Revisiting the Edges Dissolution Approximation

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Abstract

We study the edges dissolution approximation (EDA) of \cite{2}. We begin by repeating an observation from \cite{2}, namely that in the dyad-independent case, the exact result is tractable. We then observe that taking the sparse limit of the exact result leads to a different approximation than that in \cite{2}. We prove that this new approximation is better than the old approximation for sparse dyad-independent models, and we show via simulation that the new approximation tends to perform better than the old approximation for sparse models with sufficiently weak dyad-dependence. We then turn to general dyad-dependent models, proving that both the old and new approximations are asymptotically exact as the time step size goes to zero, for arbitrary dyad-dependent terms and some dyad-dependent constraints. In demonstrating this result, we identify a Markov chain, defined for any sufficiently small time step, whose cross-sectional and durational behavior is exactly that we desire of the EDA. This Markov chain can be simulated, and we do so for a dyad-dependent model, showing that it eliminates the biases present with either of the dyad-independent-derived approximations.

Keywords: Exponential-family random graph models (ergms); Markov chain Monte Carlo; Separable temporal exponential-family random graph models (stergms).

1 Introduction

Exponential-family random graph models (ergms) are a class of models that specify probability distributions on networks in terms of cross-sectional network statistics \cite{11}. Temporal exponential-family random graph models (tergms) are
a discrete-time generalization of ergms that model transitions between network states in terms of (possibly time-dependent) network statistics. Separable tergms (stergms) are a subclass of tergms in which the dynamics of tie formation and dissolution can be separated within each time step.

While the statistical theory for tergms has been well developed, the practical estimation of these models remains a formidable computational challenge. To date, there is no generally successful estimation strategy available. One approach for estimating certain simple examples of the stergms of origin, leveraging the (relative) ease of estimating ergms, is the "edges dissolution approximation" (EDA), originally presented in [2]. This approach combines coefficient estimates from an ergm (modeling prevalence of relevant cross-sectional network structures) with specified durations of ties in order to obtain formation and dissolution coefficients for a stergm.

To apply the EDA as presented in [2], one fits an ergm, containing the cross-sectional terms of interest, to data for a single cross-sectional network (possibly specified by target statistics). The stergm dissolution coefficients are calculated directly from the target edge durations by equating the dissolution probability to one over the target duration (where duration may vary by dyad type according to a dyad-independent submodel of the ergm). The formation coefficients are then obtained by taking the ergm coefficients and subtracting off the corresponding dissolution coefficients, where the formation model terms are the same as those in the ergm. This approach has been used in many applied contexts and is justified asymptotically in the dyad-independent case by the arguments in [2].

Here, we improve our understanding of the EDA in several ways. We begin, as in [2], with the case of dyad-independent ergms. In Section 3.1 we note that when the original ergm is dyad-independent, we can write down a dyad-independent stergm with arbitrarily specified dyad-by-dyad mean edge durations, all of whose cross-sectional statistics are distributed identically to those of the ergm, provided only that the cross-sectional and durational targets are consistent with each other, in the sense that the odds of any edge under the ergm cannot exceed its duration under the stergm. (This consistency condition always holds if every edge has probability less than or equal to 1/2 under the ergm, regardless of the durational targets.) This amounts to nothing more than a proper interpretation of the GMME (given in [2]) for the formation coefficient of a stergm with formation and dissolution models each consisting solely of the edges term, where the dissolution coefficient has been fixed by the specification of a mean edge duration and the formation coefficient is then determined by the specification of a mean density.

We observe that this general result reduces in the sparse limit to a simple approximation that differs from that in [2]. We prove that this new approximation outperforms the old approximation for sparse, dyad-independent models, in the sense that the error in cross-sectional edge probability is smaller. Since errors are expected to change continuously with coefficient values, if we perturb off of a sparse dyad-independent model, we expect that the new approximation will continue to have smaller errors than the old approximation in some neigh-
borhood of the initial model, and we demonstrate this behavior via simulations in Section 3.2. However, the neighborhood where the new approximation is better than the old approximation may not include models of real interest, and even when it does, both the old and new approximations can have large errors when the dyad-dependence is not weak. Thus, we are inclined to gain a better understanding of behavior in the strongly dyad-dependent regime.

In this direction, we prove in Section 3.3 that both the old and new approximations are asymptotically exact for arbitrary dyad-dependent terms and some dyad-dependent constraints, as the size of the tergm time step goes to zero. The technical conditions on the constraints in order for them to be covered by our proof are as follows: for asymptotic cross-sectional exactness, the graph whose vertices are network states satisfying the constraints and whose edges connect network states differing in edge state on exactly one dyad must be connected; for asymptotic durational exactness, we additionally require that the constraints do not ever prevent us from toggling off an edge unless that edge is unconditionally fixed by the constraints (in which case its duration is not of interest). These asymptotic exactness results justify (in the dyad-dependent case) a suggestion in [2] to improve the behavior of the approximation by increasing the duration.

In the course of the asymptotic exactness proof, we write down transition probabilities that define a Markov chain having the same cross-sectional equilibrium distribution as the ergm and also having the desired mean edge durations (up to an overall rescaling of the time step size). This Markov chain is not in general a true tergm, but may be regarded as a sort of limit of tergms in which the time step size has become infinitesimal. This “infinitesimal time tergm” can be simulated using an ergm Metropolis-Hastings algorithm with a suitable choice of proposal (though this may not be optimally efficient). We simulate this Markov chain for one of the dyad-dependent models considered in Section 3.2, showing that it eliminates the biases present with either of the dyad-independent-derived approximations.

All the tergms we work with in this paper will be defined by a formation model and a dissolution model, together with (cross-sectional) constraints. In this sense, they will all be of the separable type [7], with the technical exception of dyad-dependent constraints, which we impose on the instantaneous network rather than the union or intersection networks. These constraints will not be relevant until Section 3.3. We will use the term stergm to refer to the model in Section 3.1 and the more general term tergm in Section 3.3 and Section 4.

Additionally, the formation and dissolution models of the (s)tergms we work with will themselves be ergm models. This means that beyond the one-step memory implied by the use of union and intersection networks, the (s)tergm is memoryless. We will use the (imperfect) term memoryless to refer to (s)tergms whose formation and dissolution models are both ergm models. While such memoryless (s)tergms are not the most general class of tergms, they will suffice for our purposes.
2 Materials and Methods

We will use a mix of formal derivations and simulations in this paper. Simulations use R [10] and the statnet suite of packages [12].

3 Results

3.1 The Dyad-Independent Case

Dyad-independent models are defined by having only dyad-independent terms and constraints, meaning that the factors that influence the formation of a tie do not depend on the state of other dyads. In this section, we focus on dyad-independent models, deriving exact results for the formation coefficients (essentially repeating an argument in [2]), defining a new approximation for sparse networks, deriving the errors in both the old and new approximations, and deriving the regime in which the new approximation performs better than the old approximation.

3.1.1 Notation

Any dyad-independent ergm is fully specified by its linear predictors for each free dyad (and its edge states for fixed dyads, which will not be of interest to us). It will be useful to have simple notation that allows us to work with these linear predictors without getting bogged down in irrelevant details. For a fixed but arbitrary free dyad, we therefore let $0 < p < 1$ denote its edge probability under the ergm, and $\theta = \logit(p)$ its linear predictor. (Note that we do not care what (dyad-independent) terms occur in the original ergm, only what the linear predictors are.) Likewise, the behavior of this dyad under a memoryless, dyad-independent stergm is fully specified by the formation linear predictor, denoted by $\theta^+$, and the dissolution linear predictor, denoted by $\theta^-$. For later use, we define $q$ to be the “formation probability” as given by the relation $\theta^+ = \logit(q)$, with the convention that $\logit(1) = +\infty$.

For the dyad under consideration, we let $1 \leq D \leq \infty$ denote the mean edge duration target. For memoryless dyad-independent stergms, specifying the dissolution linear predictor $\theta^-$ is equivalent to specifying the mean duration $D$ via the relation $\theta^- = \logit(1 - 1/D) = \log(D - 1)$, with the conventions $\logit(0) = \log(0) = -\infty$.

3.1.2 Overview of Results

As we are dealing with dyad-independent ergm models, we will be able to focus on one dyad at a time. Regarding the ergm as inducing an edges-only model on the single dyad under consideration, the prescription set forth in [2] is to take

$$\begin{align*}
\theta^+ &= \theta - \log(D - 1), \\
\theta^- &= \log(D - 1).
\end{align*}$$
As noted above, $\theta^-$ is fixed by $D$ alone. Given this value of $\theta^-$, the choice of value for $\theta^+$ is supposed to render equilibrium edge probability approximately that of the original ergm.

In Section 3.1.4 we show that both the target mean duration $D$ and ergm edge probability $p$ can be matched exactly by the stergm when and only when $p \leq \frac{1}{1 - p}$, i.e. $D - \exp(\theta) \geq 0$, and that the stergm linear predictors accomplishing this exact matching are uniquely given by

$$\begin{align*}
\theta^+ &= \theta - \log(D - \exp(\theta)), \\
\theta^- &= \log(D - 1).
\end{align*}$$

(2)

This is identical to (1) when and only when $\theta = 0$, i.e, $p = 1/2$. It was observed in [2] that (1), applied to the network as a whole, works extremely well for any homogeneous mean edge duration when the full ergm is an edges-only model with mean density equal to 1/2, and we now see that it matches the exact result in that case. As $D \to +\infty$, we have $\log(D - \exp(\theta)) = \log(D - 1) \to 0$ like $(1 - \exp(\theta))/(D - 1)$, so (1) and (2) agree asymptotically in the long-duration limit, where it was observed in [2] that (1) works extremely well for an edges-only ergm of any mean density. The difference between (1) and (2) is most pronounced at low duration: for any $\theta < 0$, as $D \to 1^+$ we have $\log(D - \exp(\theta)) = \log(D - 1) \to +\infty$. The exact result (2) is effectively the formula for the GMME $\hat{\theta}^+$ in (3.3) of [2], though this use of (3.3) does not seem to be highlighted there. We will provide a derivation in our notation, for completeness.

The transformation (2) could be implemented in practice, using a suitably defined operator term [8]. However, for a direct implementation without operator terms, it is more convenient to have $\theta^+ - \theta^-$ independent of $\theta$, as was the case in [2]. This occurs naturally in the sparse limit, which corresponds to $\theta \ll 0$; since $D \geq 1$, we can then approximate $\theta - \log(D - \exp(\theta))$ as $\theta - \log(D)$, so that the prescription (2) becomes

$$\begin{align*}
\theta^+ &= \theta - \log(D), \\
\theta^- &= \log(D - 1).
\end{align*}$$

(3)

The only difference between (1) and (3) is that the former subtracts $\log(D - 1)$ from $\theta$ to obtain $\theta^+$ whereas the latter subtracts $\log(D)$. In the argument given in [2] for the general dyad-independent case, this difference can be traced back to the decision to discard both the 1 and the $-\hat{O}_{ij}$ after equation (4.4); retaining the 1 would result in (3).

Note that while we have assumed the model is dyad-independent to reach this point, we can apply the idea of (1) and (3) to dyad-dependent models as well. More explicitly, we obtain the formation model and coefficients by starting with the ergm model and coefficients, and then either adjusting the coefficient values or adding an additional term with the appropriate coefficient to effect the “correction” of $-\log(D - 1)$ or $-\log(D)$. This is the approach taken when simulating dyad-dependent models in Section 3.2 below.
3.1.3 Heuristic Derivation in the Sparse Limit

Here we give a heuristic derivation of the log(D) correction (3) in the sparse limit before turning to the formal derivation of the general result (2) in Section 3.1.4. We use notation as in Section 3.1.1. We wish to find the formation probability q that gives the dyad in question cross-sectional probability p under a memoryless dyad-independent ergodic where it has mean edge duration D. In equilibrium, the probability to form a tie on this dyad must equal the probability to dissolve a tie on this dyad, so as to conserve the total probability that there is a tie on this dyad. We start with a tie with probability p, and given that we start with a tie, we dissolve it with probability 1/D. We start with a non-tie with probability 1−p, and given that we start with a non-tie, we form a tie with probability q. Thus (1−p)q = p/D, or q = p/(1−p).D. We have θ+ = logit(q) and θ = logit(p); in the sparse limit p ≪ 1, we may approximate logit(p) by log(p), (p/(1−p)) by p/D, and logit(q) = logit(p/(1−p)) by log(p/D); the statement log(p/D) = log(p) − log(D) is then the statement that θ+ = θ − log(D) in the sparse limit.

Note that this heuristic is equivalent to that commonly used in biostatistics and epidemiology when representing the relationship between disease prevalence, incidence and duration (our p, q and D respectively [1]. The general form of that relation is p = qD, and the equivalent “sparse limit” is p = qD.

3.1.4 Formal Derivation of the Exact Solution

Consider a fixed but arbitrary free dyad. We continue to use the notation introduced in Section 3.1.1 with the addition that the random variable y denotes the edge state on the dyad in question, so that y = 1 indicates an edge and y = 0 indicates no edge.

The finite irreducible Markov chain on y (across time steps) possesses a unique stationary distribution π. Let T = (Tij)0≤i,j≤1 denote the single time step transition probability matrix for y, and let πi denote π(y = i) for i = 0, 1. We have

$$
\pi_1 = (\pi T)_1 = \pi_0 T_{01} + \pi_1 T_{11} = (1 - \pi_1) T_{01} + \pi_1 (1 - T_{10}).
$$

We also know that

$$
T_{01} = q
$$

and

$$
T_{10} = 1/D
$$

so that

$$
0 = (1 - \pi_1) q - \pi_1 / D.
$$
Solving this equation for \( \pi_1 \) yields

\[
\pi_1 = \frac{qD}{qD + 1} \tag{4}
\]

while solving it instead for \( q \) yields

\[
q = \frac{\pi_1}{(1 - \pi_1)D} \tag{5}
\]

noting \( \pi_1 < 1 \) since \( D < \infty \).

Now, suppose \( \pi_1 = p \). Then, equation (5) yields

\[
q = \frac{p}{(1 - p)D}.
\]

Conversely, suppose that \( q = \frac{p}{(1 - p)D} \). Then, equation (4) yields

\[
\pi_1 = p.
\]

Thus, \( \pi_1 = p \) if and only if \( q = \frac{p}{(1 - p)D} \).

We conclude that there exists a memoryless dyad-independent stergm giving this dyad its ergm edge probability \( p \) and its target mean edge duration \( D \) if and only if \( \frac{p}{(1 - p)D} \leq 1 \), with the corresponding formation and dissolution linear predictors uniquely determined as \( \theta^+ = \logit \left( \frac{p}{(1 - p)D} \right) \) and \( \theta^- = \log(D - 1) \). Since \( \theta = \logit(p) \) is given, we obtain after simplification that

\[
\theta^+ = \theta - \log(D - \exp(\theta))
\]

as claimed.

Applying the above argument to each free dyad yields the desired result. This approach gives each free dyad the same equilibrium edge probability under the stergm as it had under the original ergm. Since both the ergm and the stergm are dyad-independent, this means that every cross-sectional network state has the same probability under the ergm as it has under the stergm. By implication, this means that every cross-sectional statistic – regardless of whether it is in the ergm or not, dyad-independent or not – has the same distribution under the ergm and under the stergm.

### 3.1.5 Formal Derivation of the Approximation Errors

In this section we derive and compare the errors of the old and new approximations (1) and (3), assuming that the model and constraints are dyad-independent. We focus on a single dyad, with notation as in Section 3.1.1. By the assumption of dyad-independence, the mean duration will be matched exactly, so the error will be entirely in the equilibrium edge probability. The target value is \( p \), the ergm edge probability, and we let \( p_{\text{old}} \) and \( p_{\text{new}} \) denote the equilibrium edge probabilities in the stergm using the old and new approximations, respectively. We can determine \( p_{\text{old}} \) and \( p_{\text{new}} \) by equating the exact results (2) for
\( p_{\text{old}} \) and \( p_{\text{new}} \) to the approximations (1) and (3) for \( p \) (with the same value of \( D \) throughout, since we know all of (1)-(3) yield \( D \) as the mean duration), and then solving for what \( p_{\text{old}} \) and \( p_{\text{new}} \) must be in order for these equations to be satisfied.

In order to do the derivation only once, we let \( \alpha \) be a parameter taking values in \( \{0, 1\} \) and define \( p_\alpha \) by

\[
\logit(p_\alpha) - \log(D - \exp(\logit(p_\alpha))) = \logit(p) - \log(D - \alpha)
\]

so that \( p_{\text{new}} = p_0 \) and \( p_{\text{old}} = p_1 \). Noting that

\[
\logit(p_\alpha) - \log(D - \exp(\logit(p_\alpha))) = -\log\left(\frac{D}{\exp(\logit(p_\alpha))} - 1\right)
\]

we obtain

\[
-\log\left(\frac{D}{\exp(\logit(p_\alpha))} - 1\right) = \logit(p) - \log(D - \alpha).
\]

Solving for \( p_\alpha \), we find

\[
p_\alpha = p \cdot \frac{D}{D + p + \alpha(p - 1)}.
\]

Thus we have the relative error

\[
\frac{p_{\text{old}} - p}{p} = \frac{D}{D + p + \alpha(p - 1)} - 1 = \frac{-p - \alpha(p - 1)}{D + p + \alpha(p - 1)}.
\]

This means that

\[
\frac{p_{\text{old}} - p}{p} = \frac{-2p + 1}{D + 2p - 1}
\]

and

\[
\frac{p_{\text{new}} - p}{p} = \frac{-p}{D + p}.
\]

We would like to identify for what values of \( p \) and \( D \) we have

\[
|p_{\text{new}} - p| < |p_{\text{old}} - p|
\]

or, equivalently,

\[
\left|\frac{p_{\text{new}} - p}{p}\right| < \left|\frac{p_{\text{old}} - p}{p}\right|.
\]

From the formulas above, this condition is equivalent to

\[
pD + 2p^2 - p < | - 2p + 1(D + p)|.
\]

If \( p > 1/2 \), this becomes

\[
pD + 2p^2 - p < (2p - 1)(D + p) = 2pD + 2p^2 - D - p
\]
which has no solutions as \( p < 1 \) and \( D \geq 1 \). If instead \( p \leq 1/2 \), the condition is

\[
pD + 2p^2 - p < (1 - 2p)(D + p) = D + pD - 2p^2,
\]
i.e.

\[
4p^2 - p(2 - 3D) - D < 0.
\]

The quadratic equation

\[
4p^2 - p(2 - 3D) - D = 0
\]
has roots

\[
\frac{2 - 3D \pm \sqrt{4 + 4D + 9D^2}}{8}
\]
and \( 4p^2 - p(2 - 3D) - D < 0 \) precisely when \( p \) lies strictly between these roots, as the parabola opens upwards. It is clear that the lower root

\[
\frac{2 - 3D - \sqrt{4 + 4D + 9D^2}}{8}
\]
is negative, whereas \( p \) is constrained to be positive. The formula for the upper root

\[
\frac{2 - 3D + \sqrt{4 + 4D + 9D^2}}{8}
\]
defines a positive, monotonically decreasing function of \( D \in [1, \infty) \), with limiting values \( \sqrt{\frac{17}{8}} - 1 \) as \( D \to 1^+ \) and \( \frac{1}{3} \) as \( D \to +\infty \).

In other words, the error (relative or absolute) in the equilibrium edge probability is smaller with the new approximation precisely when

\[
p < \frac{2 - 3D + \sqrt{4 + 4D + 9D^2}}{8},
\]
which in particular includes the range \( p \leq \frac{1}{3} \) for any value of \( D \).

3.2 Behavior of Dyad-Independent Approximations for Dyad-Dependent Models

Dyad-dependent models are defined by having at least one dyad-dependent term or constraint, meaning that the factors that influence the formation of a tie may depend on the state of other dyads. In this section, we examine how the old and new dyad-independent-derived approximations (i.e. (1) and (3)) behave on models with some commonly used dyad-dependent terms: terms that specify some part of the degree sequence and terms that allow for triad-formation bias. We utilize simulation (rather than formal arguments) to explore these issues.
3.2.1 Simulation setup

To exhibit the behavior of the old and new approximations near dyad-independence, we performed a series of simulations of \texttt{edges + degree(1)} models on a 1000 node undirected network. We used mean degrees of 0.7, 1.0, 1.3, and 2.0, and \texttt{degree(1)} targets of 200 to 600 in steps of 100, whose range includes the mean \texttt{degree(1)} value for an edges-only model of each mean degree used. (Thus, a dyad-independent model is within the range of models we simulate for each mean degree.) We included durations of 15, 50, and 100, to exhibit how errors change with duration when all other variables are held fixed.

We also performed simulations for various \texttt{edges + degree(1) + degree(2) + gwesp(0.5, fixed = TRUE)} models on a 1000 node undirected network, analogous to those of the original paper, but using \texttt{gwesp} throughout (rather than a mix of \texttt{triangle} and \texttt{gwesp}). We used a mean degree of 2.0, a \texttt{degree(1)} target of 200, a \texttt{degree(2)} target of 350, and \texttt{gwesp(0.5, fixed = TRUE)} targets ranging from 3 to 300 (considering that an isolated \texttt{triangle} counts as three \texttt{gwesp}). We again included durations of 15, 50, and 100.

3.2.2 Simulation Results

The results of the \texttt{edges + degree(1)} simulations described in Section 3.2.1 are shown in Figures 1-4. The horizontal axes correspond to different \texttt{degree(1)} targets, and the vertical axes correspond to the relative errors in the network statistics. The dashed green horizontal lines mark zero error, and the solid purple vertical lines mark the mean \texttt{degree(1)} statistic for an edges-only model of the same mean degree (thus indicating where “dyad-independence” lies on the horizontal axes). The expectation that the new approximation is nearly exact for sparse, dyad-independent models is then supported by the fact that at the dyad-independent value of \texttt{degree(1)} (i.e., the purple line), the error with the new approximation (i.e., the red line) is very close to zero (i.e., the green line), regardless of duration. More generally, Figures 1-4 may be understood as demonstrating that in a neighborhood of a sparse, dyad-independent model, the new approximation outperforms the old approximation. The size of this neighborhood will vary from model to model, and in general we do not have any way of predicting how large it will be, or whether it will contain specific dyad-dependent models of interest. Both the new and old approximations tend to become more accurate as duration increases, consistent with observations made in [2]. Also included on these plots are the results of simulating the Markov chain R defined in Section 3.3, showing that it eliminates the bias present in either of the dyad-independent-derived approximations across the full range of models tested.

The results of the \texttt{edges + degree(1) + degree(2) + gwesp(0.5, fixed = TRUE)} simulations are shown in Figure 5. We found that substantially increasing the number of proposals per time step resulted in different trends for the old approximation than those shown in [2], suggesting the higher number of proposals is needed to allow equilibration of the Metropolis-Hastings Markov
A further tenfold increase in proposals (beyond the number used for Figure 5) produced largely similar results, suggesting the number used for Figure 5 was sufficient to capture the main trends. What we see in terms of errors is something of a mixed bag, with the new approximation generally outperforming the old for edges, degree(2), and gvesp, but underperforming the old for degree(1). This illustrates the point that for an arbitrary dyad-dependent model, there is no guarantee which approximation will be better (regardless of duration); the new approximation tends to do better than the old approximation near dyad-independence, but if we stray sufficiently far from dyad-independent models, we cannot predict which approximation will be better, and results may be mixed even within a single model.

3.3 Theoretical Results for Dyad-Dependent Models

Having seen that neither dyad-independent-derived approximation works well across the board for dyad-dependent models, we would like to gain a better understanding of the general dyad-dependent case. We do so here, proving that both of the dyad-independent-derived approximations are asymptotically exact for models with arbitrary dyad-dependent terms and some dyad-dependent constraints, as the size of the tergm time step goes to zero. In the course of the proof, we identify in Section 3.3.2 a Markov chain that has the desired cross-sectional and durational behavior not just asymptotically but at any sufficiently small time step. Notation used in this section is independent of that used in earlier sections.

3.3.1 General Setup and Notation

Suppose given an ergm with arbitrary terms and constraints. All networks we consider will have the same node set as the ergm. Thus, the only thing potentially varying from one network state to the next is the edge set. We will call a network state valid if its edge set satisfies the constraints.

To prove cross-sectional exactness results, we will need the following assumption on the constraints:

(i) the graph whose vertices are valid network states and whose edges connect valid network states that differ in edge state on exactly one dyad is connected.

To prove durational exactness results, we will need the following additional assumption on the constraints:

(ii) given a valid network state, any edge in that network that is not unconditionally fixed by the constraints can be toggled off without violating the constraints.

Thus, for an upper bound on degree we will obtain both cross-sectional and durational exactness results, for a lower bound on degree we will obtain only cross-sectional exactness results, and for a fixed number of edges constraint we
will obtain no exactness results. We will call an edge free if it is not unconditionally fixed by the constraints, and we will consider durations only for free edges.

Suppose also given a vector of positive durations $\vec{D}_0$, indexed by a positive integer $k$ corresponding to some dyad-independent notion of dyad type. (Homogeneous dissolution models are allowed, regarding a scalar as a vector of length 1.) We define $\vec{D} = \lambda \vec{D}_0$, where $\lambda$ is a positive scalar whose value we will regard as a variable parameter, and write $D_k$ for the $k$th component of $\vec{D}$. The interpretation is that $\vec{D}_0$ is given in some specific units (say days, weeks, years, ...) and $\lambda^{-1}$ signifies the fraction of that time unit that is represented by a single tergm time step, making $\vec{D}$ the vector of durations in units of the tergm time step.

We let $\theta$ denote the canonical coefficients of the ergm, and $g$ the network statistics of the ergm. We will use $i$ and $j$ to refer to valid network states (not nodes); these symbols will always denote valid network states, whether or not we use the term valid in referring to them. The ergm model probability is

$$\pi_i = \pi(i) \equiv \exp(\theta \cdot g(i))/C$$

where $i$ is any valid network state and

$$C = \sum_j \exp(\theta \cdot g(j)),$$

the sum being taken over all valid network states $j$.

### 3.3.2 Exactness of Infinitesimal Time EDAs

We now define an “infinitesimal time step EDA tergm transition probability matrix” $R$ for sufficiently large values of the parameter $\lambda$ (relating $\vec{D}$ and $\vec{D}_0$ in the manner described in Section 3.3.1) as follows. If $i$ and $j$ are valid network states and $j$ equals $i$ plus one edge of type $k$, then

$$R_{ij} = \pi(j) \pi(i) \cdot 1_D^k.$$ 

If $i$ and $j$ are valid network states and $j$ equals $i$ minus one edge of type $k$, then

$$R_{ij} = \frac{1}{D_k}.$$ 

If $i$ and $j$ are valid network states that differ in edge state on more than one dyad, then

$$R_{ij} = 0.$$ 

If $i$ is any valid network state, then

$$R_{ii} = 1 - \sum_{j \neq i} R_{ij}.$$ 

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For $\lambda$ sufficiently large, this $R$ is a well-defined transition probability matrix on the state space of valid networks. (More specifically, for any valid $i$, we have $\sum_{j \neq i} R_{ij} = O(1/\lambda)$, and this will be $\leq 1$ for all valid $i$ when $\lambda$ is sufficiently large.)

By construction, $R$ satisfies detailed balance with respect to the ergm distribution $\pi$. Since $R$ is finite and irreducible, $\pi$ is the unique stationary distribution of $R$.

Observe that under the assumptions stated in Section 3.3.1 for durational exactness, given any valid network state $i$ and any free edge of type $k$ in $i$, the probability under $R$ to transition from $i$ to the state $j$ that equals $i$ minus the edge in question is exactly $\frac{1}{D_k}$. Under $R$, there are no other (positive probability) transitions out of $i$ that involve dissolving the edge in question, so this immediately implies that the mean duration of any free edge of type $k$ is $D_k$ (with a geometric distribution) under $R$.

We have thus shown that $R$ has precisely the cross-sectional and durational behavior we desire of the EDA (i.e., the ergm’s cross-sectional network distribution and the specified mean edge durations with geometric distributions), even though the ergm may have dyad-dependence. For this reason, it may be of interest to simulate $R$ directly (which presents its own set of challenges); see the appendix for more on this. In the present argument, we will use $R$ to approximate the true EDA tergm transition probability matrix with duration $\vec{D}$ so as to show that this latter transition probability matrix has the desired durational and cross-sectional behavior asymptotically as $\lambda \to \infty$.

Intuitively, we may think of $R$ as an approximate EDA tergm transition probability matrix (across time steps, not for a Metropolis-Hastings algorithm within time step) with duration $\vec{D} = \lambda \vec{D}_0$ where $\lambda \gg 1$ is so big that transitions involving more than one change can be ignored, and where we have dropped the normalizing constant from the off-diagonal transition probabilities and replaced $\frac{1}{D_k-1}$ with $\frac{1}{D_k}$ to fix durations. Somewhat more formally, from our analysis of $R$ and the true EDA tergm transition probability matrix $T$ given below, we can see that if we expand $T$ in powers of the small parameter $\lambda^{-1}$, then $R$ corresponds exactly to keeping the 0th and 1st order terms in this expansion, dropping all higher order terms. Thus, if we express the tergm time step $dt$ as $dt \propto \lambda^{-1}$, then we obtain $R$ from $T$ by regarding $dt$ as a formal infinitesimal: $dt$ itself is not zero, but $(dt)^2 = 0$.

### 3.3.3 Asymptotic Exactness of Discrete Time EDAs

For valid network states $i$ and $j$, let $i \cup j$ denote the network whose edges are precisely those that occur in either $i$ or $j$, and let $i \cap j$ denote the network whose edges are precisely those that occur in both $i$ and $j$. (All of $i, j, i \cup j,$ and $i \cap j$ have the same node set.) We additionally let $|(i \cup j)_k|$ denote the number of edges of type $k$ in $i \cup j$, and $|(i \cap j)_k|$ denote the number of edges of type $k$ in $i \cap j$.

Note that even if $i$ and $j$ are valid, the networks $i \cup j$ and $i \cap j$ need not be valid (if the constraints are dyad-dependent). We will assume that $\pi$ has been
extended (by its usual formula) to be defined on \( i \cup j \) whenever \( i \) and \( j \) are valid, but that it is normalized with respect to the space of valid networks only. (Since the dissolution model does not directly depend on the original ergm model, we will not need \( \pi(i \cap j) \), only \( \pi(i \cup j) \).)

We now let \( T \) denote the true EDA tergm transition probability matrix with duration \( \vec{D} \). We will use the old convention (1) in writing out the details below, but the result applies just as well to the new convention (3), whose transition probability matrix differs from that of the old by \( O(1/\lambda^2) \).

If \( i \) and \( j \) are any valid network states (including the possibility that \( i = j \)), we have

\[
T_{ij} = \frac{1}{C_i} \frac{\pi(i \cup j)}{\pi(i)} \prod_k \frac{1}{(D_k - 1)^{(|i \cup j)_k| - |(i' \cup j')_k|}}
\]

where

\[
C_i = \sum_j \frac{\pi(i \cup j)}{\pi(i)} \prod_k \frac{1}{(D_k - 1)^{(|i \cup j)_k| - |(i' \cup j')_k|}}
\]

so that \( \sum_j T_{ij} = 1 \) for all \( i \). It is apparent that

\[
C_i = 1 + O(1/\lambda).
\]

We wish to show that \( T = R + O(1/\lambda^2) \). When \( i \) and \( j \) differ by two or more edge states, we clearly have

\[
T_{ij} = O(1/\lambda^2).
\]

Since \( R_{ij} = 0 \) for such \( i \) and \( j \), this means \( T_{ij} = R_{ij} + O(1/\lambda^2) \) when \( i \) and \( j \) differ by two or more edge states. When \( j \) equals \( i \) plus one edge of type \( k \), we have

\[
T_{ij} = \frac{1}{C_i} \frac{\pi(j)}{\pi(i)} \frac{1}{D_k - 1} = \frac{1}{C_i} R_{ij} \frac{D_k}{D_k - 1}
\]

and when \( j \) equals \( i \) minus one edge of type \( k \), we have

\[
T_{ij} = \frac{1}{C_i} \frac{1}{D_k - 1} = \frac{1}{C_i} R_{ij} \frac{D_k}{D_k - 1}
\]

Since \( \frac{D_k}{D_k - 1} = 1 + O(1/\lambda) \), \( C_i = 1 + O(1/\lambda) \), and off-diagonal entries in \( R \) are manifestly \( O(1/\lambda) \), this implies that \( T_{ij} = R_{ij} + O(1/\lambda^2) \) when \( i \) and \( j \) differ by a single edge state. We have thus shown that \( T_{ij} = R_{ij} + O(1/\lambda^2) \) for all \( i \neq j \); since both \( T \) and \( R \) have row sum 1, this implies that \( T = R + O(1/\lambda^2) \), as desired.

We define a \( \lambda \)-dependent matrix \( \delta \) by

\[
T = R + \delta
\]

so that \( \delta = O(1/\lambda^2) \). By our explicit definition of \( R \), we see that

\[
R = I + \frac{\eta}{\lambda}
\]
where $I$ is the identity and $\eta$ is a fixed matrix (independent of $\lambda$).

Since $\pi$ is the unique stationary distribution of $R$ for any $\lambda$ (sufficiently large that $R$ is well-defined as a transition probability matrix), the left nullspace of $\eta$ is precisely span $\{\pi\}$. (If there were a (real) vector $\sigma \notin \text{span} \{\pi\}$ with $\sigma \eta = 0$, then as $\pi_i > 0$ for all valid $i$ we will have all entries of $\pi + \alpha \sigma$ positive for sufficiently small positive $\alpha$. Renormalizing $\pi + \alpha \sigma$ to a probability vector produces a stationary distribution of $R$ that is distinct from $\pi$, contradicting uniqueness.) The positive, continuous function $v \mapsto |v\eta|$ on the compact set $\{v \in \text{span} \{\pi\}^\perp : |v| = 1\}$ thus admits a positive lower bound $c > 0$.

Since the transition probability matrix $T$ is finite and irreducible for any $\lambda$, it possesses a unique $\lambda$-dependent stationary distribution which we choose to write as $\pi + \epsilon$ where $\epsilon$ is a $\lambda$-dependent perturbation to the ergm distribution $\pi$. By definition

$$\pi + \epsilon = (\pi + \epsilon)T = (\pi + \epsilon)(R + \delta) = \pi + \epsilon + \frac{\eta}{\lambda} + (\pi + \epsilon)\delta.$$ 

Rearranging,

$$\epsilon\eta = -\lambda(\pi + \epsilon)\delta = O(1/\lambda)$$

since $\delta$ is $O(1/\lambda^2)$ and $\pi + \epsilon$ is $O(1)$ (being a probability vector). We now write

$$\epsilon = \beta\pi + \pi^\perp$$

where $\beta$ is a $\lambda$-dependent scalar and $\pi^\perp$ is a $\lambda$-dependent element of $(\text{span} \{\pi\})^\perp$.

By our observations above about the left nullspace of $\eta$, we have

$$c|\pi^\perp| \leq |\pi^\perp \eta| = |\epsilon\eta| = O(1/\lambda)$$

thus showing that $|\pi^\perp| = O(1/\lambda)$ since $c > 0$. Letting $\vec{1}$ denote the vector of 1s, we have

$$1 = \vec{1} \cdot (\pi + \epsilon) = \vec{1} \cdot \pi + \vec{1} \cdot \epsilon = 1 + \vec{1} \cdot (\beta\pi + \pi^\perp) = 1 + \beta + \vec{1} \cdot \pi^\perp$$

thus showing

$$\beta = -\vec{1} \cdot \pi^\perp = O(1/\lambda).$$

Since $\epsilon = \beta\pi + \pi^\perp$ and both $\beta$ and $\pi^\perp$ are $O(1/\lambda)$ (while $\pi$ is of course $O(1)$), we have $\epsilon = O(1/\lambda)$. Since $\pi + \epsilon$ is the stationary distribution of $T$, this shows that the stationary distribution of $T$ converges to $\pi$ as $\lambda \to \infty$, proving asymptotic cross-sectional exactness for EDAs with dyad-dependent ergm model terms (and some dyad-dependent constraints).

We still need to note that mean durations are asymptotically correct, under the required assumptions stated in Section 3.3.1. This is true in the relative sense: for any $0 < \epsilon < 1$ (having nothing to do with the $\epsilon$ above), there is a $\lambda_0(\epsilon)$ such that $\lambda > \lambda_0(\epsilon)$ implies all free edges of type $k$ have mean duration between $(1 - \epsilon)D_k$ and $(1 + \epsilon)D_k$ under $T$. The reason is that free edges of type $k$ have dissolution probability exactly $\frac{1}{D_k}$ under $R$ and $T = R + O(1/\lambda^2)$; taking $\lambda$ sufficiently large (depending on the given $\epsilon$), we can guarantee that the
dissolution probability under $T$ of any free edge of type $k$ in any valid network state is between $\frac{1}{D_k}$ and $\frac{1}{(1-\epsilon)D_k}$, thus guaranteeing its mean duration is between $(1-\epsilon)D_k$ and $(1+\epsilon)D_k$ (and its cumulative distribution function is sandwiched between those of a geometric distribution with mean $(1+\epsilon)D_k$ and a geometric distribution with mean $(1-\epsilon)D_k$).

4 Discussion

We have presented a new form of the EDA for sparse networks, proven asymptotic exactness of the EDA for a broad class of dyad-dependent models, and identified a Markov chain possessing the desired cross-sectional and durational properties at any sufficiently small time step. Here, we provide some further commentary on these results.

Generally speaking, we expect the greatest benefit of the new approximation (3) over the old approximation (1) to be for sparse models with weak dyad-dependence and short duration. While (3) may be better than (1) for some strongly dyad-dependent models, there does not seem to be a good way to tell when this is the case short of simulating both approximations and examining the errors. It may be of interest to use the general result (2) if edge probabilities differ substantially from both 0 and 1/2. All of (1)-(3) become equivalent in the long-duration limit.

In the presentation of [2], the dissolution model for the EDA tergm was taken to be a submodel of the original ergm. It should be clear from the argument in Section 3.1 that this is unnecessary. More explicitly, given the ergm and durational targets, we can achieve the linear predictors (3) by taking the formation model of the EDA tergm to be the original ergm model plus any additional (dyad-independent) terms needed to capture the granularity of the durational targets; the coefficients of the formation model terms are chosen to satisfy (3).

All of (1)-(3) were derived under the assumption of dyad-independence. They can all have substantial errors for short-duration, strongly dyad-dependent models, regardless of density. The general way to improve their behavior while continuing to use discrete-time tergms is to shrink the size of the tergm time step, which obviates issues both of incorrect density (e.g., using the sparse result (1) for a non-sparse network) and of dyad-dependent interactions differing between the instantaneous and formation (i.e. union) networks. The validity of this approach (first suggested in [2]) is justified by the asymptotics in Section 3.3.

In principle, one could avoid these issues (of dyad-dependence and incorrect density) by using the “infinitesimal time tergm” $R$ defined in Section 3.3.2. As proven there, $R$ has precisely the cross-sectional and durational behavior we are trying to achieve with the EDA. There are drawbacks to using $R$, however. It is not a discrete-time tergm, and therefore machinery that exists for simulating discrete-time tergms (e.g., the tergm package [9]) cannot be used directly. While ergm machinery can be used instead (as noted in Section 10.1), “general” approaches to this may be inefficient for complex models, requiring either a high
degree of patience or some purpose-built algorithms for the task at hand. Also, one generally needs to incorporate some knowledge of edge probabilities under the ergm in order to ensure that $R$ is properly normalized; while this information is in principle contained in the ergm, it may not always be easy to extract in the required form, without wastefully inaccurate estimates.

It should be noted, however, that efficiency issues also exist for discrete-time EDA tergms. For example, the gweep model in Section 3.2 requires a large number of proposals in each discrete time step when using a general-purpose proposal with a high gweep target statistic, likely because dyads that would close triads are relatively rare and not stratified on in proposal dyad selection. The needs for efficiently simulating $R$ and for efficiently simulating the corresponding discrete-time EDA tergm are not entirely dissimilar. The additional burden of simulating $R$ comes primarily from the need to ensure it is properly normalized. While this may not be as onerous as e.g. computing the normalizing constant for a complex dyad-dependent ergm, it does require estimates of a somewhat similar nature. These estimates do not have to be perfect, but the more wasteful they are the less efficient the simulation will be.

Finally, we note that while we have focused exclusively on EDA tergms in this paper, the full class of tergms (and even stergms) is much more general. While data limitations may preclude taking advantage of this generality in some cases, the ability to estimate tergms in general would be of great practical value. Ultimately, a method for doing so may obviate the considerations of this paper.

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6 Declaration of Interest Statement

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Here we consider the problem of simulating the Markov chain $R$ introduced above. We will approach this assuming separate proposal and accept/reject steps, as in a Metropolis-Hastings algorithm (though $R$ has not been presented as a Metropolis-Hastings chain). For $i$ and $j$ differing in edge state on exactly one dyad, we have

$$R_{ij} = \frac{\pi(i \cup j)}{\pi(i)} \cdot \frac{1}{D_k}.$$

We desire a proposal with $P(j|i) \geq R_{ij}$ for all such $i, j$; having proposed $j$ from $i$, we then accept the move with probability $R_{ij} P(j|i)$ (which can be calculated from $P(j|i)$ and existing ergm machinery). This produces a Markov chain with the required transition probabilities.

The parameter $\lambda$ should always be taken large enough that $\sum_{j \neq i} R_{ij} \leq 1$ for all $i$, but can be taken larger as needed to ensure that $\frac{R_{ij}}{P(j|i)} \leq 1$ for all $i, j$ differing on a single dyad, for a given choice of proposal. In fact, the latter condition implies the former, since $\sum_{j \neq i} P(j|i) \leq 1$. Since the amount of real time represented by one time step (i.e., one proposal) is proportional to $\lambda^{-1}$, the larger we take $\lambda$, the more proposals we need to simulate a given amount of real time. It is thus generally preferable to take $\lambda$ as small as possible, which means coming up with a proposal $P(j|i)$ that matches $R_{ij}$ as closely as possible (when $\lambda$ is chosen just large enough that $\sum_{j \neq i} R_{ij} \leq 1$ for all $i$).

This is basically the problem of constructing a sampler for dyads that, given initial network state $i$, proposes toggling a given edge of type $k$ with relative weight $\frac{1}{D_k}$, and proposes toggling a given non-edge of type $k$ with relative weight $\frac{\pi(i \cup j)}{\pi(i)} \cdot \frac{1}{D_k}$ where $j$ is $i$ with the non-edge in question toggled on, in which case $\pi(i \cup j)/\pi(i)$ is simply the conditional odds of the dyad in question being an edge (given the rest of the edge states in $i$). In general this is not an easy problem to solve, but approximate solutions can work, as long as we increase $\lambda$ as needed to compensate for the error.

In (very) sparse networks, the conditional odds of a tie are often much less than 1, so it would be nice to restrict attention to the subset of valid networks that we are ever likely to visit when choosing the value of $\lambda$. That this is a legitimate thing to do (assuming we do not disconnect the state space in the process) can be seen as follows. Suppose we have a reasonable (strict) upper bound $N_E$ on the maximum number of edges that we are ever likely to see when simulating the ergm in question (this would be larger than the mean number
of edges, but, in many cases, not many times larger than the mean number of edges). We consider the Markov chain $R$ with state space restricted to networks having $N_E$ or fewer edges, where off-diagonal transition probabilities for $R$ in the restricted state space are the same as those for $R$, and where the self-transition probabilities for networks having exactly $N_E$ edges are increased as needed to compensate for removal of transitions to networks with more than $N_E$ edges. One verifies directly that $R$ satisfies detailed balance for $\pi$ restricted to networks with $N_E$ or fewer edges (and suitably renormalized), as $R$ satisfies detailed balance for $\pi$. Since $R$ and $\overline{R}$ have the same edge off-toggle probabilities on the restricted state space, the durations in $\overline{R}$ are the same as those in $R$. We can thus think of simulating $\overline{R}$ instead of $R$, using $\overline{R}_{ij} = R_{ij}$ when $i$ and $j$ both have $N_E$ or fewer edges and differ in edge state on exactly one dyad. Provided $\lambda$ is large enough to properly normalize $\overline{R}$ (on its restricted state space), we have a well-defined Markov chain with the desired properties.

We now consider some specific proposals (referencing by name some proposals in the statnet packages \cite{12}). To keep the discussion simple, we will restrict attention to homogeneous dissolution, and we will assume that the ergm is “uniformly sparse” in the sense that the conditional odds of an edge are always \leq 1. The simplest proposal we can imagine in this case is essentially randomtoggle: we choose $\lambda$ so that $\lambda D_0$ is equal to the number of dyads in the network, and we propose toggling dyads uniformly at random, rejecting those proposals that would violate the constraints, and accepting the others with probability $\lambda D_0 R_{ij}$, where $i$ and $j$ have their usual significance. It is easy to see that this proposal and choice of $\lambda$ satisfy the requirements outlined above. From intuition gained in the ergm regime, however, we expect this proposal to be inefficient (since the network is assumed sparse); a TNT-analogue would be more appropriate. We can specify such an analogue as follows. Suppose $c \leq 1$ is an upper bound for the conditional odds of any edge (we often have $c \ll 1$ for large, (very) sparse networks), and suppose $N_E$ is a (strict) upper bound for the maximum number of edges we are ever likely to encounter. With $N$ denoting the number of dyads in the network, we let $\lambda = 2 D_0^{-1} \max(\frac{N - N_E}{N + N_E}, cN)$, and our TNT-analogue proposal proposes toggling on a given non-edge with probability $\frac{1}{2N}$, and toggling off a given edge with probability $\frac{1}{2N_E} + \frac{1}{2N}$, with no change occurring with the remaining probability. For large, sparse, homogeneous models, we expect $cN$ to be roughly the mean number of edges, and $N_E$ to be within a reasonable factor of this mean, so overall $\lambda$ should be roughly on the order of twice the number of edges divided by the duration in natural units. The minimum number of proposals per unit real time is expected to be about twice the number of edges divided by the duration (half on-toggles, half off-toggles). In practice, heterogeneity is of great interest, so we are inclined to do better than the uniform odds estimate $c$ above. This leads naturally to stratified proposals, bearing some similarity to the StratTNT family of proposals already implemented in the existing ergm and tergm framework. Dyad-independent stratification is probably simplest, and can capture a fair amount of the odds variation for some models, but various dyad-dependent effects (especially “local” effects such as degree) could also be taken into account efficiently (some similar things are already done with
degree-based constraints in the bounded-degree proposals).

Finally, we consider when $R$ can be simulated as an ergm Metropolis-Hastings algorithm. We desire a proposal for which

$$\min \left( \frac{\pi(j)}{\pi(i)} \cdot \frac{P(i|j)}{P(j|i)}, 1 \right) \cdot P(j|i) = \frac{\pi(i \cup j)}{\pi(i)} \cdot \frac{1}{D}$$

whenever $i$ equals $j$ plus/minus one edge. For the TNT-analogue described above, if the odds bound $c$ satisfies $c \leq \frac{N_E}{N + N_N}$, then our desired transition probability equation is satisfied with $\frac{1}{2N_E} + \frac{1}{2N} = \frac{1}{D}$, i.e. $\lambda = 2D_0^{-1} \frac{N_N - N_E}{N + N_N}$. We may then simulate $R$ using the ergm Metropolis-Hastings algorithm with this modified version of TNT. More generally, we could always obtain the desired transition probabilities from an ergm Metropolis-Hastings algorithm that gives one (sufficiently small) probability to proposing an on-toggle of any non-edge and another (sufficiently small) probability to proposing an off-toggle of any edge, such that the ratio $\frac{\pi(j)}{\pi(i)} \cdot \frac{P(i|j)}{P(j|i)}$ is always less than (or equal to) 1 when $j$ equals $i$ plus one edge. In that sense, $R$ is never more general than an ergm Metropolis-Hastings algorithm (though the proposal we have just described may be far from optimal). This remains true (with obvious modification to the proposal) even if heterogeneous dissolution is allowed. The assumption of uniform sparsity is also not required.

Ultimately, the seemingly greater requirements imposed on the user in order to simulate $R$ (as opposed to a true discrete time EDA tergm) may limit its usefulness. It is probably worth noting, however, that existing experience with the discrete time EDA for non-trivial models shows that “all-purpose” proposals such as (discord)TNT may perform very inefficiently, and the need to develop more specialized proposals in the discrete time tergm case is not unlike the need develop $P(j|i)$ matching $R_{ij}$. 
Figure 1: Relative errors for edges and degree(1) statistics with old and new approximations for a 1000 node undirected network with mean degree 0.7 and a range of degree(1) targets and durations.
Figure 2: Relative errors for edges and degree(1) statistics with old and new approximations for a 1000 node undirected network with mean degree 1.0 and a range of degree(1) targets and durations.
Figure 3: Relative errors for edges and degree(1) statistics with old and new approximations for a 1000 node undirected network with mean degree 1.3 and a range of degree(1) targets and durations.
Figure 4: Relative errors for edges and degree(1) statistics with old and new approximations for a 1000 node undirected network with mean degree 2.0 and a range of degree(1) targets and durations.
Figure 5: Relative errors for edges, degree(1), degree(2), and gwesp(0.5, fixed = TRUE) statistics with old and new approximations for a 1000 node undirected network with mean degree 2.0, degree(1) target 200, degree(2) target 350, and a range of gwesp(0.5, fixed = TRUE) targets and durations.