \in \mathcal{Y}((\vec{\mathbf{Y}})^{\text{obs}})\}] \end{aligned}$$

Therefore, this estimator is biased, with bias decreasing as a function of R_2 . An adjusted estimator could then be

$$\frac{1}{R_1 - 1} \sum_{r_1=1}^{R_1} \{\overline{t(\vec{Y}^{(r_1,:)})} - \overline{t(\vec{Y}^{(:,,:)})}\}^2 - \frac{1}{R_2} \frac{1}{R_1} \sum_{r_1=1}^{R_1} \frac{1}{R_2 - 1} \sum_{r_2=1}^{R_2} \{t(\vec{Y}^{(r_1,r_2)}) - \overline{t(\vec{Y}^{(r_1,:)})}\}^2.$$

Law of Total Variance method This approach takes advantage of the Law of Total Variance to write:

$$\begin{aligned} \text{Var}_{\vec{Y}}[\tau\{\hat{\beta} \mid \text{obs}(\vec{Y})\}] &= \Psi(\hat{\beta}) - \mathbb{E}_{\vec{Y}}[\Psi\{\hat{\beta} \mid \text{obs}(\vec{Y})\}], \\ &\approx \frac{1}{R_1 R_2 - 1} \sum_{r_1=1}^{R_1} \sum_{r_2=1}^{R_2} \{t(\vec{Y}^{(i,j)}) - \overline{t(\vec{Y}^{(:,,:)})}\}^2 \\ &\quad - \frac{1}{R_1} \sum_{r_1=1}^{R_1} \frac{1}{R_2 - 1} \sum_{r_2=1}^{R_2} \{t(\vec{Y}^{(i,j)}) - \overline{t(\vec{Y}^{(i,:)})}\}^2, \end{aligned}$$

an unbiased (except perhaps from MCMC autocorrelation) estimator with an added benefit that some of the simulation error in the minuend and the subtrahend cancels. We derive its properties as follows.

Suppose that each $\vec{Y}^{(r_1)}$ induces a distribution of $t(\vec{Y}^{(r_1,r_2)})$ with conditional variance $\sigma_{r_1}^2$ (i.e., $\text{Var}\{t(\vec{Y}^{(r_1,r_2)}) \mid \vec{Y}^{(r_1,r_2)} \in \mathcal{Y}((\vec{Y}^{(r_1)})^{\text{obs}})\} = \sigma_{r_1}^2$). The unbiased estimator is

$$\tilde{\sigma}_{r_1}^2 = \frac{1}{R_2 - 1} \sum_{r_2=1}^{R_2} \{t(\vec{Y}^{(r_1,r_2)}) - \overline{t(\vec{Y}^{(r_1,:)})}\}^2$$

We wish to estimate the expected variance and, under the unconstrained process, $\mathbb{E}(\sigma_{r_1}^2) = \sigma^2$. Suppose that $\text{Var}(\sigma_{r_1}^2) = \alpha$. Then, the estimator

$$\tilde{\sigma}^2 = \frac{1}{R_1} \sum_{r_1=1}^{R_1} \tilde{\sigma}_{r_1}^2$$

has expectation

$$\begin{aligned} \mathbb{E}(\tilde{\sigma}^2) &= \frac{1}{R_1} \sum_{r_1=1}^{R_1} \mathbb{E}(\tilde{\sigma}_{r_1}^2) = \frac{1}{R_1} \sum_{r_1=1}^{R_1} \mathbb{E}_{\sigma_{r_1}^2} \{\mathbb{E}_{\tilde{\sigma}_{r_1}^2}(\tilde{\sigma}_{r_1}^2 \mid \sigma_{r_1}^2)\} \\ &= \frac{1}{R_1} \sum_{r_1=1}^{R_1} \mathbb{E}_{\sigma_{r_1}^2} \{\sigma_{r_1}^2\} = \sigma^2, \end{aligned}$$

so it is unbiased regardless of R_2 , R_1 , and the distribution of $t(\vec{Y}^{(r_1, r_2)})$.

To approximate its variance, we must assume a conditional distribution $t(\vec{Y}^{(r_1, r_2)}) | \vec{Y}^{(r_1)}$. If it is approximately normal,

$$\tilde{\sigma}_{r_1}^2 | \sigma_{r_1}^2 \sim \frac{\sigma_{r_1}^2}{R_2 - 1} \chi_{R_2 - 1}^2.$$

Its variance is

$$\begin{aligned} \mathbb{V}\text{ar}(\tilde{\sigma}^2) &= \frac{1}{R_1^2} \sum_{r_1=1}^{R_1} \mathbb{V}\text{ar}(\tilde{\sigma}_{r_1}^2) \\ &= \frac{1}{R_1^2} \sum_{r_1=1}^{R_1} [\mathbb{E}_{\sigma_{r_1}^2} \{ \mathbb{V}\text{ar}_{\tilde{\sigma}_{r_1}^2} (\tilde{\sigma}_{r_1}^2 | \sigma_{r_1}^2) \} + \mathbb{V}\text{ar}_{\sigma_{r_1}^2} \{ \mathbb{E}_{\tilde{\sigma}_{r_1}^2} (\tilde{\sigma}_{r_1}^2 | \sigma_{r_1}^2) \}] \\ &= \frac{1}{R_1^2} \sum_{r_1=1}^{R_1} [\mathbb{E}_{\sigma_{r_1}^2} \left\{ \frac{2\sigma_{r_1}^4(R_2 - 1)}{(R_2 - 1)^2} \right\} + \mathbb{V}\text{ar}_{\sigma_{r_1}^2} \{ \sigma_{r_1}^2 \}] \\ &= \frac{1}{R_1^2} \sum_{r_1=1}^{R_1} \left[\frac{2}{R_2 - 1} \mathbb{E}_{\sigma_{r_1}^2} \{ \sigma_{r_1}^4 \} + \alpha \right] \\ &= \frac{1}{R_1^2} \sum_{r_1=1}^{R_1} \left[\frac{2}{R_2 - 1} \{ \mathbb{E}_{\sigma_{r_1}^2}^2 (\sigma_{r_1}^2) + \mathbb{V}\text{ar}(\sigma_{r_1}^2) \} + \alpha \right] \\ &= \frac{1}{R_1^2} \sum_{r_1=1}^{R_1} \left[\frac{2}{R_2 - 1} \{ \sigma^4 + \alpha \} + \alpha \right] = \frac{1}{R_1} \left[\frac{2}{R_2 - 1} \sigma^4 + \left(\frac{2}{R_2 - 1} + 1 \right) \alpha \right]. \end{aligned}$$

A corollary of this is that increasing R_2 can only increase the precision up to a point, whereas provided $R_2 \geq 2$, increasing R_1 increases precision without limit. Nonetheless, if $\sigma^4 \gg \alpha$, it may be worthwhile to increase R_2 , since conditional simulation is computationally cheaper.

C.2 Simulation-based Score Test for Dataset Effects

Here, we describe two variants of the simulation score test for dataset effects. For our purposes, the null hypothesis is the candidate model, which does not include explicit dataset effects, and the alternative is the same model with an explicit dataset effect. Rejection of the null hypothesis therefore implies that the dataset effect is not ignorable.

In a minimal exponential family, the score function is the difference between the observed value of sufficient statistic present in the full model but

not in the reduced model and its expected value under the MLE of the reduced model. The score test in question can therefore be conducted by the following simulation (Krivitsky 2012):

- 12 1. Specify a statistic $t_{\text{dataset}}(\vec{\mathbf{y}})$ that is not a part of the candidate model
13 and that contains an explicit dataset effect.
- 14 2. Simulate complete network datasets $\vec{\mathbf{Y}}^{(1)}, \dots, \vec{\mathbf{Y}}^{(R)} \stackrel{\text{i.i.d.}}{\sim} \text{ERGM}(\hat{\beta})$ from
15 the candidate model.
- 16 3. Evaluate the sample quantile
17

$$21 q \stackrel{\text{def}}{=} \frac{1}{R} \sum_{r=1}^R \mathbb{I}\{t_{\text{dataset}}(\vec{\mathbf{y}}) \leq t_{\text{dataset}}(\vec{\mathbf{Y}}^{(r)})\}$$

- 22 4. Then, $2 \min(q, 1 - q)$ is a score test P -value for the null hypothesis
23 $\theta_{\text{dataset}} = 0$.

In our application, a straightforward $t_{\text{dataset}}(\vec{\mathbf{y}}) = \sum_{s \in H} |\mathbf{y}_s|$: separate density for networks in the H dataset, which only depends on the completely observed networks. (A test statistic that uses partially observed networks would require further adjustment along the lines of Section 4.2.)

A joint test for several network features is also possible: if $\mathbf{t}_{\text{dataset}}(\vec{\mathbf{y}})$ is vector-valued, then, with \mathbf{m} the estimate of $\mathbb{E}\{\mathbf{t}_{\text{dataset}}(\vec{\mathbf{Y}})\}$ and V the estimate of $\text{Var}\{\mathbf{t}_{\text{dataset}}(\vec{\mathbf{Y}})\}$, both obtained by simulation, $\chi^2 = \{\mathbf{m} - \mathbf{t}_{\text{dataset}}(\vec{\mathbf{y}})\}^\top V^{-1} \{\mathbf{m} - \mathbf{t}_{\text{dataset}}(\vec{\mathbf{y}})\}$ provides an omnibus score test. Unlike the quantile-based test, this test relies on approximate normality of $\mathbf{t}_{\text{dataset}}(\vec{\mathbf{Y}})$, which can be guaranteed by a sufficiently large sample of networks.

D Parametrisation and Network-Level Design Matrices

In Section 3.2, when we described the framework for modelling effects of network-level properties on its relational structure, we expressed it under the assumption that dimension p of the sufficient statistic $\mathbf{g}_s(\cdot)$ did not vary between networks, and nor did the dimension q of the network-level covariate vector \mathbf{z}_s , and $\boldsymbol{\theta}_s \stackrel{\text{def}}{=} (\mathbf{z}_s \boldsymbol{\beta})^\top$. An implication of this is that every network-level covariate has the potential to affect every ERGM parameter.

This is often not the desired behaviour. For example, in *Model 1*, a network's edge count statistic is modelled by network size, location in Brussels, and whether the data were gathered on the weekend (but no intercept); whereas the 2-star and triangle counts are modelled with network size and intercept both. The family role mixing effects are assumed to be constant (net of others), with the exception of contacts between older female adults and older male adults, which also have the presence of a child as a predictor.

We claimed that provided that we could fix some elements of $\boldsymbol{\beta}$ at 0, no generality was lost, and we illustrate this here for *Model 1* as follows.

Firstly, we construct a design matrix based on the superset of network properties used in *Model 1*. This is illustrated for a selection of households in Table D1.

Secondly, for all networks we construct a statistic vector that is a superset of all sufficient statistics used in the model. Where a statistic is inapplicable (e.g., number of triangles in a network of size 2), it will simply be 0. Recalling the definition of $|\mathbf{y}_{X,Y}|$ from Section B.1, the following vector results:

$$\mathbf{g}_s(\mathbf{y}) = \left[|\mathbf{y}|, \sum_{i=1}^{n_s} \binom{|\mathbf{y}_i|}{2}, \sum_{1 \leq i < j < k \leq n_s} y_{i,j} y_{j,k} y_{k,i}, |\mathbf{y}_{\text{OFA,OMA}}|, \{\text{other role mixing}\} \right],$$

containing, respectively, the number of edges, the number of 2-stars, the number of triangles, the number of relations between older female adults and older male adults, and the rest of the mixing counts for family roles enumerated in Section 5.1 and elsewhere.

Lastly, constrain $\boldsymbol{\beta}$ as shown in Table D2.

In practice, this approach, while technically supported by `ergm.multi`, is unnecessarily cumbersome and computationally inefficient. We refer the

Table D1: Network properties and resulting network-level covariates for a selection of networks.

| ID | household size (n_s) | Network-level properties | | | | Design matrix (\mathbf{z}_s) | | | | | |
|-------|--------------------------|--------------------------|-----------------|------------------------|-----------|----------------------------------|---------------|--------------------|------------|--------------|--|
| | | post code in Brussels | day of the week | a child aged ≤ 12 | Intercept | $\log(n_s)$ | $\log^2(n_s)$ | Brussels post code | on weekend | child absent | |
| H1 | 5 | No | Weekday | Present | 1 | 1.61 | 2.59 | 0 | 0 | 0 | |
| H199 | 7 | Yes | Weekend | Present | 1 | 1.95 | 3.79 | 1 | 1 | 0 | |
| E79 | 2 | No | Weekend | Absent | 1 | 0.69 | 0.48 | 0 | 1 | 1 | |
| E276 | 3 | No | Weekday | Present | 1 | 1.10 | 1.21 | 0 | 0 | 0 | |
| E474 | 3 | No | Weekday | Absent | 1 | 1.10 | 1.21 | 0 | 0 | 1 | |
| E672 | 4 | No | Weekday | Present | 1 | 1.39 | 1.92 | 0 | 0 | 0 | |
| E870 | 2 | No | Weekday | Absent | 1 | 0.69 | 0.48 | 0 | 0 | 1 | |
| E1067 | 2 | No | Weekday | Absent | 1 | 0.69 | 0.48 | 0 | 0 | 1 | |
| E1265 | 3 | No | Weekday | Absent | 1 | 1.10 | 1.21 | 0 | 0 | 1 | |
| E1463 | 4 | No | Weekend | Present | 1 | 1.39 | 1.92 | 0 | 1 | 0 | |

Table D2: Constraints on β to implement *Model 1*. Zeros denote parameters fixed at 0, dots free parameters.

| | $ \mathbf{y} $ | $\sum_{i=1}^{n_s} \binom{ \mathbf{y}_i }{2}$ | $\sum_{1 \leq i < j < k \leq n_s} y_{i,j} y_{j,k} y_{k,i}$ | $ \mathbf{y}_{\text{OFA,OMA}} $ | other role mixing |
|--------------------|----------------|--|--|---------------------------------|-------------------|
| Intercept | 0 | . | . | . | . |
| $\log(n_s)$ | . | . | . | 0 | 0 |
| $\log^2(n_s)$ | . | . | . | 0 | 0 |
| Brussels post code | . | 0 | 0 | 0 | 0 |
| on weekend | . | 0 | 0 | 0 | 0 |
| child absent | 0 | 0 | 0 | . | 0 |

reader to the code to reproduce the analysis and `ergm.multi` documentation and tutorials for the recommended approach.

For Peer Review Only

E Capacity to Detect Misspecification

To illustrate misspecification detection, we fit three reduced models based on *Model 1*:

Model 0m: minimal model a model with only edge count, 2-star, and triangle statistics, with their linear and quadratic network size effects, and weekend and Brussels edge effects;

Model 1d: exclude dyad-dependent effects a submodel of *Model 1* excluding the dyad-dependent 2-star and triangle effects;

Model 1n: exclude network size (n) effects a submodel of *Model 1* excluding linear and quadratic network size effects.

A comparison of their specification to that of the other models is given in Table F1.

Hypothesis testing for network size effect misspecification Full ANOVA tables are given in Tables E1. In *Model 1n* (Table (a)), which lacks network size effects, tests on residuals reject the hypothesis of fit for edges, 2-stars, and triangles (P -vals. < 0.001 , < 0.001 , and < 0.001 , respectively). In *Model 0m* (Table (b)), which does incorporate them, none do (P -vals. 0.90, 0.83, and 0.81, respectively). *Model 1d* (Table (c)), which has network size effects for density (edge count) but not other features rejects hypothesis of fit for triangles ($P < 0.001$) and nearly so for 2-stars ($P = 0.06$) but not for edges ($P = 0.40$). Thus, the method appears to be capable of detecting and identifying network size effect misspecification with some detail.

Residual plots for dataset and network size effects Turning to residual plots, Figure E1 shows the edge residual plots for *Model 1* (Panel (a)), *Model 1n* (Panel (b) and (c)), and *Model 0m* (Panel (d)). Observe that unlike the *Model 1*'s, *Model 0m*'s residuals for households without a child are systematically different from those with a child (from either dataset). Thus, the dataset effect is not ignorable. On the other hand, the lack of network size effects in *Model 1n* does not appear to be noticeable in either Panel (b) or Panel (c).

Residual plots for age effects We can also construct residual plots for actor-level statistics and plot them against actor attributes. This allows us to diagnose whether age effects in particular have been adequately modelled by our categories. Figure E2 shows the edge residual plots for *Model 1*

Table E1: Analyses of variance for fitting residuals against household size (represented as a categorical predictor, with a dummy variable for each size).

(a) *Model 1n* (no network size effects)

| Source | df | Sum Sq. | Mean Sq. | F | P-val. |
|---------------------|------|---------|----------|-----|---------|
| edges | | | | | |
| n_s (categorical) | 7 | 36.2 | 5.2 | 4.8 | < 0.001 |
| Residuals | 1774 | 1912.1 | 1.1 | | |
| 2-stars | | | | | |
| n_s (categorical) | 6 | 30.1 | 5.0 | 4.6 | < 0.001 |
| Residuals | 1264 | 1389.2 | 1.1 | | |
| triangles | | | | | |
| n_s (categorical) | 6 | 28.5 | 4.7 | 4.5 | < 0.001 |
| Residuals | 1264 | 1341.0 | 1.1 | | |

(b) *Model 0m* (minimal model)

| Source | df | Sum Sq. | Mean Sq. | F | P-val. |
|---------------------|------|---------|----------|------|--------|
| edges | | | | | |
| n_s (categorical) | 7 | 2.8 | 0.40 | 0.41 | 0.898 |
| Residuals | 1774 | 1752.3 | 0.99 | | |
| 2-stars | | | | | |
| n_s (categorical) | 6 | 2.8 | 0.47 | 0.47 | 0.827 |
| Residuals | 1264 | 1252.9 | 0.99 | | |
| triangles | | | | | |
| n_s (categorical) | 6 | 3.0 | 0.50 | 0.51 | 0.805 |
| Residuals | 1264 | 1260.4 | 1.00 | | |

(c) *Model 1d* (minimal model)

| Source | df | Sum Sq. | Mean Sq. | F | P-val. |
|---------------------|------|---------|----------|-----|---------|
| edges | | | | | |
| n_s (categorical) | 7 | 8.2 | 1.17 | 1.0 | 0.404 |
| Residuals | 1774 | 1999.7 | 1.13 | | |
| 2-stars | | | | | |
| n_s (categorical) | 6 | 11.3 | 1.89 | 2.0 | 0.060 |
| Residuals | 1264 | 1183.0 | 0.94 | | |
| triangles | | | | | |
| n_s (categorical) | 6 | 20.8 | 3.46 | 4.6 | < 0.001 |
| Residuals | 1264 | 947.7 | 0.75 | | |

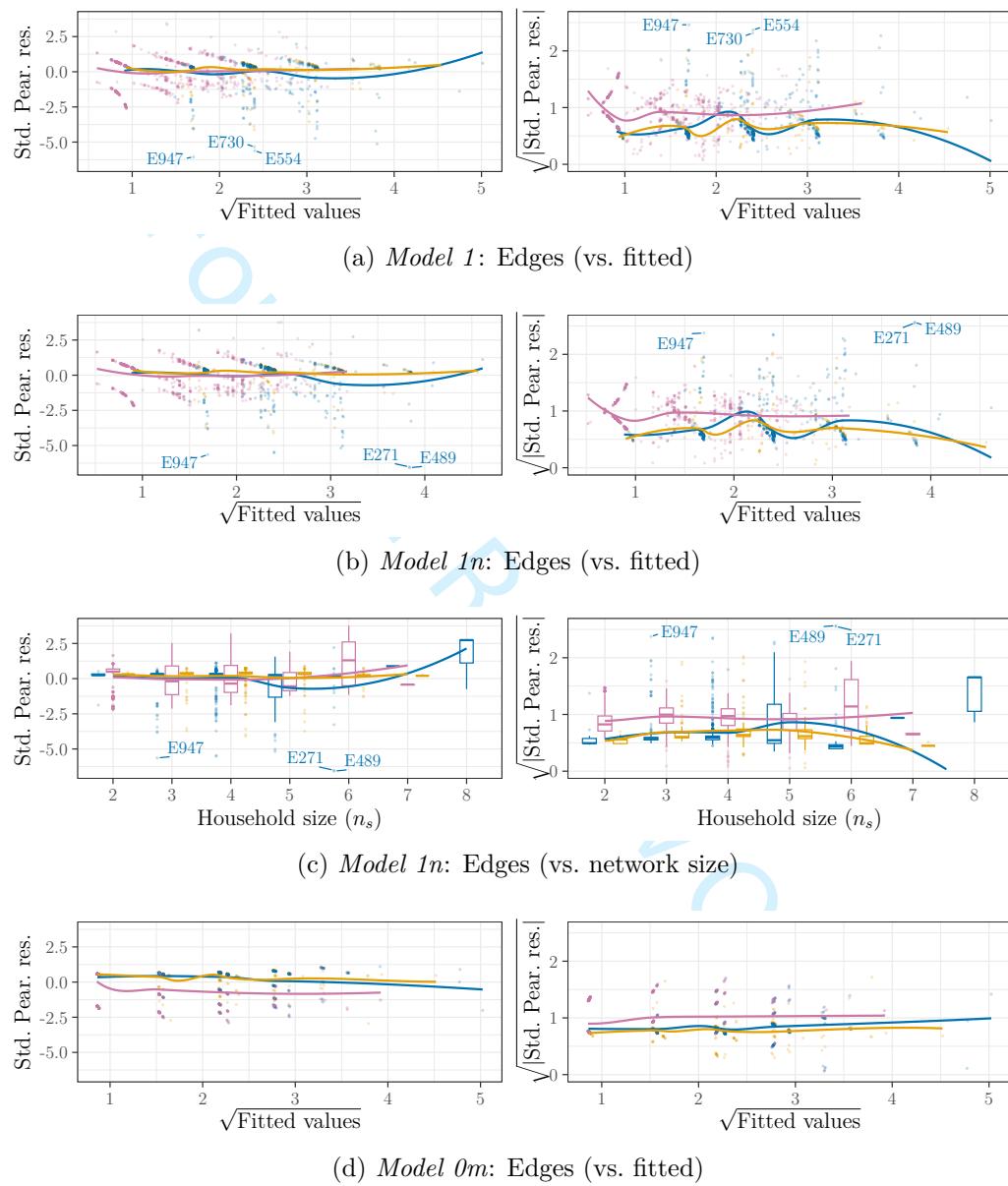


Figure E1: Pearson residual plots of network statistics for *Model 1* and its reduced models, using common vertical scales where appropriate. (Subsets: H E_{12} $E_{\bar{12}}$)

Table E2: Standard deviations of Pearson residuals for the specified network statistic under each model.

| Model | p | edges | 2-stars | triangles |
|-----------------|-----|-------|---------|-----------|
| <i>Model 0m</i> | 11 | 0.99 | 0.99 | 1.00 |
| <i>Model 1d</i> | 29 | 1.06 | 0.97 | 0.86 |
| <i>Model 1n</i> | 29 | 1.05 | 1.06 | 1.04 |
| <i>Model 1</i> | 35 | 1.00 | 0.99 | 0.98 |

(Panel (a)), *Model 1d* (Panel (b)), and *Model 0m* (Panel (c)). *Model 1* and *Model 1d*, which model age effects in similar ways, display similar overall patterns (discussed in Section 5.2 in the body of the paper), but *Model 1d* shows greater overall dispersion, consistent with the residual standard deviations discussed below. In contrast, *Model 0m*, which does not represent age effects at all, shows much clearer patterns, with residuals forming continuous curves with respect to the age, and the data subsets diverging substantially.

Pearson residual standard deviation for unaccounted-for heterogeneity In Section 4.3, we proposed a simple diagnostic for unexplained heterogeneity: that Pearson residual variances exceed 1. Residual standard deviations are given in Table E2 for *Model 1* and the three reduced models. The two models for which some standard deviations exceed 1 are *Model 1d* and *Model 1n*; it is likely that the former fails to account for heterogeneity due to dependence among the relations in the network, and the latter fails to account for heterogeneity due to network size. Despite having about a third as many free parameters, *Model 0m*, which incorporates 2-star, triangle, network size effects, and little else, shows residual standard deviations close to those of *Model 1*. This is likely because both the 2-star and the triangle statistics create positive dependence among relations in the network, absorbing the variation along the lines of Butts (2017). For small networks in particular, it might not be possible to distinguish anything but the most severe network-level heterogeneity—such as that due to network size—from more local heterogeneity.

Density error plots for network size and dataset effects Lastly, we describe an approach for assessing practical significance of lack of fit

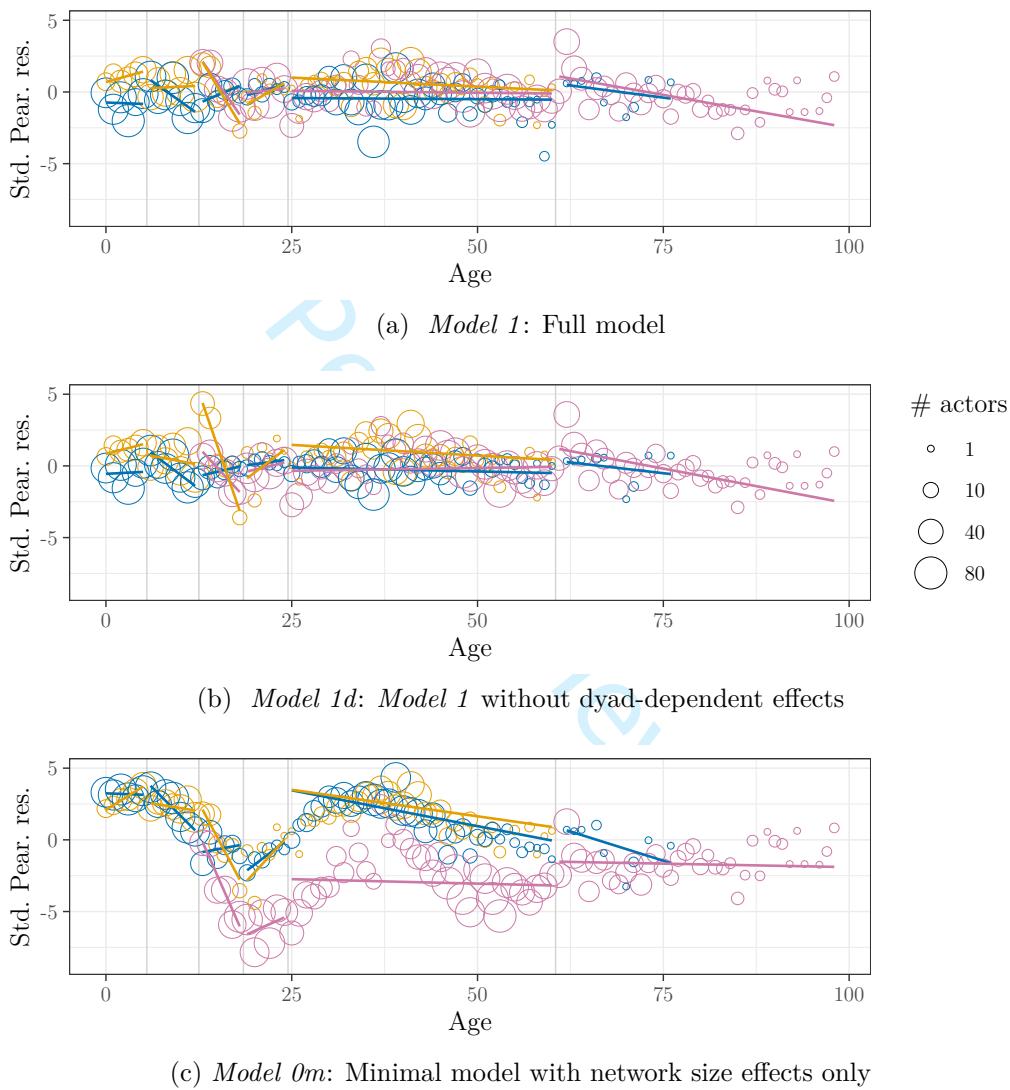


Figure E2: Pearson residual plots of edge counts broken down by actor's age and data subset. Vertical lines denote age categories. Symbol size corresponds to the number of actors it represents. (Subsets: H E_{12} $E_{\bar{12}}$)

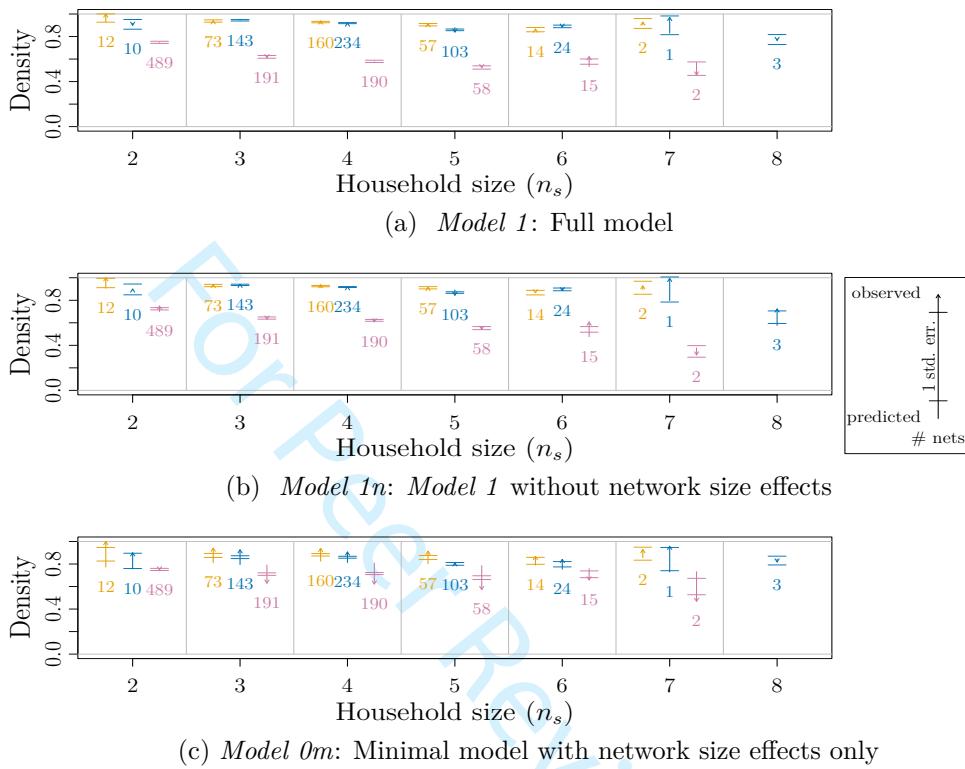


Figure E3: Average prediction errors of density. Values are averaged over the networks grouped by size and subset. (Subsets: H E_{12} $E_{\bar{12}}$)

in predicting density of contacts by contrasting the predicted and the observed/imputed densities for each combination of household size and data subset. Figure E3 provides these plots for *Model 1*, *Model 1n*, and *Model 0m*. Generally, households in H and in E_{12} tend to have similar densities for a given size, and both *Model 1* and *Model 1n* (Panels (a) and (b)) capture this. We see in Panel (b) (*Model 1n*) that removing the network size effects does not significantly affect density predictions, as the other 29 parameters adjust to compensate, but we can observe a fairly consistent trend in density errors as a function of network size: for very small and large networks, the densities are underpredicted, but for mid-sized networks, they are overpredicted. (This pattern is not found in *Model 1*'s Panel (a).) *Model 0m* (Panel (c)), as expected, shows large density prediction errors, since it does not attempt to account for household composition.

F Additional Results and Diagnostics

| | | | |
|----|-----|-----------------|----|
| 10 | F.1 | <i>Model 0m</i> | 30 |
| 11 | F.2 | <i>Model 1d</i> | 35 |
| 12 | F.3 | <i>Model 1n</i> | 41 |
| 13 | F.4 | <i>Model 0</i> | 48 |
| 14 | F.5 | <i>Model 1</i> | 55 |
| 15 | F.6 | <i>Model 1a</i> | 62 |
| 16 | F.7 | <i>Model 2</i> | 69 |
| 17 | F.8 | <i>Model 2a</i> | 76 |

A total of eight models were fit: one (0) initial, two (1 and 2) substantive, two ($1a$ and $2a$) illustrative, and three ($0m$, $1d$, and $1n$) reduced to study misspecification detection. Their motivation is described in Section 5.2 in the body of the article and in Appendix E, respectively.

Table F1 shows a side-by-side comparison of which effects were included in each model, and Table F2 gives their fit summaries (number of parameters, log-likelihood, AIC, and BIC).

In the following subsections, we provide the details for each of these models:

- full coefficient table;
- full results for common omnibus tests;
- plots of residuals vs. fitted values and network size for edge, 2-star, and triangle counts;
- plot of residuals for edges incident on actors of each age against age;
- plot of prediction errors in density by network size and subset;
- ANOVA tables for testing for unaccounted-for network size effects;
- results from regressing residuals for edges, 2-stars, and triangles on candidate network-level predictors,
- tests for dataset effect net of the model;
- sample standard deviations of Pearson residuals for some network statistics under the model; and

Table F1: Effects included in each model.

| Relationship Effect × Network-Level Effect | <i>0m</i> | <i>1d</i> | <i>1n</i> | <i>0</i> | <i>1</i> | <i>1a</i> | <i>2</i> | <i>2a</i> |
|---|-----------|-----------|-----------|----------|----------|-----------|----------|-----------|
| edges | ✓ | | | | | | | |
| × log(n_s) | ✓ | ✓ | | ✓ | ✓ | ✓ | ✓ | ✓ |
| × log ² (n_s) | ✓ | ✓ | | ✓ | ✓ | ✓ | ✓ | ✓ |
| if Brussels post code | ✓ | ✓ | ✓ | ✓ | ✓ | ✓ | ✓ | ✓ |
| if on weekend | ✓ | ✓ | ✓ | ✓ | ✓ | ✓ | ✓ | ✓ |
| if child absent | | | | | | ✓ | | |
| × log(pop. dens. in post code) | | | | | | | ✓ | |
| if city post code | | | | | | | | ✓ |
| 2-stars | ✓ | | ✓ | ✓ | ✓ | ✓ | ✓ | ✓ |
| × log(n_s) | ✓ | | ✓ | ✓ | ✓ | ✓ | ✓ | ✓ |
| × log ² (n_s) | ✓ | | ✓ | ✓ | ✓ | ✓ | ✓ | ✓ |
| triangles | ✓ | | ✓ | ✓ | ✓ | ✓ | ✓ | ✓ |
| × log(n_s) | ✓ | | ✓ | ✓ | ✓ | ✓ | ✓ | ✓ |
| × log ² (n_s) | ✓ | | ✓ | ✓ | ✓ | ✓ | ✓ | ✓ |
| Young Child with Young Child | ✓ | | ✓ | ✓ | ✓ | ✓ | ✓ | ✓ |
| Young Child with Preadolescent | ✓ | ✓ | ✓ | ✓ | ✓ | ✓ | ✓ | ✓ |
| Preadolescent with Preadolescent | ✓ | ✓ | ✓ | ✓ | ✓ | ✓ | ✓ | ✓ |
| Adolescent with Adolescent | ✓ | ✓ | ✓ | ✓ | ✓ | ✓ | ✓ | ✓ |
| Young Child with Young Adult | ✓ | ✓ | ✓ | ✓ | ✓ | ✓ | ✓ | ✓ |
| Preadolescent with Young Adult | ✓ | ✓ | ✓ | ✓ | ✓ | ✓ | ✓ | ✓ |
| Adolescent with Young Adult | ✓ | ✓ | ✓ | ✓ | ✓ | ✓ | ✓ | ✓ |
| Young Adult with Young Adult | ✓ | ✓ | ✓ | ✓ | ✓ | ✓ | ✓ | ✓ |
| Young Child with Older Female Adult | ✓ | ✓ | ✓ | ✓ | ✓ | ✓ | ✓ | ✓ |
| Preadolescent with Older Female Adult | ✓ | ✓ | ✓ | ✓ | ✓ | ✓ | ✓ | ✓ |
| Adolescent with Older Female Adult | ✓ | ✓ | ✓ | ✓ | ✓ | ✓ | ✓ | ✓ |
| Older Female Adult with Older Female Adult | ✓ | ✓ | ✓ | ✓ | ✓ | ✓ | ✓ | ✓ |
| Young Child with Older Male Adult | ✓ | ✓ | ✓ | ✓ | ✓ | ✓ | ✓ | ✓ |
| Preadolescent with Older Male Adult | ✓ | ✓ | ✓ | ✓ | ✓ | ✓ | ✓ | ✓ |
| Adolescent with Older Male Adult | ✓ | ✓ | ✓ | ✓ | ✓ | ✓ | ✓ | ✓ |
| Older Female Adult with Older Male Adult | ✓ | ✓ | ✓ | ✓ | ✓ | ✓ | ✓ | ✓ |
| if child absent | ✓ | ✓ | | ✓ | | ✓ | ✓ | ✓ |
| Older Male Adult with Older Male Adult | ✓ | ✓ | ✓ | ✓ | ✓ | ✓ | ✓ | ✓ |
| Older Female Adult with Senior | ✓ | ✓ | ✓ | ✓ | ✓ | ✓ | ✓ | ✓ |
| Older Male Adult with Senior | ✓ | ✓ | ✓ | ✓ | ✓ | ✓ | ✓ | ✓ |
| Senior with Senior | ✓ | ✓ | ✓ | ✓ | ✓ | ✓ | ✓ | ✓ |
| Adolescent with Young Child or Preadolescent | ✓ | ✓ | ✓ | ✓ | ✓ | ✓ | ✓ | ✓ |
| Young Adult with Older Adult | ✓ | ✓ | ✓ | ✓ | ✓ | ✓ | ✓ | ✓ |
| Young Child or Preadolescent with Senior | ✓ | ✓ | ✓ | ✓ | ✓ | ✓ | ✓ | ✓ |
| Adolescent or Young Adult with Senior | ✓ | ✓ | ✓ | ✓ | ✓ | ✓ | ✓ | ✓ |

Table F2: Model fit summaries. MCMC standard errors are given in parentheses.

| Model | <i>p</i> | log-likelihood | AIC | BIC |
|-----------------|----------|----------------|--------------|--------------|
| <i>Model 0m</i> | 11 | -2131.2 (0.1) | 4284.4 (0.2) | 4356.8 (0.2) |
| <i>Model 1d</i> | 29 | -2016.7 (0.0) | 4091.4 (0.0) | 4282.3 (0.0) |
| <i>Model 1n</i> | 29 | -1844.6 (0.1) | 3747.2 (0.2) | 3938.1 (0.2) |
| <i>Model 0</i> | 34 | -1823.8 (0.1) | 3715.5 (0.2) | 3939.3 (0.2) |
| <i>Model 1</i> | 35 | -1813.6 (0.1) | 3697.1 (0.2) | 3927.5 (0.2) |
| <i>Model 1a</i> | 35 | -1822.2 (0.1) | 3714.3 (0.2) | 3944.7 (0.2) |
| <i>Model 2</i> | 36 | -1812.5 (0.1) | 3696.9 (0.2) | 3933.8 (0.2) |
| <i>Model 2a</i> | 36 | -1813.1 (0.1) | 3698.2 (0.2) | 3935.1 (0.2) |

- residuals for the edge, 2-star, and triangle counts, and counts of relations for each combination of age categories older than 12, all broken down by sub-dataset.

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7 **F.1 Full results and diagnostics for *Model 0m* (the**
8 **minimal model)**

11
12 Table F3: Parameter estimates (and standard errors) for *Model 0m*.
13
14

| Relationship Effect | × Network-Level Effect | Coefficient (SE) |
|---------------------|------------------------|------------------|
| edges | | 8.05 (1.36)*** |
| | × $\log(n_s)$ | -13.68 (2.74)*** |
| | × $\log^2(n_s)$ | 5.25 (1.22)*** |
| | if Brussels post code | 0.45 (0.19)* |
| | if on weekend | 0.14 (0.04)*** |
| 2-stars | | 6.80 (0.71)*** |
| | × $\log(n_s)$ | -7.57 (0.30)*** |
| | × $\log^2(n_s)$ | 1.89 (0.13)*** |
| triangles | | -4.44 (0.96)*** |
| | × $\log(n_s)$ | 8.46 (1.36)*** |
| | × $\log^2(n_s)$ | -2.64 (0.68)*** |

29 Significance: *** ≤ 0.001 <** ≤ 0.01 <* ≤ 0.05

30
31
32
33 Table F4: Omnibus tests for selected groups of effects in *Model 0m*. Effects
34 are net of the rest of the model.
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36

| Effects | Wald χ^2 (df) | P-val. |
|----------------------------------|--------------------|---------|
| any 2-star | 1300.7 (3) | < 0.001 |
| any triangle | 145.2 (3) | < 0.001 |
| any $\log(n_s)$ or $\log^2(n_s)$ | 87776.6 (6) | < 0.001 |
| any $\log^2(n_s)$ | 451.4 (3) | < 0.001 |
| 2-star or triangle $\log^2(n_s)$ | 287.1 (2) | < 0.001 |

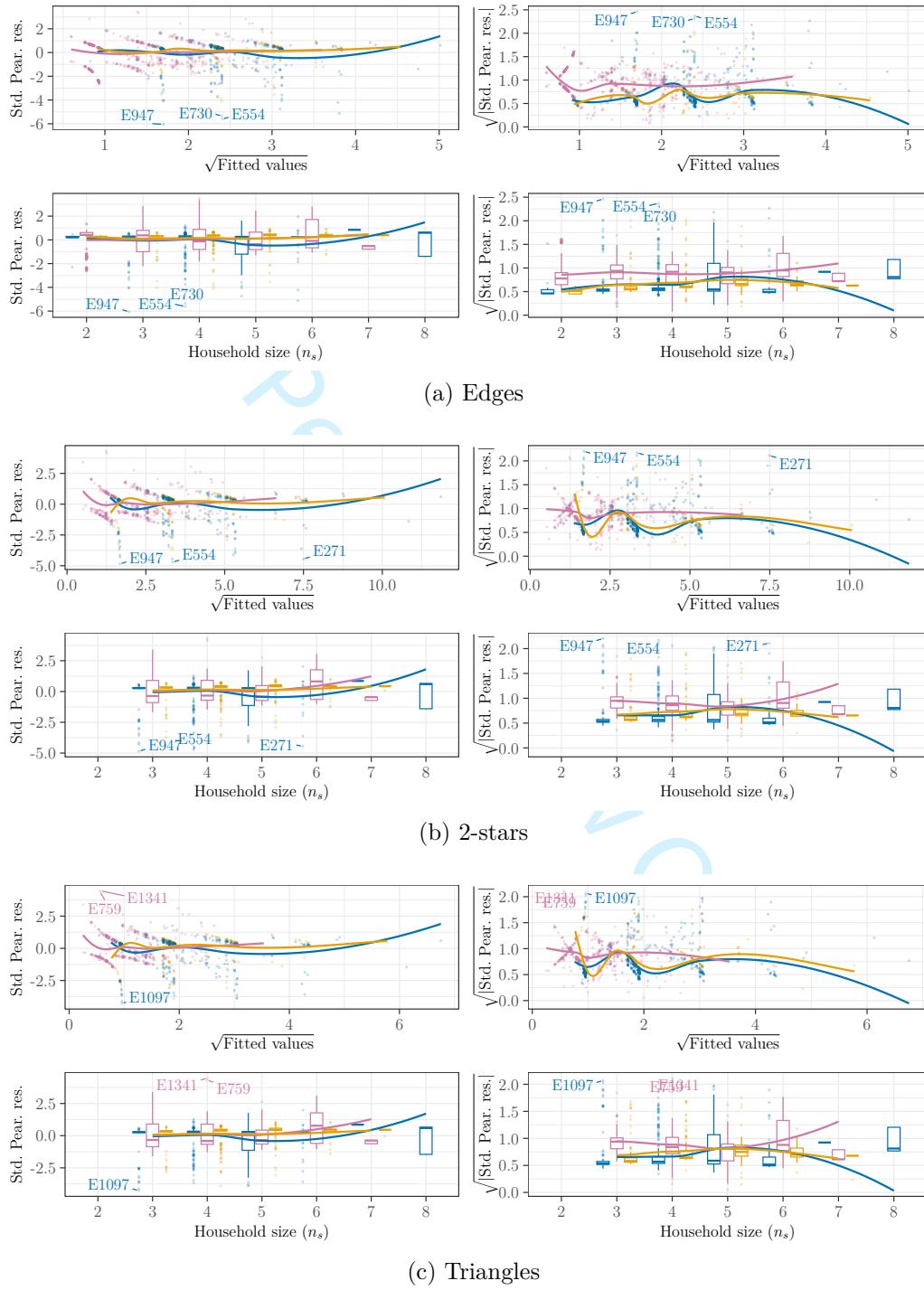


Figure F1: Residual plots of network statistics against fitted values and network size for *Model 0m*. (Subsets: H , E_{12} , $E_{\bar{12}}$)

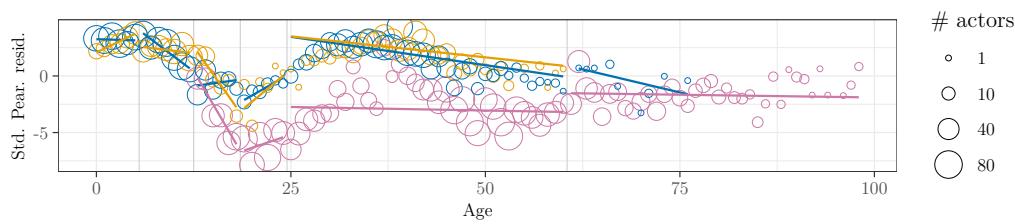


Figure F2: Residual plot for *Model 0m* of edges incident on actors of a given age against age. (Subsets: H E_{12} $E_{\bar{12}}$)

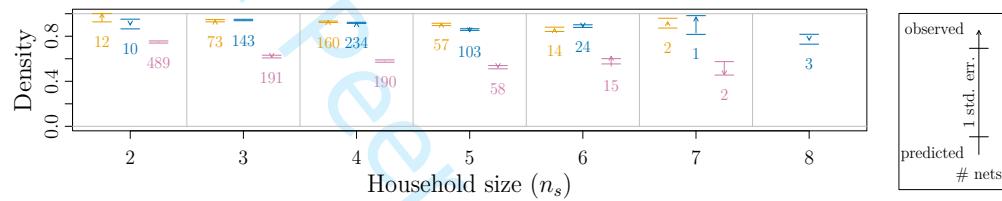


Figure F3: Average prediction errors of density in *Model 0m*. Values are averaged over the networks grouped by size and subset. (Subsets: H E_{12} $E_{\bar{12}}$)

Table F5: Analyses of variance for fitting residuals for *Model 0m* against household size (represented as a categorical predictor, with a dummy variable for each size).

| Source | df | Sum Sq. | Mean Sq. | F | P-val. |
|---------------------|------|---------|----------|------|--------|
| edges | | | | | |
| n_s (categorical) | 7 | 2.8 | 0.40 | 0.41 | 0.898 |
| Residuals | 1774 | 1752.3 | 0.99 | | |
| 2-stars | | | | | |
| n_s (categorical) | 6 | 2.8 | 0.47 | 0.47 | 0.827 |
| Residuals | 1264 | 1252.9 | 0.99 | | |
| triangles | | | | | |
| n_s (categorical) | 6 | 3.0 | 0.50 | 0.51 | 0.805 |
| Residuals | 1264 | 1260.4 | 1.00 | | |

Table F6: Regression of residuals of *Model 0m* for each network structural property on each candidate predictor.

| Relationship Effect × Network-Level Effect | Wald χ^2 (df) | P-val. |
|---|--------------------|--------|
| edges | | |
| × log(pop. dens. in post code) (linear) | 6.2 (1) | 0.013 |
| × log(pop. dens. in post code) (quadratic) | 7.1 (2) | 0.028 |
| if city post code | 1.9 (1) | 0.163 |
| if Brussels post code | 0.6 (1) | 0.450 |
| if weekend | 0.4 (1) | 0.512 |
| 2-stars | | |
| × log(pop. dens. in post code) (linear) | 5.2 (1) | 0.022 |
| × log(pop. dens. in post code) (quadratic) | 5.2 (2) | 0.073 |
| if city post code | 5.2 (1) | 0.023 |
| if Brussels post code | 0.5 (1) | 0.469 |
| if weekend | 0.0 (1) | 0.971 |
| triangles | | |
| × log(pop. dens. in post code) (linear) | 6.0 (1) | 0.014 |
| × log(pop. dens. in post code) (quadratic) | 6.0 (2) | 0.050 |
| if city post code | 5.4 (1) | 0.021 |
| if Brussels post code | 0.6 (1) | 0.428 |
| if weekend | 0.0 (1) | 0.880 |

Table F7: Tests of the null hypothesis of no effect of dataset H on the specified network statistic over and above *Model 0m*.

| | Statistic | Score χ^2 (df) | P-val. |
|---------|-----------|---------------------|----------|
| Omnibus | | 54.2 (2) | < 0.0001 |
| edges | | nonparam. | < 0.0001 |
| 2-stars | | nonparam. | < 0.0001 |

Table F8: Sample standard deviations of Pearson residuals for edge, two-star, and triangle counts in *Model 0m* for the dataset and its subsets. Values substantially greater than 1 indicate overdispersion relative to the model.

| Statistic | Overall | H | E_{12} | $E_{\bar{12}}$ |
|-----------|---------|-------|----------|----------------|
| edges | 0.993 | 0.594 | 0.719 | 1.11 |
| 2-stars | 0.995 | 0.697 | 0.751 | 1.07 |
| triangles | 0.998 | 0.762 | 0.767 | 1.05 |

Table F9: Pearson residuals for edge, two-star, triangle, and mixing counts in *Model 0m* for the dataset and its subsets. Extreme positive or negative residual values indicate that the model poorly accounts for effect of the presence of a child (the main selection criterion for the H dataset) and/or that cells in the mixing model should not have been merged. Mixing effects for which a child effect is inherent (i.e., involving a young child and/or a preadolescent but no other on one side of the relation) or which are not found in the H dataset (i.e., seniors) are also excluded.

| Effect | Overall | H | E_{12} | $E_{\bar{12}}$ |
|--|---------|-------|----------|----------------|
| edges | 0.13 | 6.81 | 6.09 | -13.55 |
| 2-stars | 0.17 | 5.52 | 4.25 | -10.96 |
| triangles | 0.17 | 5.50 | 4.18 | -10.96 |
| Adolescent with Adolescent | -4.18 | -2.84 | -0.95 | -3.36 |
| Adolescent with Young Adult | -7.86 | -3.31 | -2.33 | -6.80 |
| Young Adult with Young Adult | -7.52 | 1.35 | -2.61 | -7.82 |
| Adolescent with Older Female Adult | -1.76 | 2.53 | -0.51 | -3.55 |
| Young Adult with Older Female Adult | -10.18 | -1.42 | -2.58 | -9.80 |
| Older Female Adult with Older Female Adult | -4.88 | 0.78 | 0.41 | -5.43 |
| Adolescent with Older Male Adult | -4.11 | 1.23 | -1.09 | -5.36 |
| Young Adult with Older Male Adult | -11.08 | -1.96 | -1.53 | -10.87 |
| Older Female Adult with Older Male Adult | 3.19 | 6.63 | 7.93 | -4.97 |
| Older Male Adult with Older Male Adult | -9.39 | -1.51 | -1.67 | -9.18 |

F.2 Full results and diagnostics for *Model 1d* (dyad-independent model)

Table F10: Parameter estimates (and standard errors) for *Model 1d*.

| Relationship Effect × Network-Level Effect | Coefficient (SE) |
|---|------------------|
| edges × log(n_s) | -4.48 (0.91)*** |
| × log ² (n_s) | 1.53 (0.35)*** |
| if Brussels post code | 0.38 (0.30) |
| if on weekend | 0.34 (0.10)*** |
| Young Child with Young Child | 5.98 (0.71)*** |
| Young Child with Preadolescent | 6.24 (0.69)*** |
| Preadolescent with Preadolescent | 5.07 (0.63)*** |
| Adolescent with Adolescent | 3.27 (0.64)*** |
| Young Child with Young Adult | 5.57 (1.18)*** |
| Preadolescent with Young Adult | 2.79 (0.68)*** |
| Adolescent with Young Adult | 2.60 (0.64)*** |
| Young Adult with Young Adult | 2.75 (0.66)*** |
| Young Child with Older Female Adult | 7.01 (0.69)*** |
| Preadolescent with Older Female Adult | 6.00 (0.62)*** |
| Adolescent with Older Female Adult | 4.46 (0.61)*** |
| Older Female Adult with Older Female Adult | 3.05 (0.64)*** |
| Young Child with Older Male Adult | 6.08 (0.64)*** |
| Preadolescent with Older Male Adult | 5.44 (0.62)*** |
| Adolescent with Older Male Adult | 4.03 (0.61)*** |
| Older Female Adult with Older Male Adult | 6.54 (0.65)*** |
| if child absent | -2.57 (0.29)*** |
| Older Male Adult with Older Male Adult | 2.18 (0.64)*** |
| Older Female Adult with Senior | 3.28 (0.56)*** |
| Older Male Adult with Senior | 2.68 (0.60)*** |
| Senior with Senior | 2.93 (0.51)*** |
| Adolescent with Young Child or Preadolescent | 4.45 (0.61)*** |
| Young Adult with Older Adult | 3.21 (0.59)*** |
| Young Child or Preadolescent with Senior | 3.87 (0.92)*** |
| Adolescent or Young Adult with Senior | 5.33 (1.20)*** |

Significance: *** ≤ 0.001 <** ≤ 0.01 <* ≤ 0.05

Table F11: Omnibus tests for selected groups of effects in *Model 1d*. Effects are net of the rest of the model.

| Effects | Wald χ^2 (df) | P-val. |
|----------------------------------|--------------------|---------|
| any $\log(n_s)$ or $\log^2(n_s)$ | 32.1 (2) | < 0.001 |
| any $\log^2(n_s)$ | 19.2 (1) | < 0.001 |

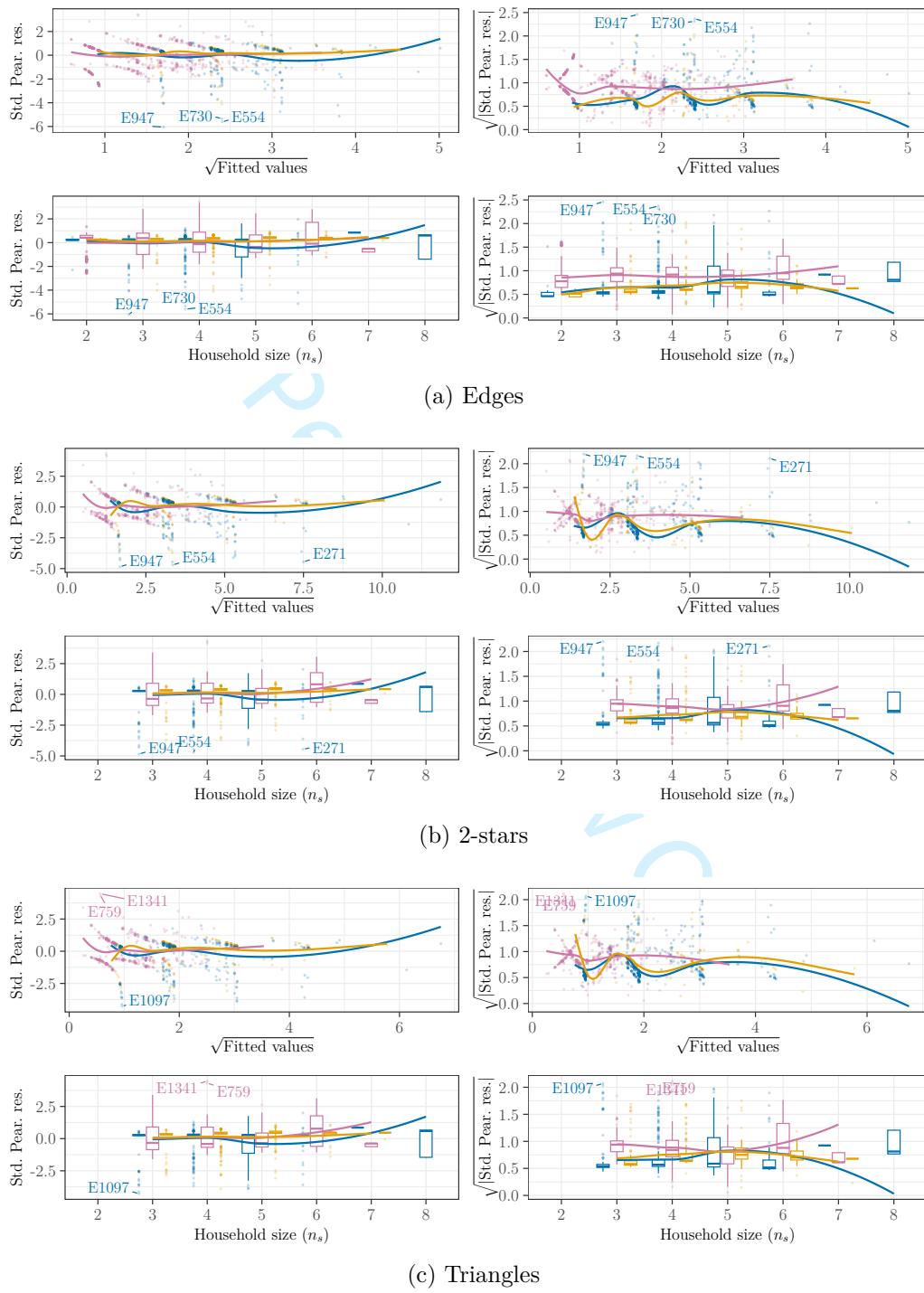


Figure F4: Residual plots of network statistics against fitted values and network size for *Model 1d*. (Subsets: E_{37}^H , E_{12} , $E_{\bar{12}}$)

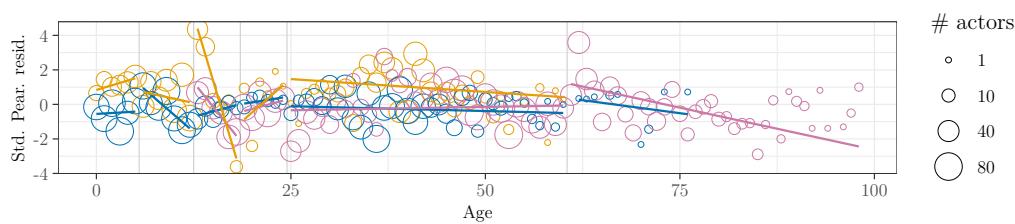


Figure F5: Residual plot for *Model 1d* of edges incident on actors of a given age against age. (Subsets: H E_{12} $E_{\bar{12}}$)

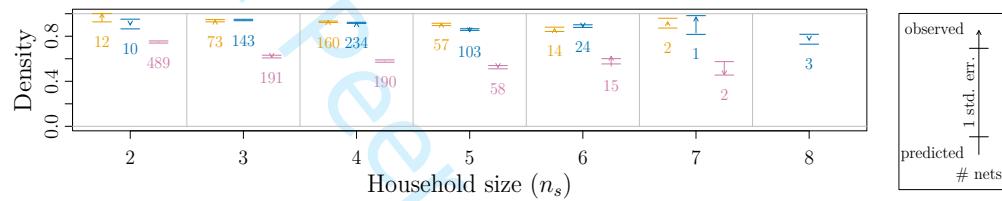


Figure F6: Average prediction errors of density in *Model 1d*. Values are averaged over the networks grouped by size and subset. (Subsets: H E_{12} $E_{\bar{12}}$)

Table F12: Analyses of variance for fitting residuals for *Model 1d* against household size (represented as a categorical predictor, with a dummy variable for each size).

| Source | df | Sum Sq. | Mean Sq. | F | P-val. |
|---------------------|------|---------|----------|-----|---------|
| edges | | | | | |
| n_s (categorical) | 7 | 8.2 | 1.17 | 1.0 | 0.404 |
| Residuals | 1774 | 1999.7 | 1.13 | | |
| 2-stars | | | | | |
| n_s (categorical) | 6 | 11.3 | 1.89 | 2.0 | 0.060 |
| Residuals | 1264 | 1183.0 | 0.94 | | |
| triangles | | | | | |
| n_s (categorical) | 6 | 20.8 | 3.46 | 4.6 | < 0.001 |
| Residuals | 1264 | 947.7 | 0.75 | | |

Table F13: Regression of residuals of *Model 1d* for each network structural property on each candidate predictor.

| Relationship Effect × Network-Level Effect | Wald χ^2 (df) | P-val. |
|---|--------------------|--------|
| edges | | |
| × log(pop. dens. in post code) (linear) | 3.7 (1) | 0.053 |
| × log(pop. dens. in post code) (quadratic) | 7.4 (2) | 0.025 |
| if city post code | 0.7 (1) | 0.387 |
| if Brussels post code | 0.0 (1) | 0.865 |
| if weekend | 2.4 (1) | 0.124 |
| 2-stars | | |
| × log(pop. dens. in post code) (linear) | 0.5 (1) | 0.477 |
| × log(pop. dens. in post code) (quadratic) | 1.1 (2) | 0.583 |
| if city post code | 0.5 (1) | 0.491 |
| if Brussels post code | 0.0 (1) | 0.890 |
| if weekend | 3.5 (1) | 0.061 |
| triangles | | |
| × log(pop. dens. in post code) (linear) | 0.3 (1) | 0.588 |
| × log(pop. dens. in post code) (quadratic) | 0.7 (2) | 0.704 |
| if city post code | 0.2 (1) | 0.648 |
| if Brussels post code | 0.0 (1) | 0.940 |
| if weekend | 3.2 (1) | 0.072 |

Table F14: Tests of the null hypothesis of no effect of dataset H on the specified network statistic over and above *Model 1d*.

| | Statistic | Score χ^2 (df) | P-val. |
|---------|-----------|---------------------|----------|
| Omnibus | | 55.3 (2) | < 0.0001 |
| edges | | nonparam. | 0.0002 |
| 2-stars | | nonparam. | < 0.0001 |

Table F15: Sample standard deviations of Pearson residuals for edge, two-star, and triangle counts in *Model 1d* for the dataset and its subsets. Values substantially greater than 1 indicate overdispersion relative to the model.

| Statistic | Overall | H | E_{12} | $E_{\bar{12}}$ |
|-----------|---------|-------|----------|----------------|
| edges | 1.062 | 1.223 | 1.051 | 1.001 |
| 2-stars | 0.968 | 1.098 | 0.916 | 0.907 |
| triangles | 0.865 | 0.999 | 0.808 | 0.796 |

Table F16: Pearson residuals for edge, two-star, triangle, and mixing counts in *Model 1d* for the dataset and its subsets. Extreme positive or negative residual values indicate that the model poorly accounts for effect of the presence of a child (the main selection criterion for the H dataset) and/or that cells in the mixing model should not have been merged. Mixing effects for which a child effect is inherent (i.e., involving a young child and/or a preadolescent but no other on one side of the relation) or which are not found in the H dataset (i.e., seniors) are also excluded.

| Effect | Overall | H | E_{12} | $E_{\bar{12}}$ |
|--|---------|-------|----------|----------------|
| edges | 0.33 | 3.66 | -0.83 | -0.99 |
| 2-stars | 2.90 | 5.30 | -0.19 | 0.31 |
| triangles | 5.25 | 6.55 | 0.54 | 1.70 |
| Adolescent with Adolescent | 0.15 | -0.10 | -0.06 | 0.26 |
| Adolescent with Young Adult | 0.08 | -0.55 | -0.12 | 0.31 |
| Young Adult with Young Adult | 0.18 | 2.82 | -0.54 | -0.43 |
| Adolescent with Older Female Adult | 0.15 | 2.59 | -0.40 | -1.36 |
| Young Adult with Older Female Adult | 0.42 | -0.03 | -0.18 | 0.50 |
| Older Female Adult with Older Female Adult | -0.02 | 1.61 | 2.02 | -0.87 |
| Adolescent with Older Male Adult | 0.12 | 2.80 | -0.57 | -1.35 |
| Young Adult with Older Male Adult | -0.61 | -0.50 | 0.91 | -0.83 |
| Older Female Adult with Older Male Adult | -0.01 | 0.16 | 0.50 | -0.24 |
| Older Male Adult with Older Male Adult | 0.07 | -0.68 | -0.22 | 0.19 |

F.3 Full results and diagnostics for *Model 1n* (*Model 1* without network size effects)

Table F17: Parameter estimates (and standard errors) for *Model 1n*.

| Relationship Effect × Network-Level Effect | Coefficient (SE) |
|---|------------------|
| edges if Brussels post code | 0.08 (0.19) |
| if on weekend | 0.15 (0.06)** |
| 2-stars | -1.04 (0.06)*** |
| triangles | 3.02 (0.17)*** |
| Young Child with Young Child | 1.06 (0.41)** |
| Young Child with Preadolescent | 1.45 (0.37)*** |
| Preadolescent with Preadolescent | 0.58 (0.23)* |
| Adolescent with Adolescent | 0.26 (0.25) |
| Young Child with Young Adult | 2.41 (1.01)* |
| Preadolescent with Young Adult | -0.06 (0.36) |
| Adolescent with Young Adult | 0.46 (0.23)* |
| Young Adult with Young Adult | 0.14 (0.28) |
| Young Child with Older Female Adult | 2.86 (0.36)*** |
| Preadolescent with Older Female Adult | 2.19 (0.21)*** |
| Adolescent with Older Female Adult | 1.24 (0.16)*** |
| Older Female Adult with Older Female Adult | -0.11 (0.28) |
| Young Child with Older Male Adult | 1.75 (0.24)*** |
| Preadolescent with Older Male Adult | 1.27 (0.18)*** |
| Adolescent with Older Male Adult | 0.62 (0.16)*** |
| Older Female Adult with Older Male Adult | 2.63 (0.27)*** |
| if child absent | -1.25 (0.29)*** |
| Older Male Adult with Older Male Adult | -1.01 (0.30)*** |
| Older Female Adult with Senior | 0.77 (0.21)*** |
| Older Male Adult with Senior | -0.12 (0.21) |
| Senior with Senior | 0.53 (0.15)*** |
| Adolescent with Young Child or Preadolescent | 0.59 (0.19)** |
| Young Adult with Older Adult | 0.39 (0.10)*** |
| Young Child or Preadolescent with Senior | 0.55 (0.46) |
| Adolescent or Young Adult with Senior | 2.26 (0.88)* |

Significance: *** ≤ 0.001 ** ≤ 0.01 * ≤ 0.05

Table F18: Omnibus tests for selected groups of effects in *Model 1n*. Effects are net of the rest of the model.

| Effects | Wald χ^2 (df) | P-val. |
|--------------|--------------------|---------|
| any 2-star | 264.6 (1) | < 0.001 |
| any triangle | 304.5 (1) | < 0.001 |

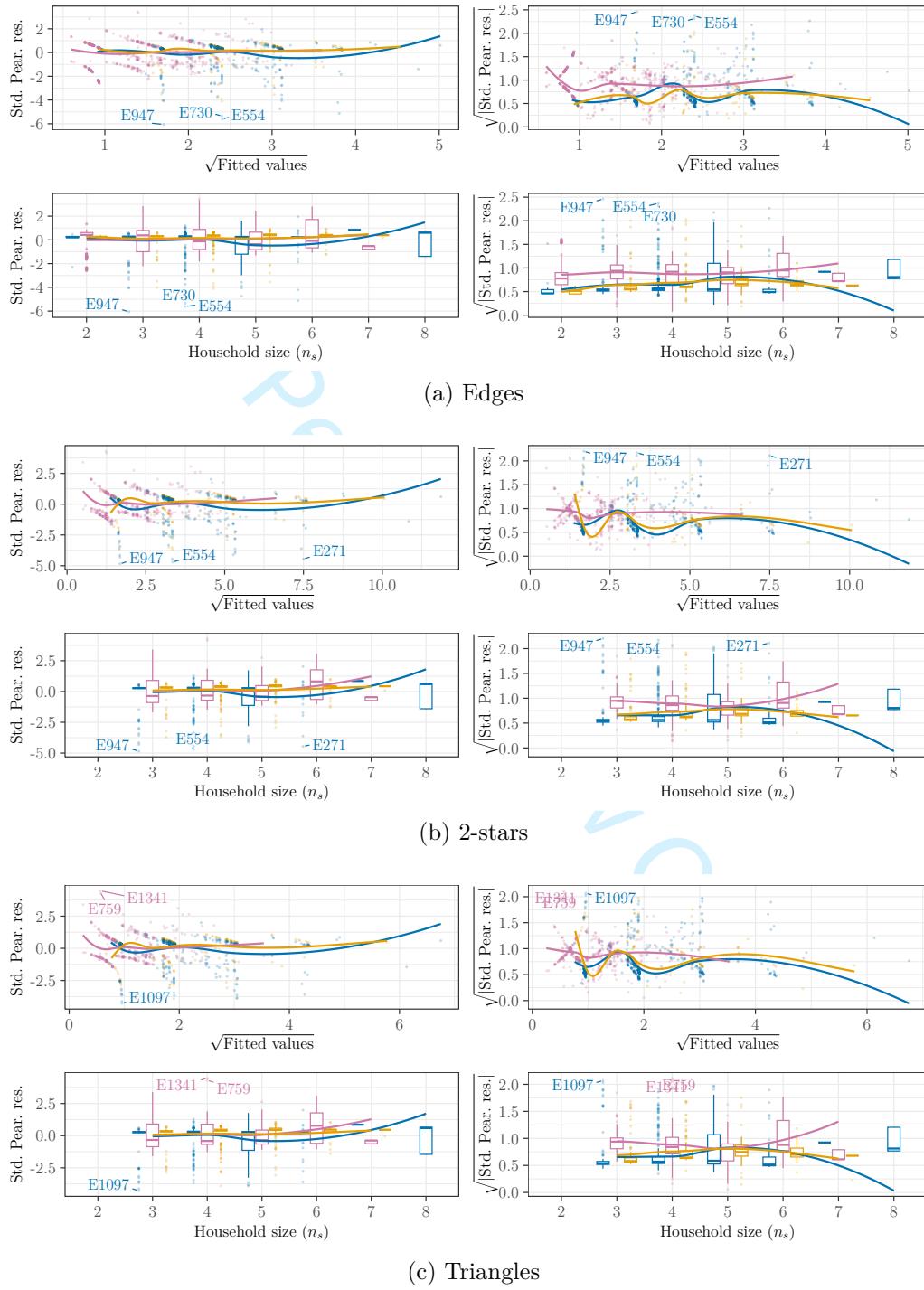


Figure F7: Residual plots of network statistics against fitted values and network size for *Model 1n*. (Subsets: E_{43}^H , E_{12} , $E_{\bar{12}}$)

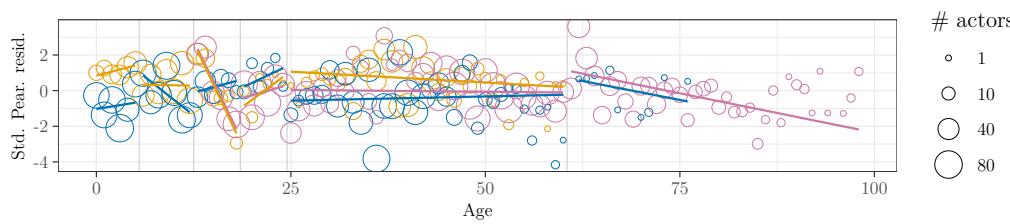


Figure F8: Residual plot for *Model 1n* of edges incident on actors of a given age against age. (Subsets: H E_{12} $E_{\bar{12}}$)

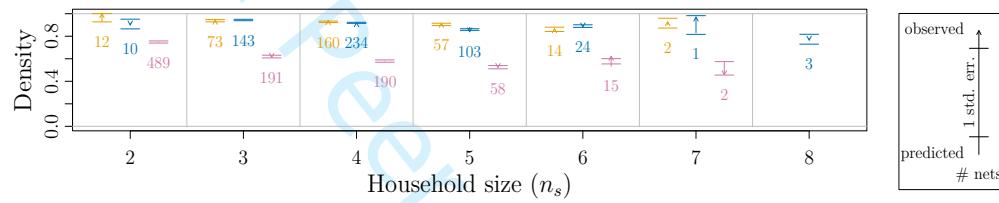


Figure F9: Average prediction errors of density in *Model 1n*. Values are averaged over the networks grouped by size and subset. (Subsets: H E_{12} $E_{\bar{12}}$)

Table F19: Analyses of variance for fitting residuals for *Model 1n* against household size (represented as a categorical predictor, with a dummy variable for each size).

| Source | df | Sum Sq. | Mean Sq. | F | P-val. |
|---------------------|------|---------|----------|-----|---------|
| edges | | | | | |
| n_s (categorical) | 7 | 36.2 | 5.2 | 4.8 | < 0.001 |
| Residuals | 1774 | 1912.1 | 1.1 | | |
| 2-stars | | | | | |
| n_s (categorical) | 6 | 30.1 | 5.0 | 4.6 | < 0.001 |
| Residuals | 1264 | 1389.2 | 1.1 | | |
| triangles | | | | | |
| n_s (categorical) | 6 | 28.5 | 4.7 | 4.5 | < 0.001 |
| Residuals | 1264 | 1341.0 | 1.1 | | |

Table F20: Regression of residuals of *Model 1n* for each network structural property on each candidate predictor.

| Relationship Effect × Network-Level Effect | Wald χ^2 (df) | P-val. |
|---|--------------------|--------|
| edges | | |
| × log(pop. dens. in post code) (linear) | 4.2 (1) | 0.041 |
| × log(pop. dens. in post code) (quadratic) | 4.6 (2) | 0.099 |
| if city post code | 1.5 (1) | 0.225 |
| if Brussels post code | 0.4 (1) | 0.511 |
| if weekend | 0.5 (1) | 0.475 |
| 2-stars | | |
| × log(pop. dens. in post code) (linear) | 1.4 (1) | 0.231 |
| × log(pop. dens. in post code) (quadratic) | 1.4 (2) | 0.488 |
| if city post code | 1.7 (1) | 0.197 |
| if Brussels post code | 0.3 (1) | 0.606 |
| if weekend | 0.5 (1) | 0.497 |
| triangles | | |
| × log(pop. dens. in post code) (linear) | 1.4 (1) | 0.236 |
| × log(pop. dens. in post code) (quadratic) | 1.4 (2) | 0.493 |
| if city post code | 1.4 (1) | 0.241 |
| if Brussels post code | 0.4 (1) | 0.531 |
| if weekend | 0.2 (1) | 0.640 |

Table F21: Tests of the null hypothesis of no effect of dataset H on the specified network statistic over and above *Model 1n*.

| Statistic | Score χ^2 (df) | P-val. |
|-----------|---------------------|--------|
| Omnibus | 4.9 (2) | 0.0855 |
| edges | nonparam. | 0.0768 |
| 2-stars | nonparam. | 0.2214 |

Table F22: Sample standard deviations of Pearson residuals for edge, two-star, and triangle counts in *Model 1n* for the dataset and its subsets. Values substantially greater than 1 indicate overdispersion relative to the model.

| Statistic | Overall | H | E_{12} | $E_{\bar{12}}$ |
|-----------|---------|-------|----------|----------------|
| edges | 1.05 | 0.835 | 1.18 | 1.02 |
| 2-stars | 1.06 | 0.837 | 1.16 | 1.07 |
| triangles | 1.04 | 0.857 | 1.12 | 1.05 |

Table F23: Pearson residuals for edge, two-star, triangle, and mixing counts in *Model 1n* for the dataset and its subsets. Extreme positive or negative residual values indicate that the model poorly accounts for effect of the presence of a child (the main selection criterion for the H dataset) and/or that cells in the mixing model should not have been merged. Mixing effects for which a child effect is inherent (i.e., involving a young child and/or a preadolescent but no other on one side of the relation) or which are not found in the H dataset (i.e., seniors) are also excluded.

| Effect | Overall | H | E_{12} | $E_{\bar{12}}$ |
|--|---------|-------|----------|----------------|
| edges | 0.22 | 1.68 | -0.85 | -0.11 |
| 2-stars | 0.54 | 1.13 | -0.37 | 0.34 |
| triangles | 0.50 | 0.95 | -0.46 | 0.52 |
| Adolescent with Adolescent | 0.37 | -1.71 | 0.96 | 0.65 |
| Adolescent with Young Adult | 0.33 | -1.78 | 1.76 | 0.05 |
| Young Adult with Young Adult | 0.13 | 1.95 | -0.48 | -0.45 |
| Adolescent with Older Female Adult | 0.13 | 2.09 | -0.60 | -0.67 |
| Young Adult with Older Female Adult | 0.52 | -0.29 | 0.47 | 0.48 |
| Older Female Adult with Older Female Adult | 0.01 | 0.86 | -0.03 | -0.12 |
| Adolescent with Older Male Adult | 0.12 | 1.56 | -0.73 | -0.40 |
| Young Adult with Older Male Adult | -0.47 | -0.97 | 1.29 | -0.65 |
| Older Female Adult with Older Male Adult | -0.04 | 0.04 | -0.06 | -0.04 |
| Older Male Adult with Older Male Adult | 0.02 | -1.80 | -2.97 | 0.72 |

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8 **F.4 Full results and diagnostics for *Model 0* (initial**
9 **model)**

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12 Table F24: Parameter estimates (and standard errors) for *Model 0*.
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| Relationship Effect × Network-Level Effect | Coefficient (SE) |
|---|------------------|
| edges × log(n_s) | -14.30 (3.01)*** |
| × log ² (n_s) | 5.72 (1.36)*** |
| if Brussels post code | 0.12 (0.19) |
| if on weekend | 0.13 (0.05)* |
| 2-stars | 0.74 (0.86) |
| × log(n_s) | -0.63 (0.47) |
| × log ² (n_s) | -0.15 (0.11) |
| triangles | 9.53 (0.93)*** |
| × log(n_s) | -8.39 (1.47)*** |
| × log ² (n_s) | 2.46 (0.76)** |
| Young Child with Young Child | 8.40 (1.55)*** |
| Young Child with Preadolescent | 8.90 (1.54)*** |
| Preadolescent with Preadolescent | 7.98 (1.51)*** |
| Adolescent with Adolescent | 7.58 (1.50)*** |
| Young Child with Young Adult | 9.59 (1.83)*** |
| Preadolescent with Young Adult | 7.19 (1.52)*** |
| Adolescent with Young Adult | 7.64 (1.51)*** |
| Young Adult with Young Adult | 7.57 (1.50)*** |
| Young Child with Older Female Adult | 10.28 (1.52)*** |
| Preadolescent with Older Female Adult | 9.66 (1.50)*** |
| Adolescent with Older Female Adult | 8.79 (1.48)*** |
| Older Female Adult with Older Female Adult | 7.23 (1.52)*** |
| Young Child with Older Male Adult | 9.13 (1.49)*** |
| Preadolescent with Older Male Adult | 8.84 (1.48)*** |
| Adolescent with Older Male Adult | 8.07 (1.48)*** |
| Older Female Adult with Older Male Adult | 9.06 (1.48)*** |
| Older Male Adult with Older Male Adult | 6.29 (1.50)*** |
| Older Female Adult with Senior | 8.06 (1.47)*** |
| Older Male Adult with Senior | 7.42 (1.50)*** |
| Senior with Senior | 7.81 (1.46)*** |
| Adolescent with Young Child or Preadolescent | 7.98 (1.49)*** |
| Young Adult with Older Adult | 7.90 (1.48)*** |
| Young Child or Preadolescent with Senior | 8.14 (1.58)*** |
| Adolescent or Young Adult with Senior | 9.75 (1.74)*** |

52 Significance: *** ≤ 0.001 < ** ≤ 0.01 < * ≤ 0.05
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Table F25: Omnibus tests for selected groups of effects in *Model 0*. Effects are net of the rest of the model.

| Effects | Wald χ^2 (df) | P-val. |
|----------------------------------|--------------------|---------|
| any 2-star | 24.2 (3) | < 0.001 |
| any triangle | 143.3 (3) | < 0.001 |
| any $\log(n_s)$ or $\log^2(n_s)$ | 3561.1 (6) | < 0.001 |
| any $\log^2(n_s)$ | 19.0 (3) | < 0.001 |
| 2-star or triangle $\log^2(n_s)$ | 10.8 (2) | 0.005 |

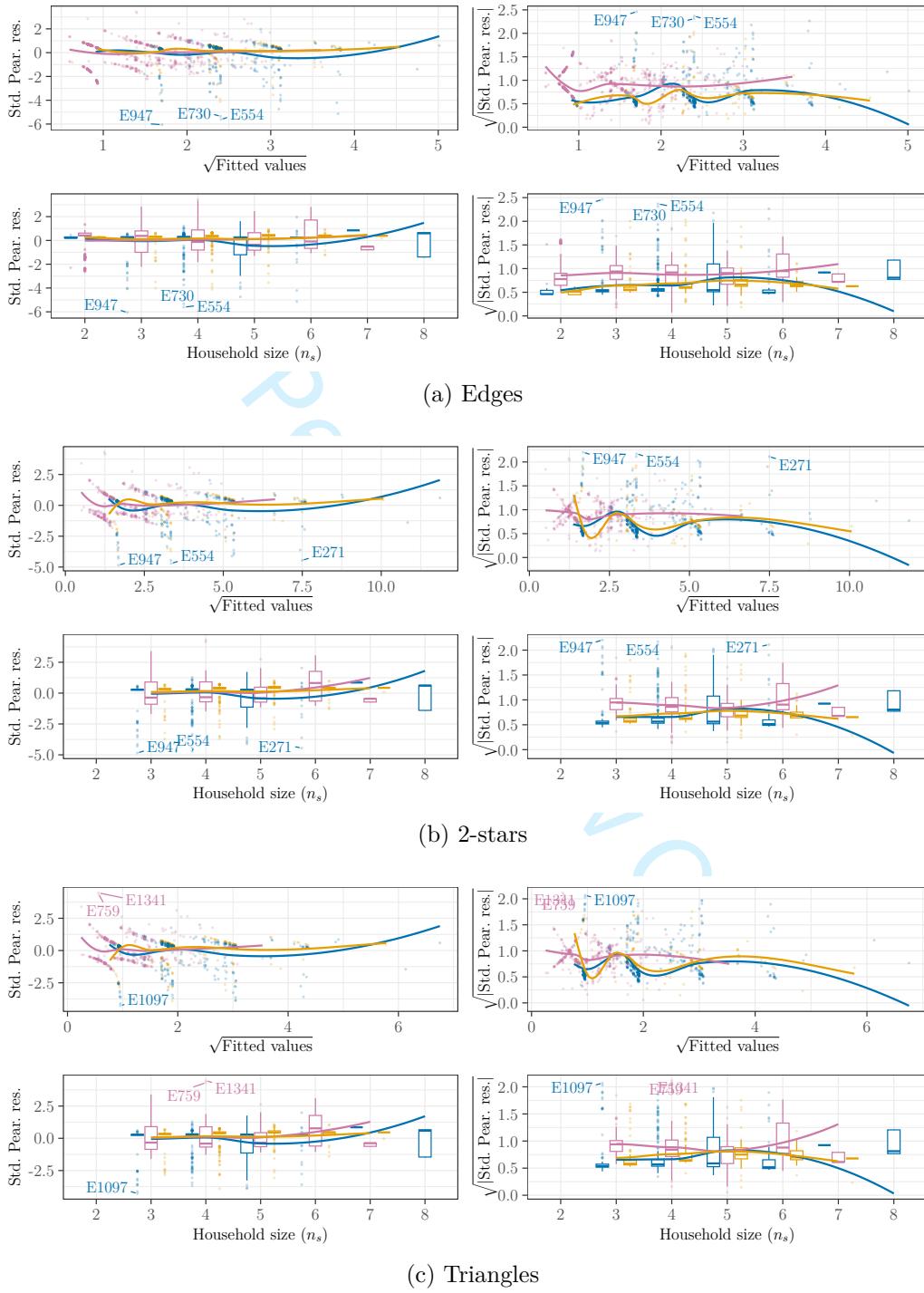


Figure F10: Residual plots of network statistics against fitted values and network size for *Model 0*. (Subsets: E_{12} $E_{\bar{12}}$)

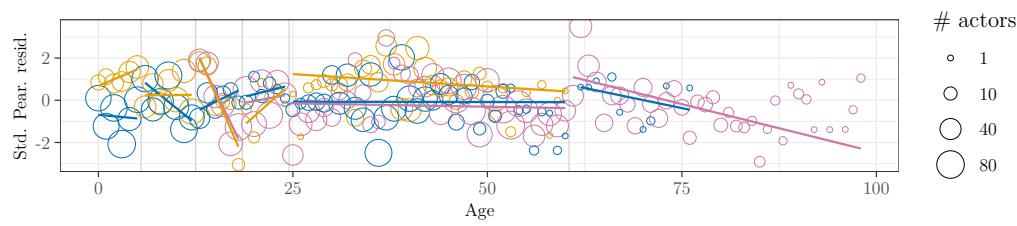


Figure F11: Residual plot for *Model 0* of edges incident on actors of a given age against age. (Subsets: H E_{12} $E_{\bar{12}}$)

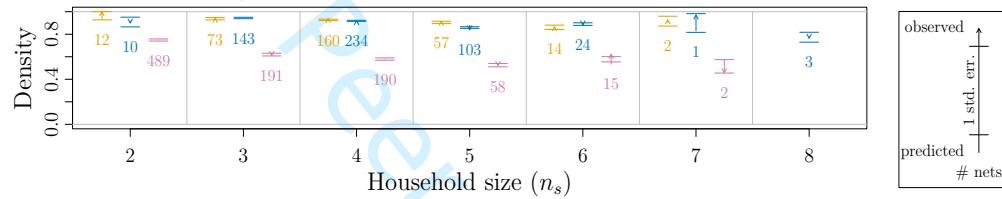


Figure F12: Average prediction errors of density in *Model 0*. Values are averaged over the networks grouped by size and subset. (Subsets: H E_{12} $E_{\bar{12}}$)

Table F26: Analyses of variance for fitting residuals for *Model 0* against household size (represented as a categorical predictor, with a dummy variable for each size).

| Source | df | Sum Sq. | Mean Sq. | F | P-val. |
|---------------------|------|---------|----------|-----|--------|
| edges | | | | | |
| n_s (categorical) | 7 | 8.9 | 1.27 | 1.3 | 0.249 |
| Residuals | 1774 | 1739.9 | 0.98 | | |
| 2-stars | | | | | |
| n_s (categorical) | 6 | 8.1 | 1.34 | 1.4 | 0.201 |
| Residuals | 1264 | 1192.0 | 0.94 | | |
| triangles | | | | | |
| n_s (categorical) | 6 | 7.3 | 1.21 | 1.3 | 0.253 |
| Residuals | 1264 | 1176.3 | 0.93 | | |

Table F27: Regression of residuals of *Model 0* for each network structural property on each candidate predictor.

| Relationship Effect × Network-Level Effect | Wald χ^2 (df) | P-val. |
|---|--------------------|--------|
| edges | | |
| × log(pop. dens. in post code) (linear) | 4.2 (1) | 0.040 |
| × log(pop. dens. in post code) (quadratic) | 5.2 (2) | 0.074 |
| if city post code | 1.1 (1) | 0.292 |
| if Brussels post code | 0.6 (1) | 0.426 |
| if weekend | 1.0 (1) | 0.320 |
| 2-stars | | |
| × log(pop. dens. in post code) (linear) | 0.7 (1) | 0.393 |
| × log(pop. dens. in post code) (quadratic) | 0.8 (2) | 0.680 |
| if city post code | 1.5 (1) | 0.222 |
| if Brussels post code | 0.1 (1) | 0.766 |
| if weekend | 0.5 (1) | 0.501 |
| triangles | | |
| × log(pop. dens. in post code) (linear) | 0.7 (1) | 0.413 |
| × log(pop. dens. in post code) (quadratic) | 0.8 (2) | 0.667 |
| if city post code | 1.4 (1) | 0.243 |
| if Brussels post code | 0.2 (1) | 0.679 |
| if weekend | 0.3 (1) | 0.564 |

Table F28: Tests of the null hypothesis of no effect of dataset *H* on the specified network statistic over and above *Model 0*.

| Statistic | Score χ^2 (df) | P-val. |
|-----------|---------------------|--------|
| Omnibus | 5.5 (2) | 0.0644 |
| edges | nonparam. | 0.0212 |
| 2-stars | nonparam. | 0.0619 |

Table F29: Sample standard deviations of Pearson residuals for edge, two-star, and triangle counts in *Model 0* for the dataset and its subsets. Values substantially greater than 1 indicate overdispersion relative to the model.

| Statistic | Overall | H | E_{12} | $E_{\bar{12}}$ |
|-----------|---------|-------|----------|----------------|
| edges | 0.991 | 0.771 | 1.022 | 1.03 |
| 2-stars | 0.972 | 0.817 | 1.002 | 1.03 |
| triangles | 0.966 | 0.861 | 0.974 | 1.02 |

Table F30: Pearson residuals for edge, two-star, triangle, and mixing counts in *Model 0* for the dataset and its subsets. Extreme positive or negative residual values indicate that the model poorly accounts for effect of the presence of a child (the main selection criterion for the H dataset) and/or that cells in the mixing model should not have been merged. Mixing effects for which a child effect is inherent (i.e., involving a young child and/or a preadolescent but no other on one side of the relation) or which are not found in the H dataset (i.e., seniors) are also excluded.

| Effect | Overall | H | E_{12} | $E_{\bar{12}}$ |
|--|---------|-------|----------|----------------|
| edges | 0.34 | 2.58 | -0.58 | -0.55 |
| 2-stars | 0.65 | 2.14 | -0.39 | -0.10 |
| triangles | 0.64 | 2.05 | -0.39 | -0.09 |
| Adolescent with Adolescent | 0.23 | -1.02 | 0.75 | 0.28 |
| Adolescent with Young Adult | 0.47 | -1.27 | 1.30 | 0.28 |
| Young Adult with Young Adult | 0.18 | 1.88 | -0.79 | -0.11 |
| Adolescent with Older Female Adult | 0.03 | 1.84 | -0.72 | -0.54 |
| Young Adult with Older Female Adult | 0.73 | -0.11 | 0.31 | 0.72 |
| Older Female Adult with Older Female Adult | -0.05 | 0.77 | 0.14 | -0.20 |
| Adolescent with Older Male Adult | 0.10 | 1.92 | -0.62 | -0.58 |
| Young Adult with Older Male Adult | -0.39 | -0.75 | 1.02 | -0.54 |
| Older Female Adult with Older Male Adult | 0.05 | 2.68 | 1.67 | -1.88 |
| Older Male Adult with Older Male Adult | 0.00 | -1.07 | -1.74 | 0.56 |

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F.5 Full results and diagnostics for *Model 1*

Table F31: Parameter estimates (and standard errors) for *Model 1*.

| Relationship Effect × Network-Level Effect | Coefficient (SE) |
|---|------------------|
| edges × log(n_s) | -14.35 (2.89)*** |
| × log ² (n_s) | 5.72 (1.29)*** |
| if Brussels post code | 0.08 (0.19) |
| if on weekend | 0.14 (0.06)* |
| 2-stars | 1.98 (0.79)* |
| × log(n_s) | -2.22 (0.41)*** |
| × log ² (n_s) | 0.36 (0.12)** |
| triangles | 5.43 (0.96)*** |
| × log(n_s) | -3.31 (1.40)* |
| × log ² (n_s) | 0.89 (0.71) |
| Young Child with Young Child | 8.63 (1.50)*** |
| Young Child with Preadolescent | 9.13 (1.49)*** |
| Preadolescent with Preadolescent | 8.21 (1.46)*** |
| Adolescent with Adolescent | 7.74 (1.44)*** |
| Young Child with Young Adult | 9.67 (1.78)*** |
| Preadolescent with Young Adult | 7.28 (1.46)*** |
| Adolescent with Young Adult | 7.76 (1.45)*** |
| Young Adult with Young Adult | 7.69 (1.45)*** |
| Young Child with Older Female Adult | 10.29 (1.46)*** |
| Preadolescent with Older Female Adult | 9.71 (1.44)*** |
| Adolescent with Older Female Adult | 8.93 (1.44)*** |
| Older Female Adult with Older Female Adult | 7.50 (1.47)*** |
| Young Child with Older Male Adult | 9.13 (1.44)*** |
| Preadolescent with Older Male Adult | 8.80 (1.43)*** |
| Adolescent with Older Male Adult | 8.24 (1.43)*** |
| Older Female Adult with Older Male Adult | 10.15 (1.45)*** |
| if child absent | -1.22 (0.30)*** |
| Older Male Adult with Older Male Adult | 6.62 (1.45)*** |
| Older Female Adult with Senior | 8.16 (1.42)*** |
| Older Male Adult with Senior | 7.55 (1.46)*** |
| Senior with Senior | 7.86 (1.41)*** |
| Adolescent with Young Child or Preadolescent | 8.11 (1.44)*** |
| Young Adult with Older Adult | 8.06 (1.43)*** |
| Young Child or Preadolescent with Senior | 8.32 (1.53)*** |
| Adolescent or Young Adult with Senior | 9.96 (1.71)*** |

Significance: *** ≤ 0.001 <** ≤ 0.01 <* ≤ 0.05

Table F32: Omnibus tests for selected groups of effects in *Model 1*. Effects are net of the rest of the model.

| Effects | Wald χ^2 (df) | P-val. |
|----------------------------------|--------------------|---------|
| any 2-star | 52.7 (3) | < 0.001 |
| any triangle | 103.1 (3) | < 0.001 |
| any $\log(n_s)$ or $\log^2(n_s)$ | 3370.3 (6) | < 0.001 |
| any $\log^2(n_s)$ | 60.8 (3) | < 0.001 |
| 2-star or triangle $\log^2(n_s)$ | 23.9 (2) | < 0.001 |

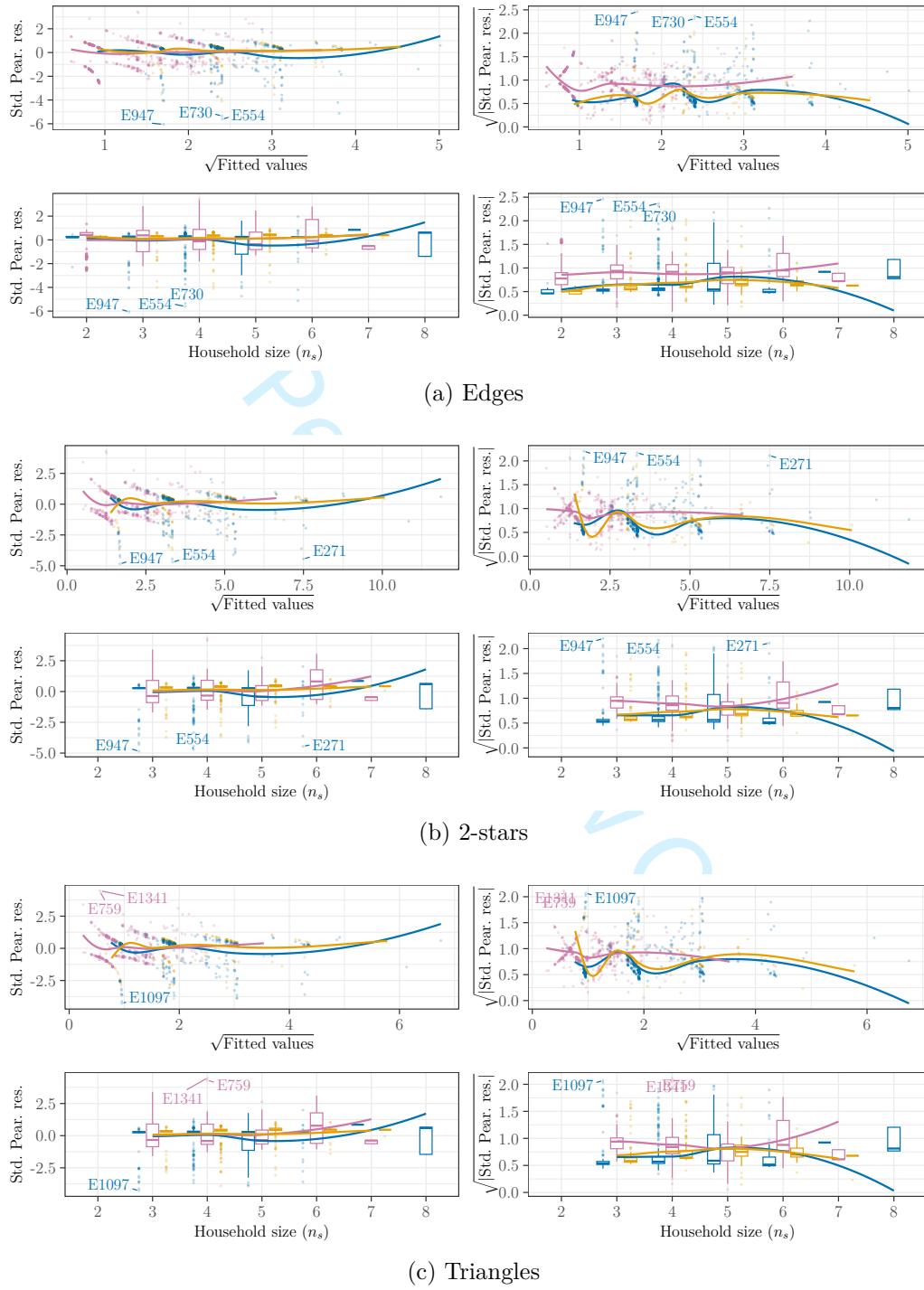


Figure F13: Residual plots of network statistics against fitted values and network size for *Model 1*. (Subsets: $\frac{H}{57}$ E_{12} $E_{\bar{12}}$)

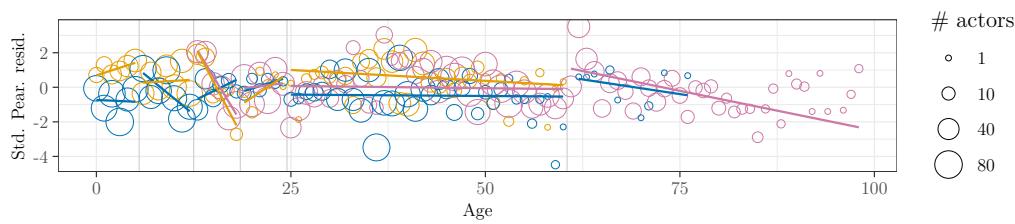


Figure F14: Residual plot for *Model 1* of edges incident on actors of a given age against age. (Subsets: H E_{12} $E_{\bar{12}}$)

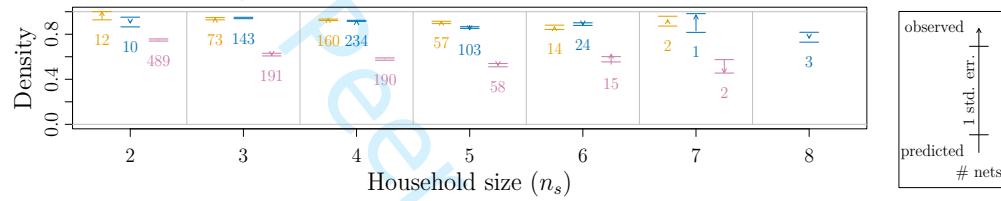


Figure F15: Average prediction errors of density in *Model 1*. Values are averaged over the networks grouped by size and subset. (Subsets: H E_{12} $E_{\bar{12}}$)

Table F33: Analyses of variance for fitting residuals for *Model 1* against household size (represented as a categorical predictor, with a dummy variable for each size).

| Source | df | Sum Sq. | Mean Sq. | F | P-val. |
|---------------------|------|---------|----------|-----|--------|
| edges | | | | | |
| n_s (categorical) | 7 | 9.5 | 1.36 | 1.4 | 0.220 |
| Residuals | 1774 | 1781.6 | 1.00 | | |
| 2-stars | | | | | |
| n_s (categorical) | 6 | 8.6 | 1.44 | 1.5 | 0.188 |
| Residuals | 1264 | 1246.0 | 0.99 | | |
| triangles | | | | | |
| n_s (categorical) | 6 | 7.7 | 1.29 | 1.3 | 0.236 |
| Residuals | 1264 | 1212.1 | 0.96 | | |

Table F34: Regression of residuals of *Model 1* for each network structural property on each candidate predictor.

| Relationship Effect × Network-Level Effect | | Wald χ^2 (df) | P-val. |
|---|--|--------------------|--------|
| edges | | | |
| × log(pop. dens. in post code) (linear) | | 4.2 (1) | 0.041 |
| × log(pop. dens. in post code) (quadratic) | | 5.2 (2) | 0.073 |
| if city post code | | 1.2 (1) | 0.270 |
| if Brussels post code | | 0.4 (1) | 0.529 |
| if weekend | | 1.2 (1) | 0.271 |
| 2-stars | | | |
| × log(pop. dens. in post code) (linear) | | 1.1 (1) | 0.304 |
| × log(pop. dens. in post code) (quadratic) | | 1.1 (2) | 0.588 |
| if city post code | | 1.5 (1) | 0.224 |
| if Brussels post code | | 0.1 (1) | 0.790 |
| if weekend | | 1.2 (1) | 0.270 |
| triangles | | | |
| × log(pop. dens. in post code) (linear) | | 1.0 (1) | 0.309 |
| × log(pop. dens. in post code) (quadratic) | | 1.0 (2) | 0.594 |
| if city post code | | 1.4 (1) | 0.235 |
| if Brussels post code | | 0.2 (1) | 0.681 |
| if weekend | | 0.8 (1) | 0.372 |

Table F35: Tests of the null hypothesis of no effect of dataset H on the specified network statistic over and above *Model 1*.

| Statistic | Score χ^2 (df) | P-val. |
|-----------|---------------------|--------|
| Omnibus | 3.1 (2) | 0.2114 |
| edges | nonparam. | 0.0839 |
| 2-stars | nonparam. | 0.1378 |

Table F36: Sample standard deviations of Pearson residuals for edge, two-star, and triangle counts in *Model 1* for the dataset and its subsets. Values substantially greater than 1 indicate overdispersion relative to the model.

| Statistic | Overall | H | E_{12} | $E_{\bar{12}}$ |
|-----------|---------|-------|----------|----------------|
| edges | 1.003 | 0.815 | 1.08 | 1.01 |
| 2-stars | 0.994 | 0.846 | 1.05 | 1.02 |
| triangles | 0.980 | 0.875 | 1.01 | 1.00 |

Table F37: Pearson residuals for edge, two-star, triangle, and mixing counts in *Model 1* for the dataset and its subsets. Extreme positive or negative residual values indicate that the model poorly accounts for effect of the presence of a child (the main selection criterion for the H dataset) and/or that cells in the mixing model should not have been merged. Mixing effects for which a child effect is inherent (i.e., involving a young child and/or a preadolescent but no other on one side of the relation) or which are not found in the H dataset (i.e., seniors) are also excluded.

| Effect | Overall | H | E_{12} | $E_{\bar{12}}$ |
|--|---------|-------|----------|----------------|
| edges | 0.24 | 1.96 | -1.40 | 0.19 |
| 2-stars | 0.38 | 1.69 | -1.17 | 0.60 |
| triangles | 0.38 | 1.64 | -1.13 | 0.59 |
| Adolescent with Adolescent | -0.02 | -1.27 | 0.18 | 0.45 |
| Adolescent with Young Adult | 0.37 | -1.47 | 0.52 | 0.53 |
| Young Adult with Young Adult | -0.05 | 1.94 | -1.07 | -0.21 |
| Adolescent with Older Female Adult | 0.01 | 1.67 | -1.26 | -0.28 |
| Young Adult with Older Female Adult | 0.60 | -0.26 | -0.09 | 0.73 |
| Older Female Adult with Older Female Adult | 0.13 | 0.78 | 0.15 | -0.01 |
| Adolescent with Older Male Adult | -0.04 | 1.40 | -1.36 | -0.18 |
| Young Adult with Older Male Adult | -0.42 | -0.86 | 0.85 | -0.53 |
| Older Female Adult with Older Male Adult | 0.09 | 0.21 | -0.04 | 0.05 |
| Older Male Adult with Older Male Adult | 0.01 | -1.22 | -1.64 | 0.52 |

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F.6 Full results and diagnostics for *Model 1a*

Table F38: Parameter estimates (and standard errors) for *Model 1a*.

| Relationship Effect × Network-Level Effect | Coefficient (SE) |
|---|------------------|
| edges × log(n_s) | -14.40 (3.54)*** |
| × log ² (n_s) | 5.79 (1.60)*** |
| if Brussels post code | 0.10 (0.19) |
| if on weekend | 0.13 (0.05)* |
| if child absent | -0.17 (0.09) |
| 2-stars | 0.51 (4.23) |
| × log(n_s) | -0.34 (4.98) |
| × log ² (n_s) | -0.25 (1.45) |
| triangles | 10.13 (10.09) |
| × log(n_s) | -9.20 (12.46) |
| × log ² (n_s) | 2.74 (3.82) |
| Young Child with Young Child | 8.50 (1.78)*** |
| Young Child with Preadolescent | 9.01 (1.78)*** |
| Preadolescent with Preadolescent | 8.09 (1.75)*** |
| Adolescent with Adolescent | 7.82 (1.74)*** |
| Young Child with Young Adult | 9.44 (1.99)*** |
| Preadolescent with Young Adult | 7.06 (1.75)*** |
| Adolescent with Young Adult | 7.89 (1.72)*** |
| Young Adult with Young Adult | 7.77 (1.75)*** |
| Young Child with Older Female Adult | 10.31 (1.75)*** |
| Preadolescent with Older Female Adult | 9.71 (1.74)*** |
| Adolescent with Older Female Adult | 8.98 (1.74)*** |
| Older Female Adult with Older Female Adult | 7.49 (1.77)*** |
| Young Child with Older Male Adult | 9.16 (1.75)*** |
| Preadolescent with Older Male Adult | 8.86 (1.72)*** |
| Adolescent with Older Male Adult | 8.27 (1.74)*** |
| Older Female Adult with Older Male Adult | 9.25 (1.73)*** |
| Older Male Adult with Older Male Adult | 6.55 (1.76)*** |
| Older Female Adult with Senior | 8.29 (1.72)*** |
| Older Male Adult with Senior | 7.65 (1.76)*** |
| Senior with Senior | 8.02 (1.71)*** |
| Adolescent with Young Child or Preadolescent | 7.94 (1.74)*** |
| Young Adult with Older Adult | 8.13 (1.74)*** |
| Young Child or Preadolescent with Senior | 8.10 (1.82)*** |
| Adolescent or Young Adult with Senior | 10.06 (2.00)*** |

Significance: *** ≤ 0.001 <** ≤ 0.01 <* ≤ 0.05

Table F39: Omnibus tests for selected groups of effects in *Model 1a*. Effects are net of the rest of the model.

| Effects | Wald χ^2 (df) | P-val. |
|----------------------------------|--------------------|---------|
| any 2-star | 23.0 (3) | < 0.001 |
| any triangle | 102.4 (3) | < 0.001 |
| any $\log(n_s)$ or $\log^2(n_s)$ | 80.6 (6) | < 0.001 |
| any $\log^2(n_s)$ | 20.4 (3) | < 0.001 |
| 2-star or triangle $\log^2(n_s)$ | 10.9 (2) | 0.004 |

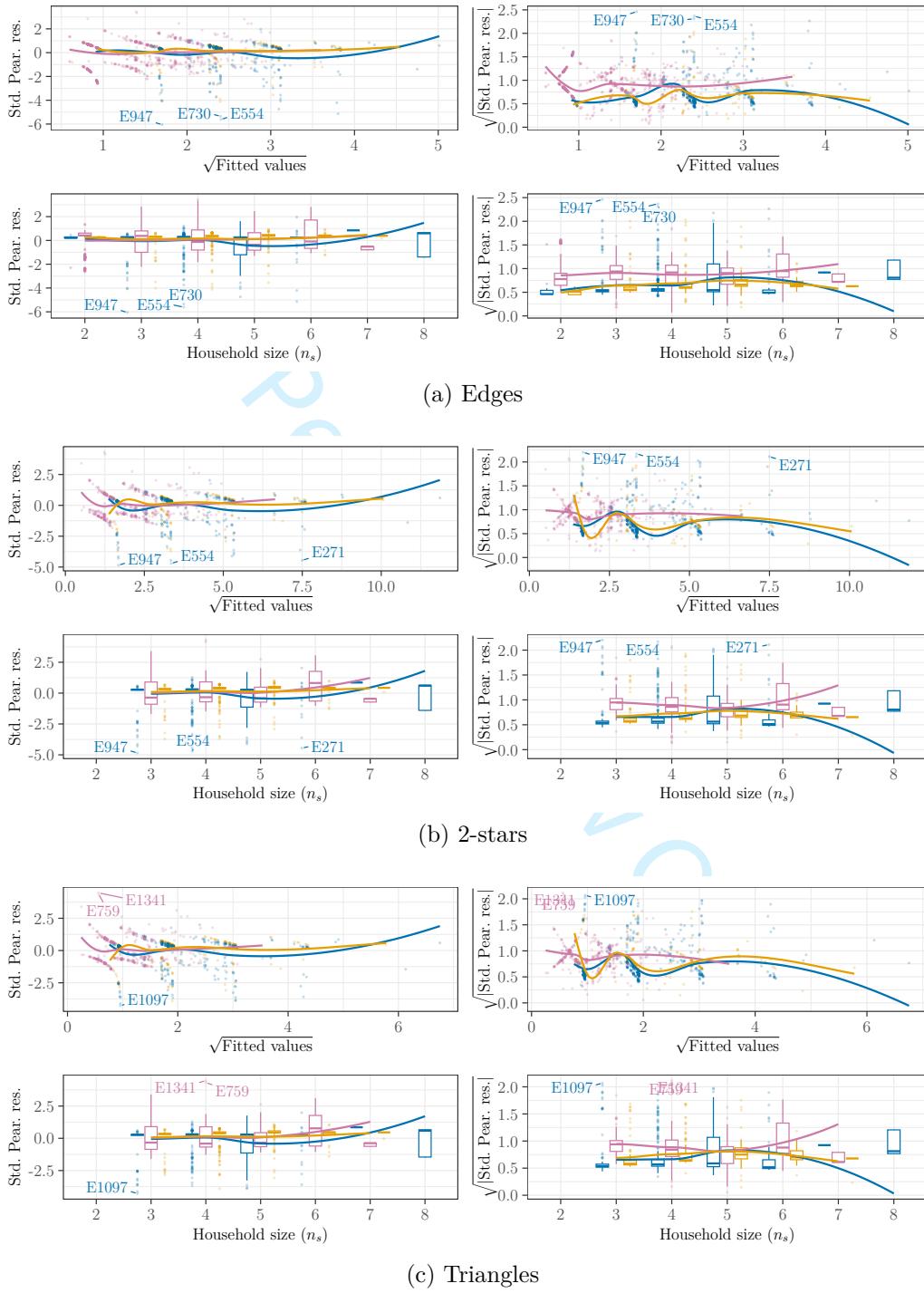


Figure F16: Residual plots of network statistics against fitted values and network size for *Model 1a*. (Subsets E_{64} , E_{12} , $E_{\bar{12}}$)

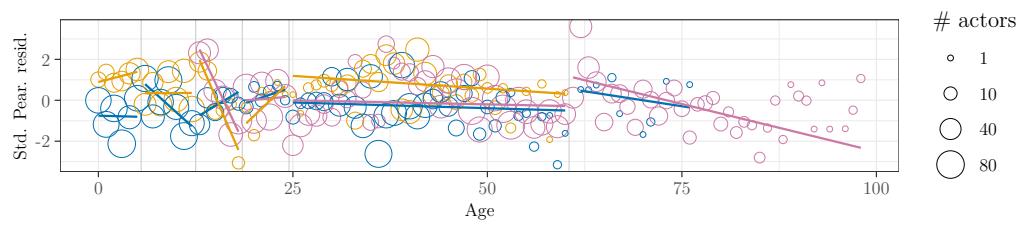


Figure F17: Residual plot for *Model 1a* of edges incident on actors of a given age against age. (Subsets: H E_{12} $E_{\bar{12}}$)

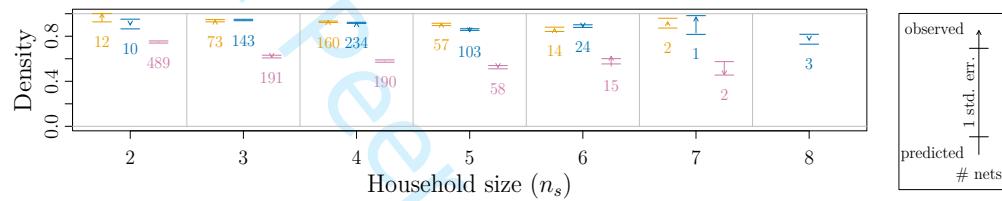


Figure F18: Average prediction errors of density in *Model 1a*. Values are averaged over the networks grouped by size and subset. (Subsets: H E_{12} $E_{\bar{12}}$)

Table F40: Analyses of variance for fitting residuals for *Model 1a* against household size (represented as a categorical predictor, with a dummy variable for each size).

| Source | df | Sum Sq. | Mean Sq. | F | P-val. |
|---------------------|------|---------|----------|-----|--------|
| edges | | | | | |
| n_s (categorical) | 7 | 9.4 | 1.34 | 1.4 | 0.219 |
| Residuals | 1774 | 1750.0 | 0.99 | | |
| 2-stars | | | | | |
| n_s (categorical) | 6 | 8.5 | 1.41 | 1.5 | 0.181 |
| Residuals | 1264 | 1202.6 | 0.95 | | |
| triangles | | | | | |
| n_s (categorical) | 6 | 7.6 | 1.27 | 1.4 | 0.230 |
| Residuals | 1264 | 1183.9 | 0.94 | | |

Table F41: Regression of residuals of *Model 1a* for each network structural property on each candidate predictor.

| Relationship Effect × Network-Level Effect | Wald χ^2 (df) | P-val. |
|---|--------------------|--------|
| edges | | |
| × log(pop. dens. in post code) (linear) | 4.1 (1) | 0.043 |
| × log(pop. dens. in post code) (quadratic) | 5.1 (2) | 0.080 |
| if city post code | 1.0 (1) | 0.312 |
| if Brussels post code | 0.6 (1) | 0.440 |
| if weekend | 1.0 (1) | 0.315 |
| 2-stars | | |
| × log(pop. dens. in post code) (linear) | 0.7 (1) | 0.399 |
| × log(pop. dens. in post code) (quadratic) | 0.8 (2) | 0.684 |
| if city post code | 1.4 (1) | 0.230 |
| if Brussels post code | 0.1 (1) | 0.769 |
| if weekend | 0.6 (1) | 0.457 |
| triangles | | |
| × log(pop. dens. in post code) (linear) | 0.7 (1) | 0.407 |
| × log(pop. dens. in post code) (quadratic) | 0.8 (2) | 0.664 |
| if city post code | 1.3 (1) | 0.249 |
| if Brussels post code | 0.2 (1) | 0.682 |
| if weekend | 0.4 (1) | 0.538 |

Table F42: Tests of the null hypothesis of no effect of dataset H on the specified network statistic over and above *Model 1a*.

| Statistic | Score χ^2 (df) | P-val. |
|-----------|---------------------|--------|
| Omnibus | 4.2 (2) | 0.1237 |
| edges | nonparam. | 0.0502 |
| 2-stars | nonparam. | 0.1160 |

Table F43: Sample standard deviations of Pearson residuals for edge, two-star, and triangle counts in *Model 1a* for the dataset and its subsets. Values substantially greater than 1 indicate overdispersion relative to the model.

| Statistic | Overall | H | E_{12} | $E_{\bar{12}}$ |
|-----------|---------|-------|----------|----------------|
| edges | 0.994 | 0.777 | 1.031 | 1.03 |
| 2-stars | 0.977 | 0.822 | 1.011 | 1.03 |
| triangles | 0.969 | 0.864 | 0.983 | 1.02 |

Table F44: Pearson residuals for edge, two-star, triangle, and mixing counts in *Model 1a* for the dataset and its subsets. Extreme positive or negative residual values indicate that the model poorly accounts for effect of the presence of a child (the main selection criterion for the H dataset) and/or that cells in the mixing model should not have been merged. Mixing effects for which a child effect is inherent (i.e., involving a young child and/or a preadolescent but no other on one side of the relation) or which are not found in the H dataset (i.e., seniors) are also excluded.

| Effect | Overall | H | E_{12} | $E_{\bar{12}}$ |
|--|---------|-------|----------|----------------|
| edges | 0.13 | 1.77 | -0.89 | -0.20 |
| 2-stars | 0.54 | 1.46 | -0.50 | 0.42 |
| triangles | 0.54 | 1.36 | -0.48 | 0.43 |
| Adolescent with Adolescent | 0.24 | -1.65 | 0.48 | 0.75 |
| Adolescent with Young Adult | 0.29 | -1.80 | 0.64 | 0.50 |
| Young Adult with Young Adult | -0.14 | 1.62 | -1.44 | -0.10 |
| Adolescent with Older Female Adult | 0.01 | 1.33 | -1.31 | 0.00 |
| Young Adult with Older Female Adult | 0.38 | -0.79 | -0.14 | 0.59 |
| Older Female Adult with Older Female Adult | 0.02 | 0.63 | -0.02 | -0.06 |
| Adolescent with Older Male Adult | 0.16 | 1.20 | -1.03 | 0.06 |
| Young Adult with Older Male Adult | -0.77 | -1.19 | 0.56 | -0.70 |
| Older Female Adult with Older Male Adult | -0.07 | 2.08 | 1.45 | -1.49 |
| Older Male Adult with Older Male Adult | -0.18 | -1.14 | -1.61 | 0.31 |

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F.7 Full results and diagnostics for *Model 2*

Table F45: Parameter estimates (and standard errors) for *Model 2*.

| Relationship Effect × Network-Level Effect | Coefficient (SE) |
|---|------------------|
| edges × log(n_s) | -13.86 (2.97)*** |
| × log ² (n_s) | 5.51 (1.33)*** |
| if Brussels post code | -0.03 (0.20) |
| × log(pop. dens. in post code) | 0.04 (0.03) |
| if on weekend | 0.13 (0.05)* |
| 2-stars | 1.12 (0.82) |
| × log(n_s) | -1.18 (0.44)** |
| × log ² (n_s) | 0.05 (0.11) |
| triangles | 7.43 (0.96)*** |
| × log(n_s) | -5.82 (1.47)*** |
| × log ² (n_s) | 1.66 (0.74)* |
| Young Child with Young Child | 8.70 (1.54)*** |
| Young Child with Preadolescent | 9.19 (1.53)*** |
| Preadolescent with Preadolescent | 8.27 (1.50)*** |
| Adolescent with Adolescent | 7.79 (1.49)*** |
| Young Child with Young Adult | 9.72 (1.83)*** |
| Preadolescent with Young Adult | 7.32 (1.50)*** |
| Adolescent with Young Adult | 7.86 (1.50)*** |
| Young Adult with Young Adult | 7.74 (1.49)*** |
| Young Child with Older Female Adult | 10.35 (1.50)*** |
| Preadolescent with Older Female Adult | 9.78 (1.49)*** |
| Adolescent with Older Female Adult | 9.00 (1.48)*** |
| Older Female Adult with Older Female Adult | 7.55 (1.51)*** |
| Young Child with Older Male Adult | 9.18 (1.49)*** |
| Preadolescent with Older Male Adult | 8.87 (1.48)*** |
| Adolescent with Older Male Adult | 8.30 (1.48)*** |
| Older Female Adult with Older Male Adult | 10.21 (1.49)*** |
| if child absent | -1.21 (0.30)*** |
| Older Male Adult with Older Male Adult | 6.70 (1.49)*** |
| Older Female Adult with Senior | 8.24 (1.47)*** |
| Older Male Adult with Senior | 7.62 (1.50)*** |
| Senior with Senior | 7.93 (1.46)*** |
| Adolescent with Young Child or Preadolescent | 8.17 (1.48)*** |
| Young Adult with Older Adult | 8.11 (1.48)*** |
| Young Child or Preadolescent with Senior | 8.38 (1.57)*** |
| Adolescent or Young Adult with Senior | 10.06 (1.77)*** |

Significance: *** ≤ 0.001 <** ≤ 0.01 <* ≤ 0.05

Table F46: Omnibus tests for selected groups of effects in *Model 2*. Effects are net of the rest of the model.

| Effects | Wald χ^2 (df) | P-val. |
|----------------------------------|--------------------|---------|
| any 2-star | 21.9 (3) | < 0.001 |
| any triangle | 114.0 (3) | < 0.001 |
| any $\log(n_s)$ or $\log^2(n_s)$ | 151.7 (6) | < 0.001 |
| any $\log^2(n_s)$ | 27.7 (3) | < 0.001 |
| 2-star or triangle $\log^2(n_s)$ | 9.9 (2) | 0.007 |

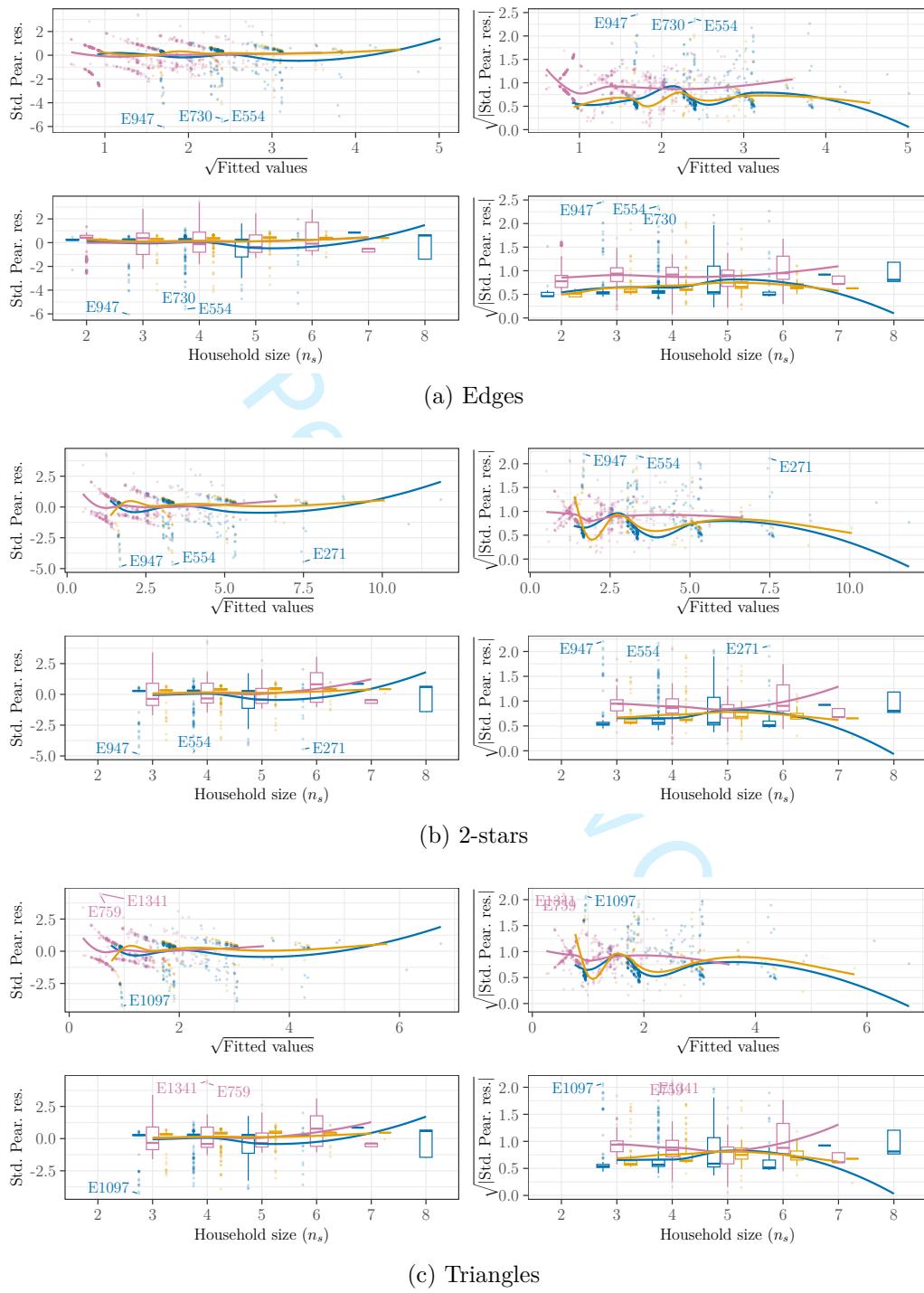


Figure F19: Residual plots of network statistics against fitted values and network size for *Model 2*. (Subsets: H E_{12} $E_{\bar{12}}$)

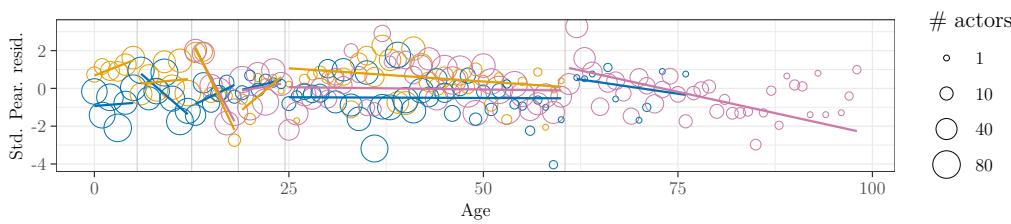


Figure F20: Residual plot for *Model 2* of edges incident on actors of a given age against age. (Subsets: H E_{12} $E_{\bar{12}}$)

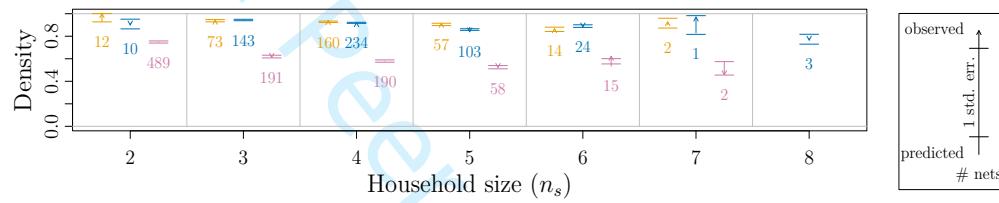


Figure F21: Average prediction errors of density in *Model 2*. Values are averaged over the networks grouped by size and subset. (Subsets: H E_{12} $E_{\bar{12}}$)

Table F47: Analyses of variance for fitting residuals for *Model 2* against household size (represented as a categorical predictor, with a dummy variable for each size).

| Source | df | Sum Sq. | Mean Sq. | F | P-val. |
|---------------------|------|---------|----------|-----|--------|
| edges | | | | | |
| n_s (categorical) | 7 | 9.2 | 1.32 | 1.3 | 0.234 |
| Residuals | 1774 | 1767.5 | 1.00 | | |
| 2-stars | | | | | |
| n_s (categorical) | 6 | 8.5 | 1.42 | 1.4 | 0.193 |
| Residuals | 1264 | 1237.6 | 0.98 | | |
| triangles | | | | | |
| n_s (categorical) | 6 | 7.7 | 1.28 | 1.3 | 0.237 |
| Residuals | 1264 | 1207.6 | 0.96 | | |

Table F48: Regression of residuals of *Model 2* for each network structural property on each candidate predictor.

| Relationship Effect × Network-Level Effect | Wald χ^2 (df) | P-val. |
|---|--------------------|--------|
| edges | | |
| × log(pop. dens. in post code) (linear) | 1.9 (1) | 0.166 |
| × log(pop. dens. in post code) (quadratic) | 2.6 (2) | 0.276 |
| if city post code | 0.6 (1) | 0.454 |
| if Brussels post code | 0.3 (1) | 0.555 |
| if weekend | 1.0 (1) | 0.321 |
| 2-stars | | |
| × log(pop. dens. in post code) (linear) | 0.3 (1) | 0.575 |
| × log(pop. dens. in post code) (quadratic) | 0.3 (2) | 0.848 |
| if city post code | 1.0 (1) | 0.325 |
| if Brussels post code | 0.0 (1) | 0.849 |
| if weekend | 0.9 (1) | 0.348 |
| triangles | | |
| × log(pop. dens. in post code) (linear) | 0.3 (1) | 0.581 |
| × log(pop. dens. in post code) (quadratic) | 0.4 (2) | 0.827 |
| if city post code | 1.0 (1) | 0.327 |
| if Brussels post code | 0.1 (1) | 0.737 |
| if weekend | 0.6 (1) | 0.440 |

Table F49: Tests of the null hypothesis of no effect of dataset H on the specified network statistic over and above *Model 2*.

| Statistic | Score χ^2 (df) | P-val. |
|-----------|---------------------|--------|
| Omnibus | 3.1 (2) | 0.2074 |
| edges | nonparam. | 0.0903 |
| 2-stars | nonparam. | 0.1558 |

Table F50: Sample standard deviations of Pearson residuals for edge, two-star, and triangle counts in *Model 2* for the dataset and its subsets. Values substantially greater than 1 indicate overdispersion relative to the model.

| Statistic | Overall | H | E_{12} | $E_{\bar{12}}$ |
|-----------|---------|-------|----------|----------------|
| edges | 0.999 | 0.814 | 1.06 | 1.02 |
| 2-stars | 0.991 | 0.846 | 1.04 | 1.02 |
| triangles | 0.979 | 0.874 | 1.01 | 1.01 |

Table F51: Pearson residuals for edge, two-star, triangle, and mixing counts in *Model 2* for the dataset and its subsets. Extreme positive or negative residual values indicate that the model poorly accounts for effect of the presence of a child (the main selection criterion for the H dataset) and/or that cells in the mixing model should not have been merged. Mixing effects for which a child effect is inherent (i.e., involving a young child and/or a preadolescent but no other on one side of the relation) or which are not found in the H dataset (i.e., seniors) are also excluded.

| Effect | Overall | H | E_{12} | $E_{\bar{12}}$ |
|--|---------|-------|----------|----------------|
| edges | 0.19 | 1.86 | -1.37 | 0.18 |
| 2-stars | 0.36 | 1.59 | -1.08 | 0.60 |
| triangles | 0.36 | 1.53 | -1.06 | 0.58 |
| Adolescent with Adolescent | 0.15 | -1.19 | 0.25 | 0.54 |
| Adolescent with Young Adult | 0.31 | -1.56 | 0.52 | 0.52 |
| Young Adult with Young Adult | 0.01 | 1.85 | -0.82 | -0.18 |
| Adolescent with Older Female Adult | 0.16 | 1.88 | -0.99 | -0.20 |
| Young Adult with Older Female Adult | 0.47 | -0.51 | -0.16 | 0.62 |
| Older Female Adult with Older Female Adult | 0.04 | 0.63 | 0.07 | -0.06 |
| Adolescent with Older Male Adult | 0.14 | 1.48 | -1.18 | -0.07 |
| Young Adult with Older Male Adult | -0.61 | -1.42 | 0.75 | -0.55 |
| Older Female Adult with Older Male Adult | 0.09 | 0.19 | -0.05 | 0.06 |
| Older Male Adult with Older Male Adult | -0.05 | -2.08 | -1.68 | 0.57 |

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F.8 Full results and diagnostics for *Model 2a*

Table F52: Parameter estimates (and standard errors) for *Model 2a*.

| Relationship Effect × Network-Level Effect | Coefficient (SE) |
|---|------------------|
| edges × log(n_s) | -14.18 (2.92)*** |
| × log ² (n_s) | 5.64 (1.31)*** |
| if Brussels post code | 0.02 (0.21) |
| if city post code | 0.07 (0.09) |
| if on weekend | 0.13 (0.06)* |
| 2-stars | 1.70 (0.81)* |
| × log(n_s) | -1.87 (0.42)*** |
| × log ² (n_s) | 0.25 (0.12)* |
| triangles | 6.16 (0.97)*** |
| × log(n_s) | -4.27 (1.42)** |
| × log ² (n_s) | 1.20 (0.72) |
| Young Child with Young Child | 8.54 (1.51)*** |
| Young Child with Preadolescent | 9.04 (1.50)*** |
| Preadolescent with Preadolescent | 8.11 (1.47)*** |
| Adolescent with Adolescent | 7.63 (1.45)*** |
| Young Child with Young Adult | 9.60 (1.79)*** |
| Preadolescent with Young Adult | 7.17 (1.48)*** |
| Adolescent with Young Adult | 7.68 (1.47)*** |
| Young Adult with Young Adult | 7.59 (1.47)*** |
| Young Child with Older Female Adult | 10.19 (1.47)*** |
| Preadolescent with Older Female Adult | 9.62 (1.46)*** |
| Adolescent with Older Female Adult | 8.84 (1.45)*** |
| Older Female Adult with Older Female Adult | 7.40 (1.48)*** |
| Young Child with Older Male Adult | 9.03 (1.46)*** |
| Preadolescent with Older Male Adult | 8.71 (1.45)*** |
| Adolescent with Older Male Adult | 8.14 (1.45)*** |
| Older Female Adult with Older Male Adult | 10.06 (1.46)*** |
| if child absent | -1.21 (0.30)*** |
| Older Male Adult with Older Male Adult | 6.52 (1.47)*** |
| Older Female Adult with Senior | 8.07 (1.44)*** |
| Older Male Adult with Senior | 7.46 (1.47)*** |
| Senior with Senior | 7.76 (1.43)*** |
| Adolescent with Young Child or Preadolescent | 8.01 (1.45)*** |
| Young Adult with Older Adult | 7.96 (1.45)*** |
| Young Child or Preadolescent with Senior | 8.23 (1.54)*** |
| Adolescent or Young Adult with Senior | 9.86 (1.72)*** |

Significance: *** ≤ 0.001 <** ≤ 0.01 <* ≤ 0.05

Table F53: Omnibus tests for selected groups of effects in *Model 2a*. Effects are net of the rest of the model.

| Effects | Wald χ^2 (df) | P-val. |
|----------------------------------|--------------------|---------|
| any 2-star | 36.1 (3) | < 0.001 |
| any triangle | 101.9 (3) | < 0.001 |
| any $\log(n_s)$ or $\log^2(n_s)$ | 1129.7 (6) | < 0.001 |
| any $\log^2(n_s)$ | 45.2 (3) | < 0.001 |
| 2-star or triangle $\log^2(n_s)$ | 17.7 (2) | < 0.001 |

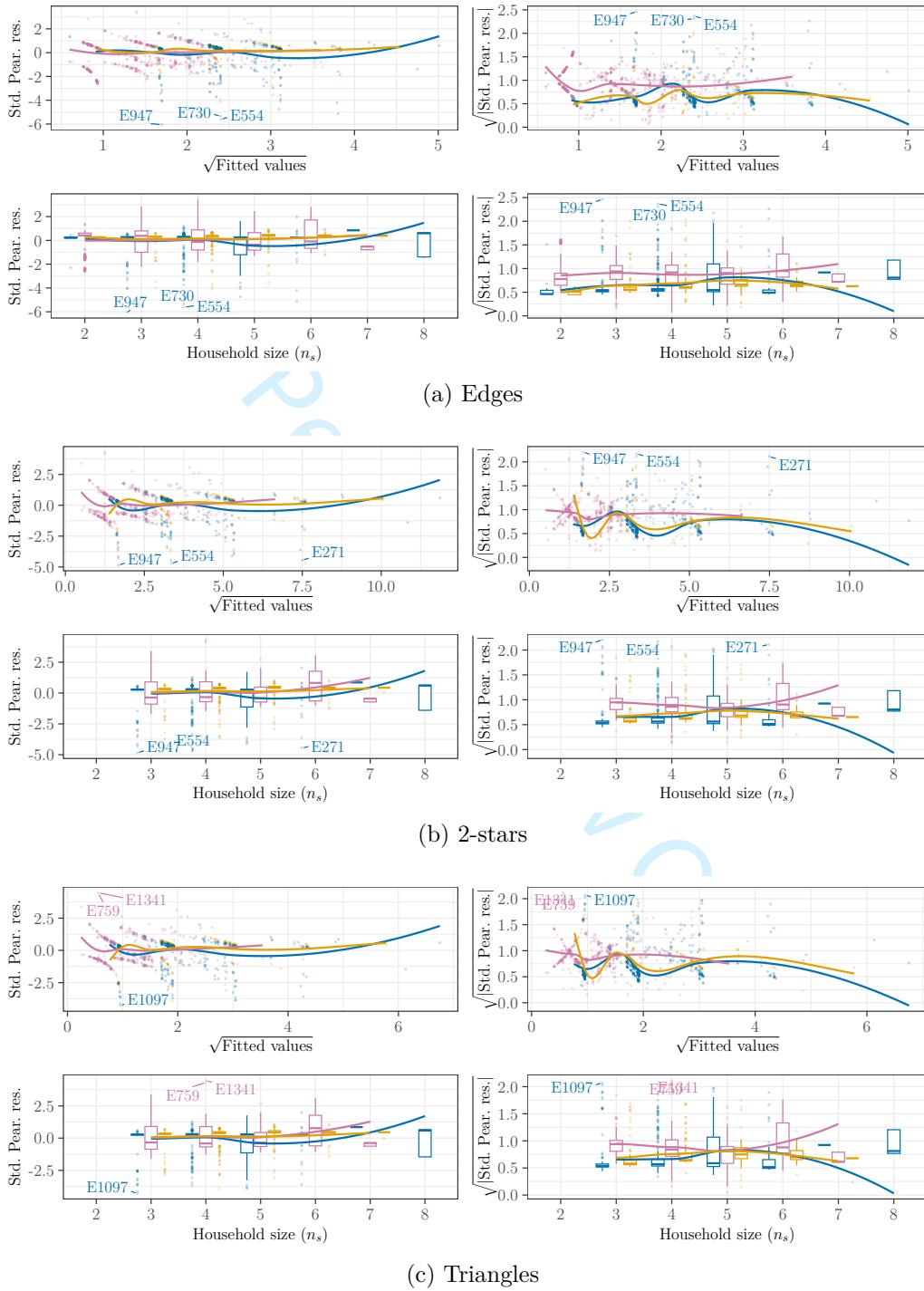


Figure F22: Residual plots of network statistics against fitted values and network size for *Model 2a*. (Subsets $\textcolor{blue}{H}$ E_{12} $E_{\bar{12}}$)
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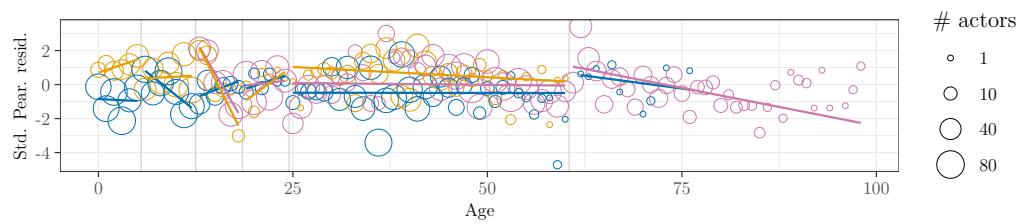


Figure F23: Residual plot for *Model 2a* of edges incident on actors of a given age against age. (Subsets: H E_{12} $E_{\bar{12}}$)

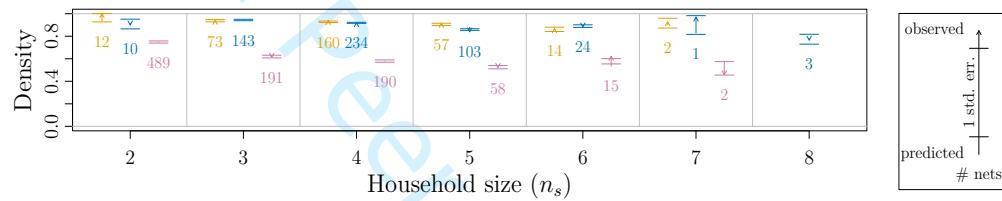


Figure F24: Average prediction errors of density in *Model 2a*. Values are averaged over the networks grouped by size and subset. (Subsets: H E_{12} $E_{\bar{12}}$)

Table F54: Analyses of variance for fitting residuals for *Model 2a* against household size (represented as a categorical predictor, with a dummy variable for each size).

| Source | df | Sum Sq. | Mean Sq. | F | P-val. |
|---------------------|------|---------|----------|-----|--------|
| edges | | | | | |
| n_s (categorical) | 7 | 9.2 | 1.32 | 1.3 | 0.234 |
| Residuals | 1774 | 1767.5 | 1.00 | | |
| 2-stars | | | | | |
| n_s (categorical) | 6 | 8.5 | 1.42 | 1.4 | 0.193 |
| Residuals | 1264 | 1237.6 | 0.98 | | |
| triangles | | | | | |
| n_s (categorical) | 6 | 7.7 | 1.28 | 1.3 | 0.237 |
| Residuals | 1264 | 1207.6 | 0.96 | | |

Table F55: Regression of residuals of *Model 2a* for each network structural property on each candidate predictor.

| Relationship Effect × Network-Level Effect | Wald χ^2 (df) | P-val. |
|---|--------------------|--------|
| edges | | |
| × log(pop. dens. in post code) (linear) | 1.9 (1) | 0.166 |
| × log(pop. dens. in post code) (quadratic) | 2.6 (2) | 0.276 |
| if city post code | 0.6 (1) | 0.454 |
| if Brussels post code | 0.3 (1) | 0.555 |
| if weekend | 1.0 (1) | 0.321 |
| 2-stars | | |
| × log(pop. dens. in post code) (linear) | 0.3 (1) | 0.575 |
| × log(pop. dens. in post code) (quadratic) | 0.3 (2) | 0.848 |
| if city post code | 1.0 (1) | 0.325 |
| if Brussels post code | 0.0 (1) | 0.849 |
| if weekend | 0.9 (1) | 0.348 |
| triangles | | |
| × log(pop. dens. in post code) (linear) | 0.3 (1) | 0.581 |
| × log(pop. dens. in post code) (quadratic) | 0.4 (2) | 0.827 |
| if city post code | 1.0 (1) | 0.327 |
| if Brussels post code | 0.1 (1) | 0.737 |
| if weekend | 0.6 (1) | 0.440 |

Table F56: Tests of the null hypothesis of no effect of dataset H on the specified network statistic over and above *Model 2a*.

| Statistic | Score χ^2 (df) | P-val. |
|-----------|---------------------|--------|
| Omnibus | 3.3 (2) | 0.1924 |
| edges | nonparam. | 0.0747 |
| 2-stars | nonparam. | 0.1201 |

Table F57: Sample standard deviations of Pearson residuals for edge, two-star, and triangle counts in *Model 2a* for the dataset and its subsets. Values substantially greater than 1 indicate overdispersion relative to the model.

| Statistic | Overall | H | E_{12} | $E_{\bar{12}}$ |
|-----------|---------|-------|----------|----------------|
| edges | 0.999 | 0.814 | 1.06 | 1.02 |
| 2-stars | 0.991 | 0.846 | 1.04 | 1.02 |
| triangles | 0.979 | 0.874 | 1.01 | 1.01 |

Table F58: Pearson residuals for edge, two-star, triangle, and mixing counts in *Model 2a* for the dataset and its subsets. Extreme positive or negative residual values indicate that the model poorly accounts for effect of the presence of a child (the main selection criterion for the H dataset) and/or that cells in the mixing model should not have been merged. Mixing effects for which a child effect is inherent (i.e., involving a young child and/or a preadolescent but no other on one side of the relation) or which are not found in the H dataset (i.e., seniors) are also excluded.

| Effect | Overall | H | E_{12} | $E_{\bar{12}}$ |
|--|---------|-------|----------|----------------|
| edges | 0.18 | 1.91 | -1.43 | 0.22 |
| 2-stars | 0.27 | 1.66 | -1.19 | 0.60 |
| triangles | 0.25 | 1.64 | -1.17 | 0.58 |
| Adolescent with Adolescent | 0.23 | -1.36 | 0.23 | 0.71 |
| Adolescent with Young Adult | 0.07 | -1.40 | 0.57 | 0.18 |
| Young Adult with Young Adult | 0.14 | 1.94 | -0.97 | -0.12 |
| Adolescent with Older Female Adult | 0.12 | 1.60 | -1.13 | -0.16 |
| Young Adult with Older Female Adult | 0.58 | -0.22 | 0.09 | 0.65 |
| Older Female Adult with Older Female Adult | -0.02 | 0.61 | -0.01 | -0.10 |
| Adolescent with Older Male Adult | 0.15 | 1.49 | -1.22 | 0.01 |
| Young Adult with Older Male Adult | -0.50 | -0.94 | 0.87 | -0.57 |
| Older Female Adult with Older Male Adult | 0.13 | 0.09 | -0.08 | 0.14 |
| Older Male Adult with Older Male Adult | -0.06 | -1.55 | -2.06 | 0.53 |

References

- Butts, C. T. 2017. "Baseline Mixture Models for Social Networks," arXiv: 1710.02773v1.
- Hoang, T. V., P. Coletti, Y. W. Kifle, K. V. Kerckhove, S. Vercruyse, L. Willem, P. Beutels, and N. Hens. 2021. "Close Contact Infection Dynamics Over Time: Insights from a Second Large-scale Social Contact Survey in Flanders, Belgium, in 2010–2011." *BMC Infectious Diseases* 21 (1): 274.
- Krivitsky, P. N. 2012. "Exponential-family Random Graph Models for Valued Networks." *Electronic Journal of Statistics* 6:1100–1128.
- Krivitsky, P. N., M. S. Handcock, and M. Morris. 2011. "Adjusting for Network Size and Composition Effects in Exponential-family Random Graph Models." *Statistical Methodology* 8 (4): 319–339.

JASA ACS Reproducibility Author Contribution Checklist

The submission includes a file `data_and_code.zip` which contains the data and the code referenced here.
R functions and classes are labelled using the convention of `<package>::<function>()` or `<pacakge>::<class>`.
R code in this document is provided in a runnable form in the accompanying `README.R` file.

Data

Abstract

1. `H_networks.touch.rds` and `E_networks.touch.rds` lists of individual `network::network` objects
21 containing the data.
2. `HHNet.rds`: a `network::network` object with metadata intended to be used in an `ergm::ergm()` call
3. `subdatasets.rds`: an R factor object indicating to which sub-dataset (Household, Egocentric with
24 child, Egocentric without child) each network belongs; used in diagnostics.
4. A collection of RDS files containing ERGM fits and diagnostic simulation results

Availability

Included with submission.

Description (Mandatory if data available)

1. Data

Permissions Data are the result of social contact surveys conducted on behalf of the research group.

Licensing information Data are available under Creative Commons Attribution–NonCommercial 4.0 license.

Link to data `H_networks.touch.rds`, `E_networks.touch.rds`, `HHNet.rds`, and `subdatasets.rds` can be found in the supplementary materials.

42 Data provenance, including identifier or link to original data if different than above

- 44 • The raw survey data from which the E dataset was constructed can be found at BLINDED.
- 45 • The original H dataset will similarly be made available on Zenodo on acceptance of the manuscript.

File format RDS (R's storage format for individual objects)

Metadata (including data dictionary) The data dictionary for the vertex attributes of the `HHNet.rds` network object can be found in the `data_dictionary.pdf` file.

Version information Version 1.0

55 2. Fit objects and diagnostics

Permissions Data are generated by the provided code from the provided dataset.

1
2
3 **Licensing information** As dataset.
4
5 **File format** RDS (R's storage format for individual objects)
6
7 **Metadata** Results and diagnostics for *Model <X>* can be found in the `Model<X>.results` subdirectory of
8 analysis. The format can be found by looking up R help for the respective function that produced it.
9
10 `fit.rds` an `ergm::ergm` object containing the fit.
11
12 `gofN_e2t.rds` a `ergm.multi::gofN` object containing Pearson residuals for the edges, 2-stars, and triangles
13 statistics for each network.
14
15 `sim_age.rds` a `gofN`-like object containing Pearson residuals for the number of ties incident on an actor
16 with a given age for ages 0–100.
17
18 `sim_mix.rds` a `gofN`-like object containing Pearson residuals for the number of ties for each combination of
19 age categories.
20
21 `simtest.rds` a `coda::mcmc.list` object containing simulated edge count and 2-star statistics pooled for all
22 H dataset networks.
23
24
25 **Version information** Having been generated from the datasets, these files are unversioned.

Code

Abstract

1. Three (3) R package source tarballs, two public (`statnet.common`, `ergm`), one blinded (`ergm.multi`).
2. R scripts to construct the dataset from a list of networks and set appropriate metadata.
3. R scripts to fit the models and run their diagnostic simulations.
4. R files to produce nonstandard diagnostics `test_dataset.R`, `density_error.R`, and `plot_age_resid.R`.

Description

1. R packages

2 **How delivered** Source code tarball form created by R CMD build. Note that they require compilation,
3 and installing them on Windows or MacOS may require installing development tools.
4
5

6 **Licensing information** GPL 3 with attribution clause
7
8

9 **Location** On GitHub: BLINDED<PACKAGE>; eventually on CRAN.
10
11

12 **Version information** Versions provided in tarball form are as follows:
13
14

15 `ergm` BLINDED
16
17 `statnet.common` BLINDED
18
19 `ergm.multi` BLINDED
20
21

2. R scripts to construct the dataset from a list of networks and set appropriate metadata

22 **How delivered** R source files in the `data` subdirectory.
23
24

25 **Licensing information** MIT license
26
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1
2
3 **Location** Included in the supplement
4

5 **Version information** No relevant versioning
6

7 **3. R scripts to fit the models and run diagnostic simulations**
8

9 **How delivered** R source files in the analysis subdirectory. See the section on reproducibility for usage
10 instructions.
11

12 **Licensing information** MIT license
13

14 **Location** Included in the supplement
15

16 **Version information** No relevant versioning
17

18 **4. Implementations of nonstandard diagnostics**
19

20 **How delivered** R source files in the analysis subdirectory. See the section on reproducibility for usage
21 instructions.
22

23 **Licensing information** MIT license
24

25 **Location** Included in the supplement
26

27 **Version information** No relevant versioning
28

29 **Optional Information**
30

31 **Hardware requirements**
32

33 There are no special hardware requirements. As these analyses involve large networks with high missingness
34 fractions, a computing cluster is helpful but not critical.
35

36 **Supporting software requirements**
37

38 Reproducing the analysis requires a number of packages from CRAN and a number of development versions
39 of Statnet Project packages, available on GitHub, as well as the experimental package `ergm.multi`. Some of
40 the other packages are required to process and format the results.
41

42 We recommend the following R commands to install the required packages.
43

```
install.packages("remotes")
library(remotes)
remotes::install_cran(c('broom', 'coda', 'dplyr', 'ggplot2', 'here', 'kableExtra',
                      'knitr', 'purrr', 'remotes', 'sessioninfo', 'stringr', 'texreg',
                      'tibble', 'tidyverse', 'xtable', 'ggrepel', 'gridExtra'))
remotes::install_github(c("statnet/statnet.common", "statnet/ergm", "statnet/ergm.multi"))
```

50 An example setup is provided below:
51

- R version 4.2.2 Patched (2022-11-10 r83330), x86_64-pc-linux-gnu
- Running under: Debian GNU/Linux bookworm/sid
- Matrix products: default
- BLAS: /usr/lib/x86_64-linux-gnublas/libblas.so.3.11.0

- LAPACK: /usr/lib/x86_64-linux-gnu/lapack/liblapack.so.3.11.0
- Base packages: base, datasets, graphics, grDevices, methods, stats, utils
- Other packages: broom 1.0.3, coda 0.19-4, dplyr 1.1.0, ergm 4.4-7158, ergm.multi 0.2.0-4102, forcats 1.0.0, ggplot2 3.4.1, ggrepel 0.9.3, gridExtra 2.3, here 1.0.1, kableExtra 1.3.4, knitr 1.42, network 1.18.1, purrr 1.0.1, readr 2.1.4, remotes 2.4.2, sessioninfo 1.2.2, statnet.common 4.8.0-411, stringr 1.5.0, texreg 1.38.6, tibble 3.1.8, tidyverse 1.3.2, xtable 1.8-4
- Loaded via a namespace (and not attached): assertthat 0.2.1, backports 1.4.1, cachem 1.0.6, cellranger 1.1.0, cli 3.6.0, codetools 0.2-19, colorspace 2.1-0, compiler 4.2.2, crayon 1.5.2, DBI 1.1.3, dbplyr 2.3.0, DEoptimR 1.0-11, digest 0.6.31, ellipsis 0.3.2, evaluate 0.20, fansi 1.0.4, fastmap 1.1.0, fs 1.6.1, gargle 1.3.0, generics 0.1.3, glue 1.6.2, googledrive 2.0.0, googlesheets4 1.0.1, grid 4.2.2, gtable 0.3.1, haven 2.5.1, hms 1.1.2, htmltools 0.5.4, httr 1.4.4, jsonlite 1.8.4, lattice 0.20-45, lifecycle 1.0.3, lpSolveAPI 5.5.2.0-17.9, lubridate 1.9.2, magrittr 2.0.3, MASS 7.3-58.2, Matrix 1.5-3, memoise 2.0.1, modelr 0.1.10, munsell 0.5.0, parallel 4.2.2, pillar 1.8.1, pkgconfig 2.0.3, R6 2.5.1, rbibutils 2.2.13, Rcpp 1.0.10, Rdpack 2.4, readxl 1.4.2, reprex 2.0.2, rlang 1.0.6, rle 0.9.2-234, rmarkdown 2.20, robustbase 0.95-0, rprojroot 2.0.3, rstudioapi 0.14, rvest 1.0.3, scales 1.2.1, stringi 1.7.12, svglite 2.1.1, systemfonts 1.0.4, tidyselect 1.2.0, timechange 0.2.0, tools 4.2.2, trust 0.1-8, tzdb 0.3.0, utf8 1.2.3, vctrs 0.5.2, viridisLite 0.4.1, webshot 0.5.4, withr 2.5.0, xfun 0.37, xml2 1.3.3, yaml 2.3.7

Instructions for Use

Reproducibility

The following assumes that the requisite packages have been installed and loaded, and the data and source files are readily available to R.

Rerunning the fitting and the diagnostics

A model is fit and diagnostic simulations are performed by executing a model runner R script (named `run_Model<X>.R`), typically as a batch job on a cluster. This script will specify the model formula and define model-specific variables, then execute the workhorse script `fit_and_run_diags.R`, which in turn will create an output subdirectory `Model<X>_results` and place the files containing the model fit and various diagnostic simulation results there. These result files are included as data item 2 above.

`ergm` and `ergm.multi` are evolving packages. Although backwards compatibility of the user interface is generally maintained, the same random seed might not always reproduce the same final results for different versions of `ergm`, and very few guarantees can be made if parallel processing is used without careful and system-specific initialisation. Thus, while the ultimate results (coefficients, standard errors, measures of fit, diagnostic plots, etc.) will be very similar from version to version and from run to run, they will not be completely identical.

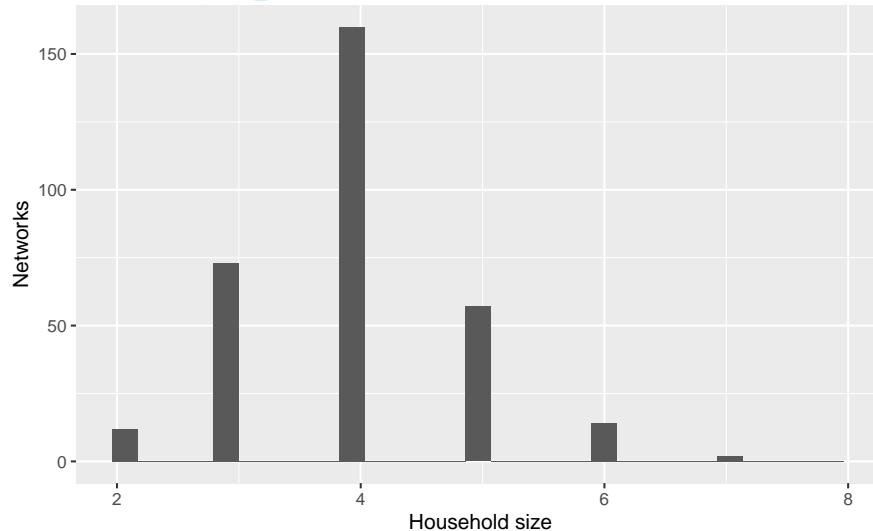
Reproducing summaries and graphics

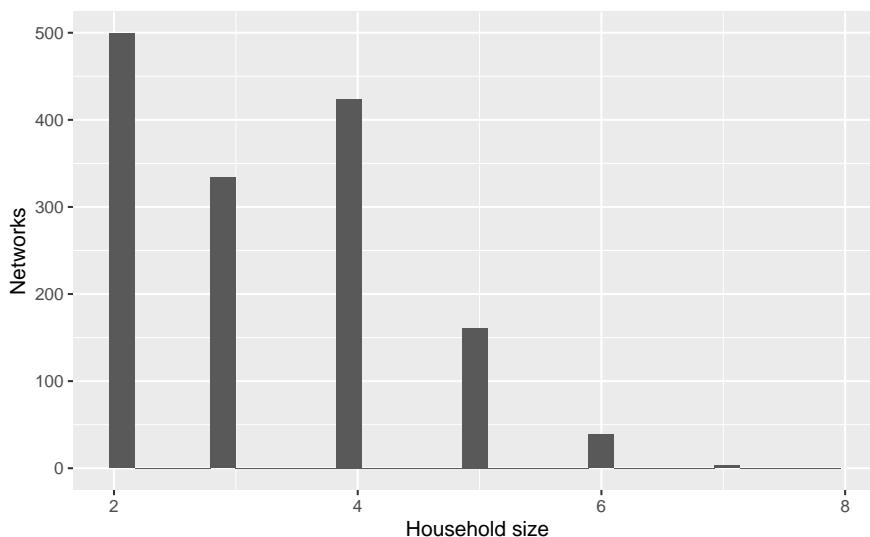
Basic data summaries The following code loads the dataset and processes data summaries:

Load and extract the network list, and define the “sub-datasets” and their colour coding:

```
HHNet <- readRDS(here("data", "HHNet.rds"))
nattrs <- as_tibble(HHNet, unit="network")
subdatasets <- readRDS(here("data", "subdatasets.rds"))
levels(subdatasets) <- c("H", "Ewc", "Enc")
subdatacol <- as.numeric(subdatasets)+1
subdatapal <- palette()
```

```
1  
2  
3 H <- readRDS(here("data","H_networks.touch.rds"))  
4 E <- readRDS(here("data","E_networks.touch.rds"))  
5  
6 Household sizes:  
7  
8 H.sizes <- sapply(H, network.size)  
9 E.sizes <- sapply(E, network.size)  
10  
11 summary(H.sizes)  
12  
13 ##      Min. 1st Qu. Median      Mean 3rd Qu.      Max.  
14 ##      2.000   3.000  4.000    3.981  4.000    7.000  
15  
16 summary(E.sizes)  
17  
18 ##      Min. 1st Qu. Median      Mean 3rd Qu.      Max.  
19 ##      2.000   2.000  3.000    3.267  4.000    8.000  
20 qplot(H.sizes, geom="histogram",xlab="Household size",ylab="Networks") +  
21   xlim(NA, max(E.sizes, H.sizes))  
22  
23  
24  
25  
26  
27  
28  
29  
30  
31  
32  
33  
34  
35  
36  
37  
38  
39 qplot(E.sizes, geom="histogram",xlab="Household size",ylab="Networks") +  
40   xlim(NA, max(E.sizes, H.sizes))  
41  
42  
43  
44  
45  
46  
47  
48  
49  
50  
51  
52  
53  
54  
55  
56  
57  
58  
59  
60
```





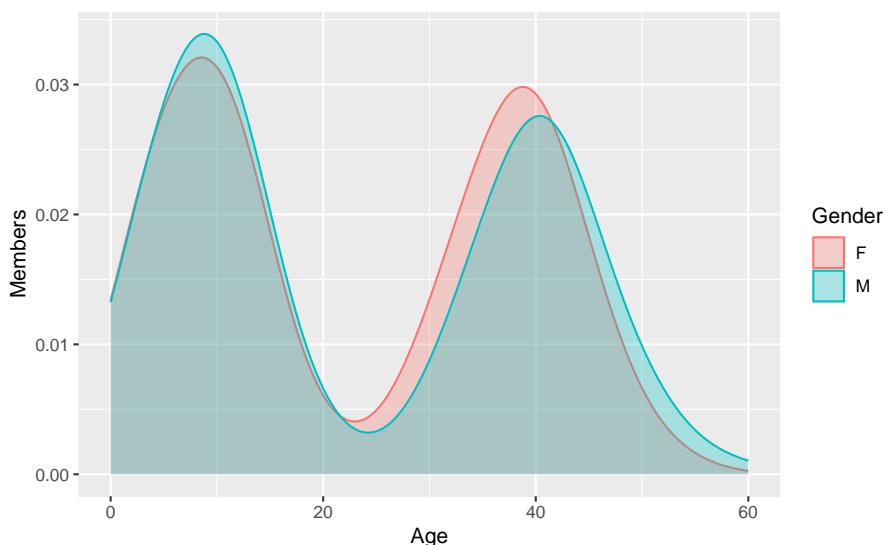
Joint age and gender distribution of H dataset household members:

```

22 H.agegender <- tibble(
23   Gender = H %>% map(get.vertex.attribute, "gender") %>% unlist,
24   Age = H %>% map(get.vertex.attribute, "age") %>% unlist
25 )
26 table(H.agegender)

27 ##      Age
28 ##      Gender  0  1  2  3  4  5  6  7  8  9 10 11 12 13 14 15 16 17 18 19 20 21 22 23
29 ##          F 10  6 16 18 23 25 18 20 24 16 25 30 30 18 17  6  3  3  4  2  4  1  1  1
30 ##          M  6 12 14 15 18 23 26 16 23 28 34 22 36 18 11  9  8  3  4  2  2  1  2  0
31 ##      Age
32 ##      Gender 24 25 26 27 28 29 30 31 32 33 34 35 36 37 38 39 40 41 42 43 44 45 46 47
33 ##          F  0  1  0  3  3  8  6 13 15  9 13 15 22 21 24 23 24 28 21 12 11 13  5  9
34 ##          M  1  0  1  1  1  1  2  7  8 13  9 14  9 17 18 20 26 24 28 21 11 13 10  8
35 ##      Age
36 ##      Gender 48 49 50 51 52 53 55 57 58 59 60
37 ##          F  6  1  1  5  0  1  2  0  0  0  0
38 ##          M  5  8  4  6  3  3  0  2  1  1  1
40 ggplot(H.agegender, aes(x=Age, fill=Gender, color=Gender)) + geom_density(alpha=.3) +
41   ylab("Members")

```



Joint age and gender distribution of E dataset household members:

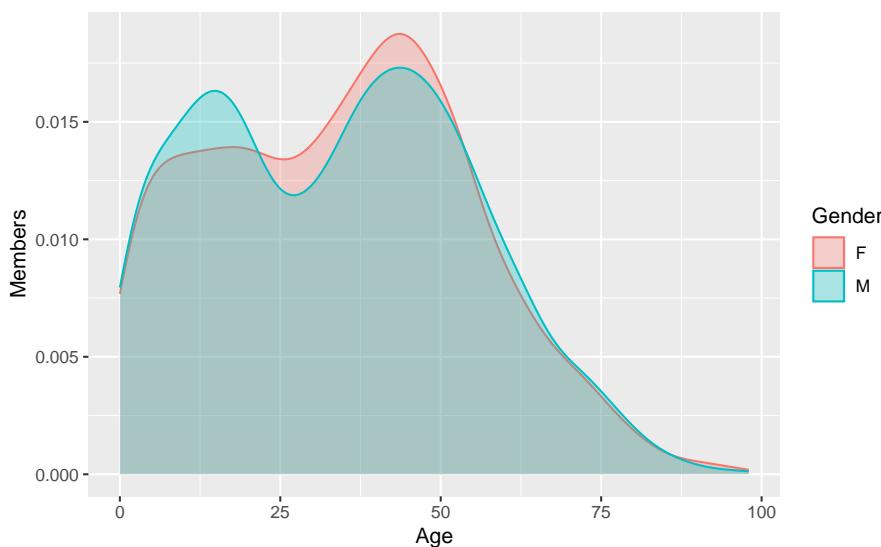
```

E.agegender <- tibble(
  Gender = E %>% map(get.vertex.attribute, "gender") %>% unlist,
  Age = E %>% map(get.vertex.attribute, "age") %>% unlist
)
table(E.agegender)

##      Age
## Gender  0  1  2  3  4  5  6  7  8  9 10 11 12 13 14 15 16 17 18 19 20 21 22 23
##   F 30 37 34 38 23 29 36 26 39 35 24 31 33 34 42 21 32 30 40 38 28 23 48 30
##   M 36 31 39 42 28 38 35 25 27 41 39 44 30 48 39 49 38 38 43 44 38 36 31 25
##      Age
## Gender 24 25 26 27 28 29 30 31 32 33 34 35 36 37 38 39 40 41 42 43 44 45 46 47
##   F 27 28 29 31 33 30 28 38 28 38 43 33 37 40 34 50 43 44 42 44 44 56 54 37
##   M 26 21 25 34 32 24 25 28 42 19 30 38 50 40 35 37 46 40 56 35 43 40 42 46
##      Age
## Gender 48 49 50 51 52 53 54 55 56 57 58 59 60 61 62 63 64 65 66 67 68 69 70 71
##   F 41 34 28 48 44 41 36 22 28 14 21 29 20 18 22 14 17 12 10 20 10 8 12 9
##   M 51 37 37 25 47 43 34 34 18 33 33 18 19 21 24 29 17 12 21 6 6 11 15 13
##      Age
## Gender 72 73 74 75 76 77 78 79 80 81 82 83 84 85 86 87 88 89 90 91 92 93 94 96
##   F 10 15 8 7 7 4 5 3 8 3 3 2 2 1 2 1 0 1 3 2 1 1 0 1 0 1
##   M 17 6 10 10 4 7 9 7 4 1 4 3 1 4 0 2 2 0 1 1 0 0 1 0
##      Age
## Gender 97 98
##   F 1 1
##   M 1 1

ggplot(E.agegender, aes(x=Age, fill=Gender, color=Gender)) + geom_density(alpha=.3) +
  ylab("Members")

```



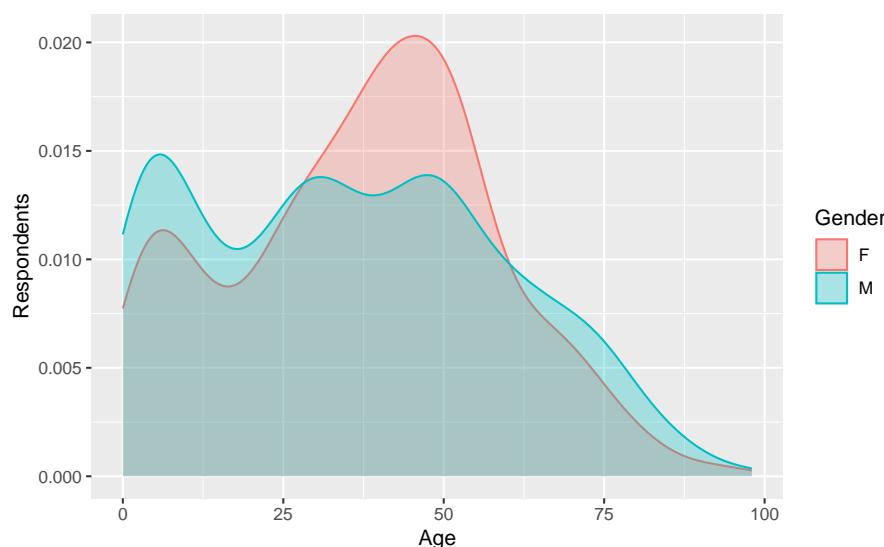
Joint age and gender distribution of *E* dataset respondents only:

```

E.resp.agegender <- tibble(
  Gender = E %>% map(vertex.attribute, "gender") %>% map_chr(1),
  Age = E %>% map(vertex.attribute, "age") %>% map_dbl(1)
)
table(E.resp.agegender)

##          Age
## Gender  0  1  2  3  4  5  6  7  8  9 10 11 12 13 14 15 16 17 18 19 20 21 22 23
##   F 12 15  8 12 11  8 12 10 13 11  3  5  9  6  7  4  6  5  9  4  5  3 11  6
##   M 18 16 17 15 16 11 12 10 10 11  9  5  6  4  6  6  8  4  7  8  7  5  5
##          Age
## Gender 24 25 26 27 28 29 30 31 32 33 34 35 36 37 38 39 40 41 42 43 44 45 46 47
##   F  8 16 11 10  8 10  8 16  9 12 16 13  9 11 12 19 14 18 18 13 19 13 22 13
##   M  6  7 11 14 18  8 13  9  9 10  8 10 11 11  6  4  6  8  9  8  9 10 12 10
##          Age
## Gender 48 49 50 51 52 53 54 55 56 57 58 59 60 61 62 63 64 65 66 67 68 69 70 71
##   F 12 15 13 21 21 18 16  8  9  5  7  6  7  5  9  3  5  6  5  6  6  4  7
##   M 16 11 10  8 16 11  8  5  2  6  6  7  6 10  8  7  6  4  8  4  2  4  5  7
##          Age
## Gender 72 73 74 75 76 77 78 79 80 81 82 83 84 85 86 87 88 90 91 92 93 97 98
##   F  2  5  2  3  6  0  2  1  4  2  0  0  2  1  1  0  0  0  1  1  1  1  0
##   M  8  5  8  4  3  3  7  1  3  1  2  2  0  4  0  2  2  1  0  0  0  1  1
ggplot(E.resp.agegender, aes(x=Age, fill=Gender, color=Gender)) + geom_density(alpha=.3) +
  ylab("Respondents")

```



Proportion of households with child ≤ 12 :

```
mean(H %>% map_lgl(get.network.attribute, "child12"))
```

```
## [1] 1
```

```
mean(H %>% map_lgl(get.network.attribute, "child12"))
```

```
## [1] 1
```

Weekday information:

```
H %>% map_lgl(get.network.attribute, "weekday") -> H_weekday
```

```
E %>% map_lgl(get.network.attribute, "weekday") -> E_weekday
```

```
mean(H_weekday)
```

```
## [1] 0.7138365
```

```
mean(E_weekday)
```

```
## [1] 0.7511962
```

Numbers of observed edges:

```
H %>% map_db1(network.edgecount) -> H.edges
```

```
E %>% map_db1(network.edgecount) -> E.edges
```

Estimated densities:

```
H.densities <- H.edges/choose(H.sizes,2)
```

```
E.densities <- E.edges/(E.sizes-1)
```

```
summary(H.densities)
```

| | Min. | 1st Qu. | Median | Mean | 3rd Qu. | Max. |
|--|------|---------|--------|------|---------|------|
|--|------|---------|--------|------|---------|------|

```
## 0.1667 1.0000 1.0000 0.9337 1.0000 1.0000
```

```
summary(E.densities)
```

| | Min. | 1st Qu. | Median | Mean | 3rd Qu. | Max. |
|--|------|---------|--------|------|---------|------|
|--|------|---------|--------|------|---------|------|

```
## 0.0000 0.5000 1.0000 0.7536 1.0000 1.0000
```

```

1
2
3   t.test(H.densities, E.densities)
4
5   ##
6   ##  Welch Two Sample t-test
7   ##
8   ## data: H.densities and E.densities
9   ## t = 13.757, df = 1235.5, p-value < 2.2e-16
10  ## alternative hypothesis: true difference in means is not equal to 0
11  ## 95 percent confidence interval:
12  ##  0.1543998 0.2057611
13  ## sample estimates:
14  ## mean of x mean of y
15  ## 0.9337227 0.7536422
16
17 Household contact densities as a function of household size and subset:
18 bind_cols(n=c(H.sizes, E.sizes), dens=c(H.densities, E.densities), subdataset=subdatasets,
19           subdatacol=subdatacol) %>%
20   group_by(n, subdataset, subdatacol) %>%
21   summarize(s=n(), dens=mean(dens)) %>%
22   ggplot(aes(ordered(n), dens, col=I(subdatacol))) +
23     geom_point() + geom_line(aes(group=subdataset)) +
24     geom_label_repel(aes(label=s)) +
25     ylim(0,1) + xlab("Household size") + ylab("Average density of contacts")
26
27
28
29
30
31
32
33
34
35
36
37
38
39
40
41
42
43
44 Mean clustering coefficient for H dataset:
45 H.triangles <- H %>% map_dbl(~summary(.~triangles))
46 H.triplets <- H %>% map_dbl(~summary(.~kstar(2)))
47
48 mean(na.omit(3*H.triangles/H.triplets))
49
50 ## [1] 0.9249176
51
52 Number of people in each subdataset of each age (needed for plots):
53 H.age <- H %>% map(get.vertex.attribute, "age") %>% unlist %>%
54   factor(levels=0:100) %>% table
55 Ewc.age <- E %>% keep(~get.network.attribute(., "child12")) %>%
56
57
58
59
60

```

| Household size | Red Line (Mean Density) | Green Line (Mean Density) | Count |
|----------------|-------------------------|---------------------------|--------------|
| 2 | 0.98 | 0.85 | 12, 10, 489 |
| 3 | 0.98 | 0.98 | 143, 73, 234 |
| 4 | 0.98 | 0.98 | 160, 57 |
| 5 | 0.95 | 0.80 | 57, 103 |
| 6 | 0.88 | 0.80 | 14, 24 |
| 7 | 0.90 | 0.98 | 1, 2 |
| 8 | - | 0.80 | 3 |

Average density of contacts

Household size

```

1
2
3   map(get.vertex.attribute, "age") %>% unlist %>% factor(levels=0:100) %>% table
4   Enc.age <- E %>% keep(~!get.network.attribute(., "child12")) %>%
5     map(get.vertex.attribute, "age") %>% unlist %>% factor(levels=0:100) %>% table
6
7 fit.agesim.weights <- rbind(H.age+Ewc.age+Enc.age, H.age, Enc.age, Ewc.age)
8
9

```

Model summaries and diagnostics The following code illustrates loading the model fit and diagnostic simulations and producing all of the summaries, tests, and diagnostic plots reported. This code works for *Model 1*, but other models can be substituted as well.

Read in the scripts:

```

15 source(here("analysis", "test_dataset.R"))
16 source(here("analysis", "plot_age_resid.R"))
17 source(here("analysis", "density_error.R"))
18

```

Load the estimates and diagnostics:

```

20 MODEL_NAME <- "Model1"
21 INDS <- list(poly_ns_eff_edges = c("N(log(n))~edges", "N(I(log(n)^2))~edges"),
22               poly_ns_eff_2stars = c("N(1)~kstar2", "N(log(n))~kstar2",
23                                     "N(I(log(n)^2))~kstar2"),
24               poly_ns_eff_triangles = c("N(1)~triangle", "N(log(n))~triangle",
25                                         "N(I(log(n)^2))~triangle"))
25
26 rds <- function(prefix, ext="rds")
27   readRDS(here("analysis", paste0(MODEL_NAME, "_results")), paste0(prefix, ".", ext)))
28 fit <- rds("fit")
29 summ <- summary(fit)
30 fit.dataset <- rds("simtest")
31 fit.gofN.e2t <- rds("gofN_e2t")
32 fit.mix <- rds("sim_mix")
33 fit.agesim <- rds("sim_age")
34

```

Coefficient table and fit information:

```

35
36 summary(fit)
37
38
39 ## Call:
40 ## ergm(formula = MODEL_FORMULA, eval.loglik = FALSE, control = control,
41 ##       verbose = 3)
42 ## 
43 ## Monte Carlo Maximum Likelihood Results:
44
45 ##                               Estimate Std. Error MCMC % z value
46 ## N(log(n))~edges           -14.35195  2.88798   0 -4.970
47 ## N(I(log(n)^2))~edges        5.72001  1.29343   0  4.422
48 ## N(as.integer(locatedInBrussel))~edges  0.07930  0.19007   0  0.417
49 ## N(as.integer(weekday == FALSE))~edges  0.13659  0.05574   0  2.450
50 ## N(1)~kstar2                 1.97808  0.79263   0  2.496
51 ## N(log(n))~kstar2          -2.22319  0.41333   0 -5.379
52 ## N(I(log(n)^2))~kstar2        0.36103  0.11600   0  3.112
53 ## N(1)~triangle                5.42612  0.96179   0  5.642
54 ## N(log(n))~triangle          -3.30696  1.39662   0 -2.368
55 ## N(I(log(n)^2))~triangle        0.88809  0.70672   0  1.257
56 ## N(1)~mm[A6G1=1YC,A6G1=1YC]  8.63310  1.49902   0  5.759
57 ## N(1)~mm[A6G1=1YC,A6G1=2PT]  9.13367  1.48898   0  6.134
58
59
60

```

```

1
2
3      ## N(1)~mm[A6G1=2PT,A6G1=2PT]           8.20816   1.45894   0   5.626
4      ## N(1)~mm[A6G1=3T,A6G1=3T]             7.73965   1.43589   0   5.390
5      ## N(1)~mm[A6G1=1YC,A6G1=4YA]          9.66997   1.77816   0   5.438
6      ## N(1)~mm[A6G1=2PT,A6G1=4YA]          7.27844   1.46101   0   4.982
7      ## N(1)~mm[A6G1=3T,A6G1=4YA]          7.76489   1.44936   0   5.357
8      ## N(1)~mm[A6G1=4YA,A6G1=4YA]          7.69187   1.44950   0   5.307
9      ## N(1)~mm[A6G1=1YC,A6G1=50FA]         10.29132  1.46104   0   7.044
10     ## N(1)~mm[A6G1=2PT,A6G1=50FA]        9.71267   1.44003   0   6.745
11     ## N(1)~mm[A6G1=3T,A6G1=50FA]        8.93307   1.43543   0   6.223
12     ## N(1)~mm[A6G1=50FA,A6G1=50FA]        7.49616   1.46984   0   5.100
13     ## N(1)~mm[A6G1=1YC,A6G1=60MA]         9.12750   1.44287   0   6.326
14     ## N(1)~mm[A6G1=2PT,A6G1=60MA]         8.79950   1.43253   0   6.143
15     ## N(1)~mm[A6G1=3T,A6G1=60MA]         8.23893   1.43210   0   5.753
16     ## N(1)~mm[A6G1=50FA,A6G1=60MA]         10.15429  1.44586   0   7.023
17     ## N(1)~mm[A6G1=60MA,A6G1=60MA]         6.62070   1.45366   0   4.554
18     ## N(1)~mm[A6G1=50FA,A6G1=7S]          8.15920   1.42290   0   5.734
19     ## N(1)~mm[A6G1=60MA,A6G1=7S]          7.55157   1.45856   0   5.177
20     ## N(1)~mm[A6G1=7S,A6G1=7S]            7.85740   1.40944   0   5.575
21     ## N(1)~Sum-T:(YC+PT)                  8.10864   1.43843   0   5.637
22     ## N(1)~Sum-YA:(OFA+OMA)              8.05579   1.43361   0   5.619
23     ## N(1)~Sum-S:(YC+PT)                 8.32393   1.53077   0   5.438
24     ## N(1)~Sum-S:(T+YA)                  9.95903   1.70784   0   5.831
25     ## N(NoChild,1)~mm[A6G1=50FA,A6G1=60MA] -1.22061  0.29750   0   -4.103
26
27      ##                                     Pr(>|z|)
28      ## N(log(n))~edges                  < 1e-04 ***
29      ## N(I(log(n)^2))~edges              < 1e-04 ***
30      ## N(as.integer(locatedInBrussel))~edges 0.67652
31      ## N(as.integer(weekday == FALSE))~edges 0.01427 *
32      ## N(1)~kstar2                     0.01257 *
33      ## N(log(n))~kstar2                < 1e-04 ***
34      ## N(I(log(n)^2))~kstar2            0.00186 **
35      ## N(1)~triangle                  < 1e-04 ***
36      ## N(log(n))~triangle              0.01789 *
37      ## N(I(log(n)^2))~triangle          0.20888
38      ## N(1)~mm[A6G1=1YC,A6G1=1YC]       < 1e-04 ***
39      ## N(1)~mm[A6G1=1YC,A6G1=2PT]       < 1e-04 ***
40      ## N(1)~mm[A6G1=2PT,A6G1=2PT]       < 1e-04 ***
41      ## N(1)~mm[A6G1=3T,A6G1=3T]       < 1e-04 ***
42      ## N(1)~mm[A6G1=1YC,A6G1=4YA]       < 1e-04 ***
43      ## N(1)~mm[A6G1=2PT,A6G1=4YA]       < 1e-04 ***
44      ## N(1)~mm[A6G1=3T,A6G1=4YA]       < 1e-04 ***
45      ## N(1)~mm[A6G1=4YA,A6G1=4YA]       < 1e-04 ***
46      ## N(1)~mm[A6G1=1YC,A6G1=50FA]      < 1e-04 ***
47      ## N(1)~mm[A6G1=2PT,A6G1=50FA]      < 1e-04 ***
48      ## N(1)~mm[A6G1=3T,A6G1=50FA]      < 1e-04 ***
49      ## N(1)~mm[A6G1=50FA,A6G1=50FA]      < 1e-04 ***
50      ## N(1)~mm[A6G1=1YC,A6G1=60MA]      < 1e-04 ***
51      ## N(1)~mm[A6G1=3T,A6G1=60MA]      < 1e-04 ***
52      ## N(1)~mm[A6G1=50FA,A6G1=60MA]      < 1e-04 ***
53      ## N(1)~mm[A6G1=60MA,A6G1=60MA]      < 1e-04 ***
54      ## N(1)~mm[A6G1=50FA,A6G1=7S]       < 1e-04 ***
55      ## N(1)~mm[A6G1=60MA,A6G1=7S]       < 1e-04 ***
56      ## N(1)~mm[A6G1=7S,A6G1=7S]       < 1e-04 ***
57
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```

```

1
2
3      ## N(1)~Sum~T:(YC+PT)           < 1e-04 ***
4      ## N(1)~Sum~YA:(OFA+OMA)       < 1e-04 ***
5      ## N(1)~Sum~S:(YC+PT)          < 1e-04 ***
6      ## N(1)~Sum~S:(T+YA)          < 1e-04 ***
7      ## N(NoChild,1)~mm[A6G1=50FA,A6G1=60MA] < 1e-04 ***
8      ##
9      ## Signif. codes: 0 '***' 0.001 '**' 0.01 '*' 0.05 '.' 0.1 ' ' 1
10     ##
11     ## Null Deviance: 7389 on 5330 degrees of freedom
12     ## Residual Deviance: 3627 on 5295 degrees of freedom
13     ##
14     ## AIC: 3697 BIC: 3927 (Smaller is better. MC Std. Err. = 0.2346)
15
16 Network size effects:  

17 nseff <- function(coef, interval, intercept=TRUE,...){  

18   d <- length(coef)-intercept  

19   xr <- interval[1]:interval[2]  

20   f <- function(x) exp(map_dbl(x, ~sum(log(.)^((1-intercept):d)*coef)))  

21   fi <- if(intercept) f else function(x) f(x)/f(2)  

22   ggplot(tibble(x=xr, y=fi(xr)), mapping=aes(x,y)) + xlim(interval[1], interval[2]) +  

23     geom_function(fun=fi) + geom_point() +  

24     xlab("$n$") + ylab("Cond. odds ratio")
25 }
26
27 nseff(coef(fit)[INDS$poly_ns_eff_edges], interval=c(2,max(E.sizes,H.sizes)),
28       intercept=FALSE)
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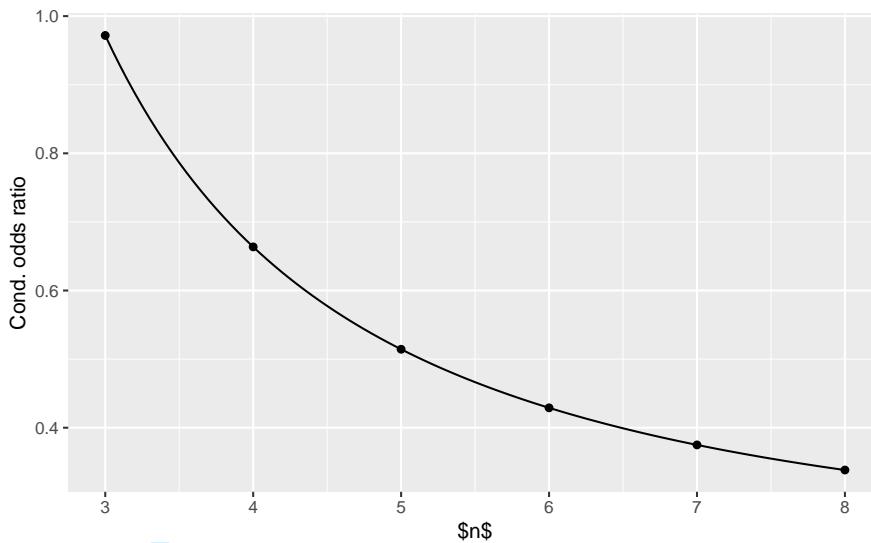
```

| \$n\$ | Cond. odds ratio |
|-------|------------------|
| 2 | 1.0 |
| 3 | 0.5 |
| 4 | 0.3 |
| 5 | 0.5 |
| 6 | 1.0 |
| 7 | 2.5 |
| 8 | 8.0 |

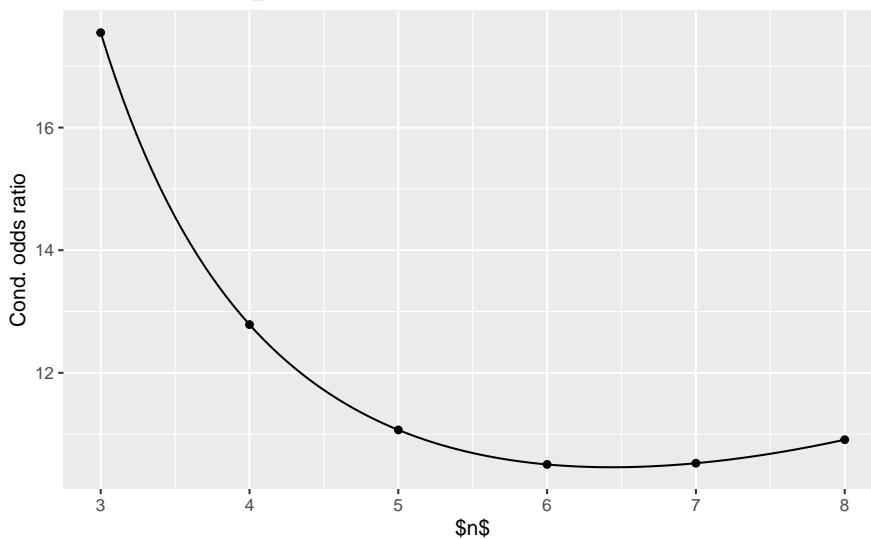
```

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```



```
nseff(coef(fit)[INDS$poly_ns_eff_triangles], interval=c(3,max(H.sizes, E.sizes)))
```



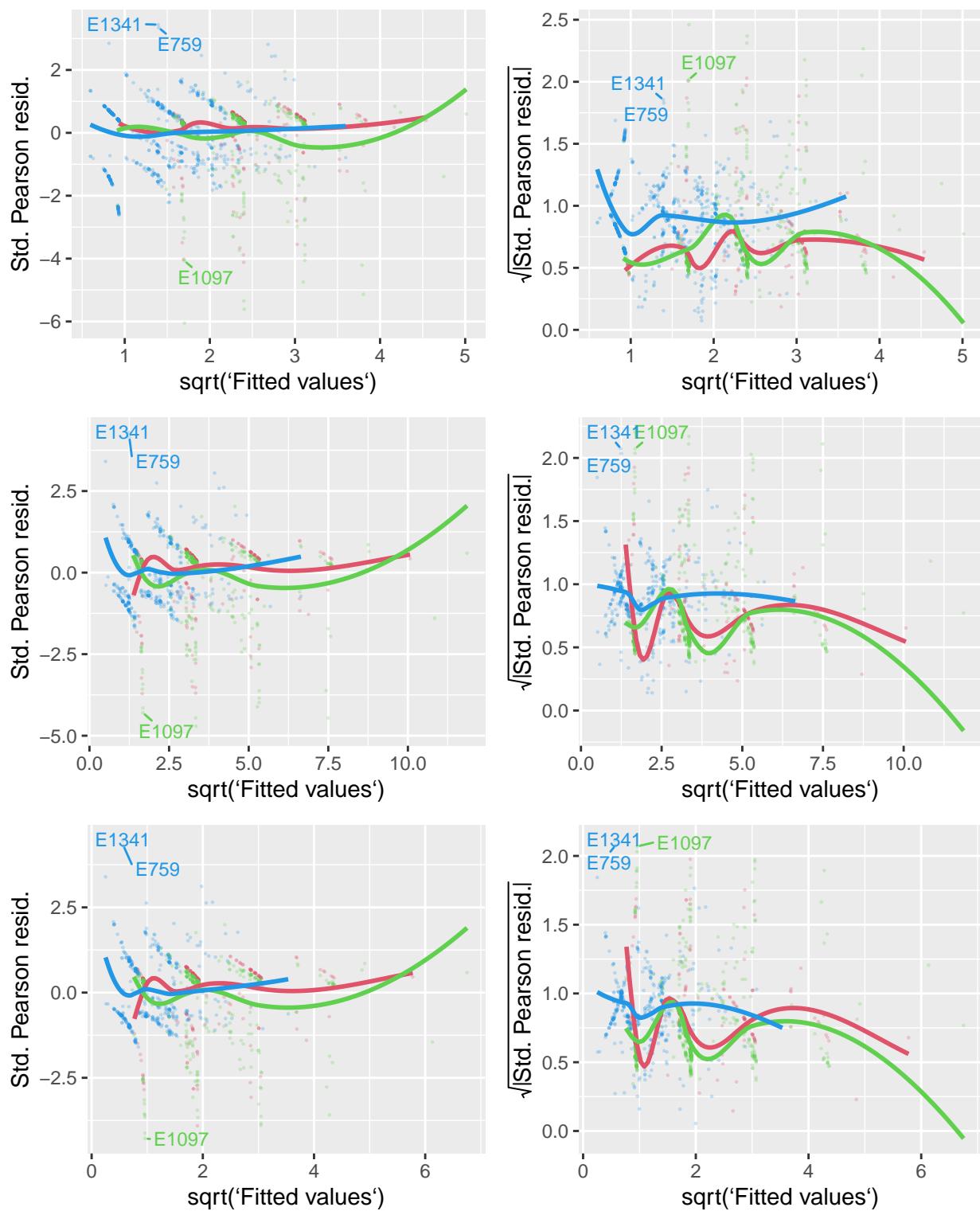
Pearson residual plots against fitted and network size:

```

net_label <- function(dataset, .network_id)
  ifelse(dataset=="Individual", paste0("E", .network_id-length(H)), paste0("H", .network_id))

grid.arrange(
  grobs=autoplot(fit.gofN.e2t,
    against=sqrt(.fitted),
    mappings=list(default=aes(col=I(subdatacol), group=subdatacol)),
    geom_args=list(point=list(alpha=1/4,size=1/8),
      text=list(size=3, min.segment.length=0)),
    id.label=net_label(dataset, .network_id)), ncol=2)

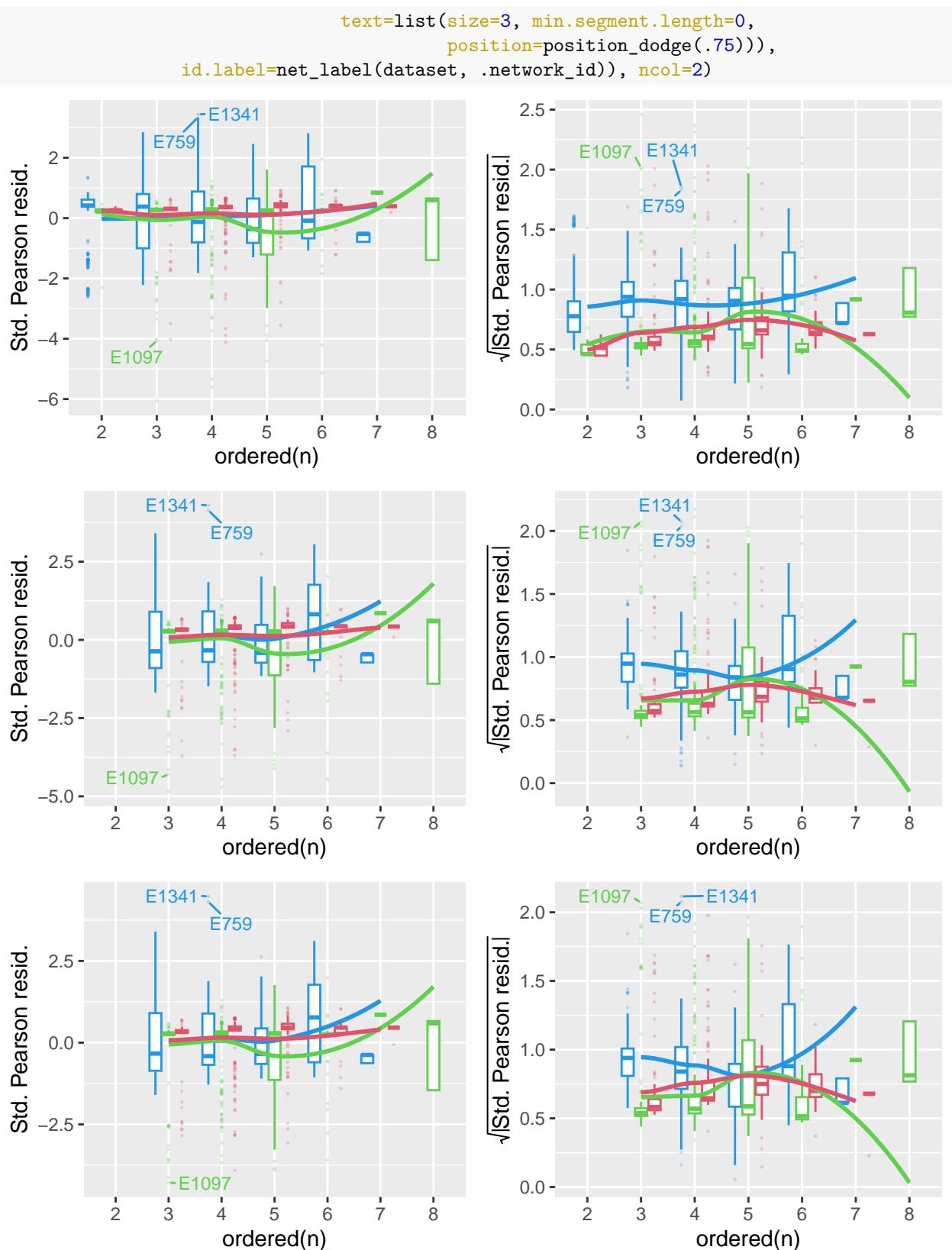
```



```

grid.arrange(
  grobs=autoplot(fit.gofN.e2t,
    against=ordered(n),
    mappings=list(default=aes(col=I(palette()[subdatacol]))),
    geom_args=list(point=list(outlier.alpha=1/4,outlier.size=1/8,
      position=position_dodge2(preserve="single"))),

```

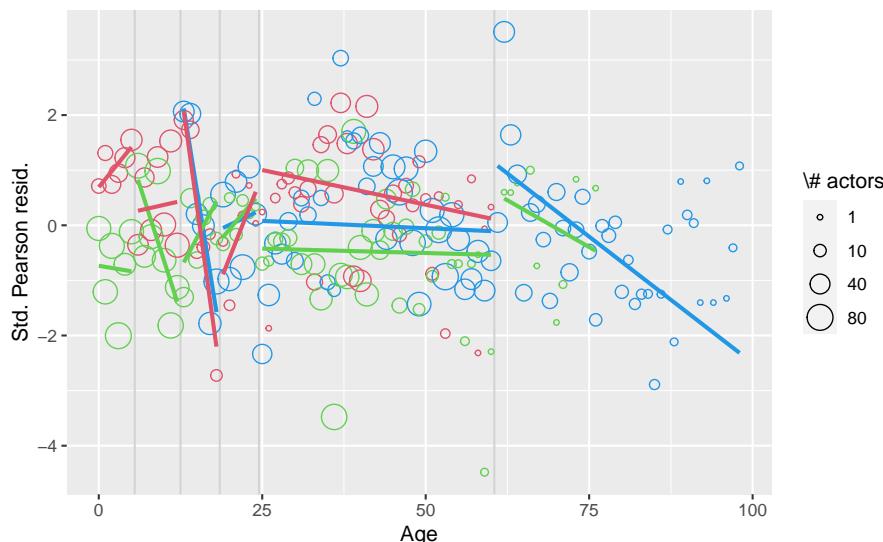


Residuals by age:

```

1
2
3
4   ggplot_age_resid(fit.agesim, weights=fit.agesim.weights, subdatasets=-1) +
5     scale_size_continuous(name="\#\# actors", breaks=c(1,10,40,80))
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```

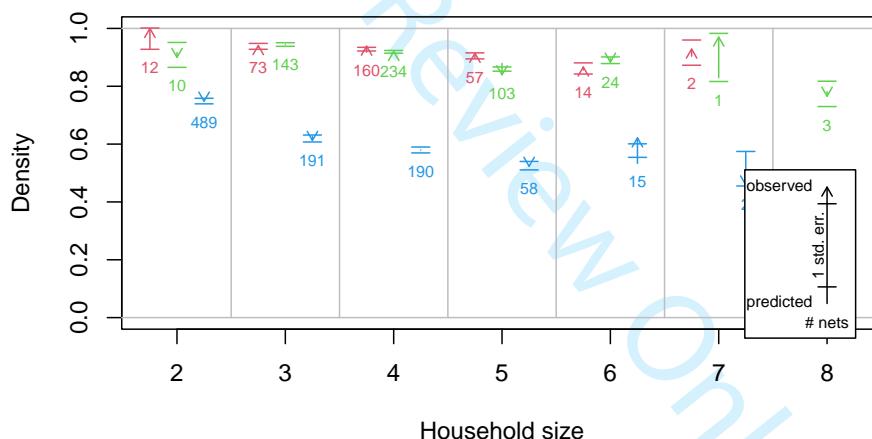


Density errors:

```

25 density_error(fit.gofN.e2t[1], subdatasets=subdatasets, arrow_scl=0.5, cex=.65,
26   key=c(8,0.25), xlab="Household size", key.title="")
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```



Network size lack of fit tests:

```

43 lm.gofN((1:3)-0+factor(n), data=fit.gofN.e2t) %>% map(anova)
44
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```

```

## $edges
## Analysis of Variance Table
##
## Response: edges
##             Df  Sum Sq Mean Sq F value Pr(>F)
## factor(n)    7   9.54  1.3627  1.3569 0.2196
## Residuals 1774 1781.56  1.0043
##
## $kstar2
## Analysis of Variance Table
##
## Response: kstar2

```

```

1
2
3      ##          Df  Sum Sq Mean Sq F value Pr(>F)
4      ## factor(n)    6     8.64 1.43967  1.4604 0.1884
5      ## Residuals 1264 1246.03 0.98578
6      ##
7      ## $triangle
8      ## Analysis of Variance Table
9      ##
10     ## Response: triangle
11     ##          Df  Sum Sq Mean Sq F value Pr(>F)
12     ## factor(n)    6     7.71 1.28502  1.3401 0.2361
13     ## Residuals 1264 1212.07 0.95892
14
15 Regression on residuals:  

16 chi2tst <- function(fit, i){
17   lst(chi2=coef(fit)[i] %*% solve(vcov(fit)[i,i]) %*% coef(fit)[i],
18       df=length(i), pval=pchisq(c(chi2), df, lower.tail=FALSE))
19 }
20
21 y <- list(edges~, kstar2~, triangle~)
22 d <- lapply(1:3, \{i) fit.gofN.e2t[i])
23 ylbl <- c("edges", "2-stars", "triangles")
24
25 x <- list(~log(popDensityM2), ~poly(log(popDensityM2), 2),
26           .~locatedInCity, .~locatedInBrussel, .~I(weekday==FALSE))
27 p <- list(2, 2:3, 2, 2, 2)
28 xlabel <- c("log(pop. dens. in post code) (linear)",
29            "log(pop. dens. in post code) (quadratic)",
30            "if city post code", "if Brussels post code", "if weekend")
31
32 tests <- expand.grid(yi=seq_along(y), xi=seq_along(x))
33 tests <- tibble(y = y[tests$yi], d = d[tests$yi], ylbl = ylbl[tests$yi],
34                  x = x[tests$xi], p = p[tests$xi], xlabel = xlabel[tests$xi])
35 test.result <- apply(tests, 1, function(.x){
36   lm.gofN(update(.x$y, .x$x), data=.x$d)[[1]] %>% chi2tst(.x$p)
37 }) %>% transpose() %>% lapply(unlist)
38
39 cbind(tests[c("ylbl", "xlabel")], test.result)
40
41      ##          ylbl          xlabel      chi2      df      pval
42      ## 1    edges    log(pop. dens. in post code) (linear) 4.1738391 1 0.04105268
43      ## 2    2-stars  log(pop. dens. in post code) (linear) 1.0559765 1 0.30413465
44      ## 3  triangles  log(pop. dens. in post code) (linear) 1.0362235 1 0.30870141
45      ## 4    edges  log(pop. dens. in post code) (quadratic) 5.2266503 2 0.07329044
46      ## 5    2-stars  log(pop. dens. in post code) (quadratic) 1.0632399 2 0.58765224
47      ## 6  triangles  log(pop. dens. in post code) (quadratic) 1.0431716 2 0.59357851
48      ## 7    edges                      if city post code 1.2167568 1 0.26999808
49      ## 8    2-stars                     if city post code 1.4762829 1 0.22435701
50      ## 9  triangles                     if city post code 1.4085300 1 0.23530057
51      ## 10   edges                      if Brussels post code 0.3964847 1 0.52891029
52      ## 11   2-stars                     if Brussels post code 0.0712551 1 0.78951805
53      ## 12  triangles                     if Brussels post code 0.1692714 1 0.68076014
54      ## 13   edges                      if weekend 1.2122593 1 0.27088513
55      ## 14   2-stars                     if weekend 1.2148431 1 0.27037507
56      ## 15  triangles                     if weekend 0.7970447 1 0.37197844
57
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```

```
1  
2  
3 Dataset tests:  
4 quantile_test_sim(fit.dataset, conf.level=FALSE)  
5  
6 ## N(1)~edges N(1)~kstar2  
7 ## 0.0838623 0.1378174  
8  
9 chisq_test_sim(fit.dataset)  
10  
11 ## [1] 0.2114477  
12 ## attr(),"statistic")  
13 ## [,1]  
14 ## [1,] 3.107555  
15 ## attr(),"parameter")  
16 ## [1] 2  
17 Standard deviations of pearson residuals:  
18 cbind(data.frame(Overall=fit.gofN.e2t %>% map("pearson") %>% map_dbl(sd, na.rm=TRUE)),  
19 fit.gofN.e2t %>% map("pearson") %>% map(tapply, subdatasets, sd, na.rm=TRUE) %>%  
20 do.call(rbind, .))  
21  
22 ## Overall H Ewc Enc  
23 ## edges 1.0031114 0.8147589 1.078155 1.014703  
24 ## kstar2 0.9943332 0.8457433 1.050852 1.016460  
25 ## triangle 0.9804052 0.8747220 1.013766 1.005475  
26
```

27 Replication

28 Vignettes and workshops for the `ergm.multi` package are under ongoing development. Their latest versions
29 can be found in the GitHub repository, on CRAN, and in the Advanced ERGM workshop BLINDED.

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