ALAAMEE: Open-source software for fitting autologistic actor attribute models

Alex Stivala^{1,*}, Peng Wang^{2,1}, and Alessandro Lomi¹

¹Università della Svizzera italiana, Via Giuseppe Buffi 13, 6900 Lugano, Switzerland ²Swinburne University of Technology, John Street, Hawthorn VIC 3122, Australia *Corresponding author: alexander.stivala@usi.ch

April 5, 2024

Abstract

The autologistic actor attribute model (ALAAM) is a model for social influence, derived from the more widely known exponential-family random graph model (ERGM). ALAAMs can be used to estimate parameters corresponding to multiple forms of social contagion associated with network structure and actor covariates. This work introduces ALAAMEE, open-source Python software for estimation, simulation, and goodness-of-fit testing for ALAAM models. ALAAMEE implements both the stochastic approximation and equilibrium expectation (EE) algorithms for ALAAM parameter estimation, including estimation from snowball sampled network data. It implements data structures and statistics for undirected, directed, and bipartite networks. We use a simulation study to assess the accuracy of the EE algorithm for ALAAM parameter estimation and statistical inference, and demonstrate the use of ALAAMEE with empirical examples using both small (fewer than 100 nodes) and large (more than 10 000 nodes) networks.

Keywords— autologistic actor attribute model, ALAAM, exponential-family random graph model, ERGM, social influence, social networks, Python software

1 Introduction

The autologistic actor attribute model (ALAAM) is a model for social influence or social contagion, the process whereby actors in a social network adopt the attitudes, opinions, or beliefs of their network neighbours. This process may also be known as diffusion, or, in economics, peer effects (Bramoullé et al., 2020). Originally introduced by Robins et al. (2001b), the ALAAM is a variant of exponential-family random graph model (ERGM) for social networks (Robins et al., 2001a; Daraganova, 2009; Daraganova and Robins, 2013; Lusher et al., 2013; Amati et al., 2018; Koskinen, 2020, 2023). As such, the ALAAM is a cross-sectional model: given a single observation of the social network and the attribute (assumed to be binary in the ALAAM) which is hypothesized to be socially contagious, the model is used to estimate parameters relating to this contagion. In the ALAAM, the network is assumed to be fixed (exogenous), and the binary outcome variable is modeled (the variable is endogenous). This in contrast to the ERGM, in which the tie variables are modeled (tie formation is an endogenous process), based on fixed actor attributes. Note that the outcome (binary) attribute of an actor in the ALAAM is allowed to depend on its values for other actors connected to it in the social network, hence the "autologistic" in the name.

Unlike the more widely known network autocorrelation model (Ord, 1975; Cliff and Ord, 1981; Doreian, 1981; Anselin, 1990; Friedkin, 1990; Leenders, 2002), in which social contagion is associated with a single parameter, the ALAAM can be used to estimate parameters corresponding to multiple forms of social contagion associated with more complex relationships between network structure, the outcome variable, and other actor attributes. This is discussed further in Stivala et al. (2020b), and the dependency assumptions and the types of terms these allow in the ALAAM are discussed in Daraganova (2009); Koskinen and Daraganova (2022).

ALAAMs can also be estimated for network data obtained via snowball sampling (Daraganova, 2009; Daraganova and Robins, 2013; Kashima et al., 2013; Stivala et al., 2020b). For a recent introduction and review of ALAAM usage, see Parker et al. (2022), and for a comprehensive survey of ALAAM applications, Stivala (2023).

The most commonly used software for ALAAM modeling is the IPNet Windows application (Wang et al., 2009), or its successor, the Windows application MPNet (Wang et al., 2014, 2022), which allows for ERGM and ALAAM modeling with undirected, directed, bipartite, and multilevel networks. Note that the widely-used R package statnet (Handcock et al., 2008; Hunter et al., 2008; Hummel et al., 2012; Handcock et al., 2022; Krivitsky et al., 2023) for ERGM modeling, does not implement ALAAM,¹ although the exponential-family random network model (ERNM), a generalization of the ERGM and ALAAM, which models both social selection and social influence simultaneously (Fellows and Handcock, 2012, 2013; Wang et al., 2024) is implemented using statnet. The only other publicly available code for ALAAM modeling is the R code for estimating Bayesian ALAAMs described by Koskinen and Daraganova (2022).

These existing implementations are limited, both by the algorithms implemented and details of their implementation, in the size of the networks on which they can practically be used. Therefore, in order to be able use ALAAMs with large (thousands of nodes or more) networks, such as, for example, those that can be collected from online social network data, an alternative is required.

This paper describes one such alternative, ALAAMEE, open-source Python code for ALAAM parameter estimation, simulation, and goodness-of-fit testing. The ALAAMEE software implements the same stochastic approximation algorithm for ALAAM parameter estimation as IPNet and MPNet do (Snijders, 2002), which is practical for networks of the order of thousands, or in some cases tens of thousands, of nodes in size or smaller. For larger networks, it also implements the "equilibrium expectation" (EE) algorithm (Byshkin et al., 2016, 2018; Borisenko et al., 2020), which has previously been used for estimating ERGM parameters for very large networks (Byshkin et al., 2018; Chakraborty et al., 2020; Stivala et al., 2019, 2020a; Stivala and Lomi, 2022)

2 The autologistic actor attribute model (ALAAM)

The ALAAM, modeling the probability of attribute Y (taking the form of a binary vector y) given the network X (a matrix of binary tie variables) can be expressed as (Daraganova and Robins, 2013):

$$\Pr(Y = y | X = x) = \frac{1}{\kappa(\theta_I)} \exp\left(\sum_I \theta_I z_I(y, x, w)\right)$$
(1)

where θ_I is the parameter corresponding to the network-attribute statistic z_I , in which the "configuration" I is defined by a combination of dependent (outcome) attribute variables y, network variables x, and actor covariates w, and $\kappa(\theta_I)$ is a normalizing quantity which ensures a proper probability distribution.

Just as for ERGM, parameter estimation for ALAAM is a computationally intractable problem, and so the maximum likelihood estimate (MLE) of the ALAAM parameters is found using Markov chain Monte Carlo (MCMC) methods (see Hunter et al. (2012) for an overview in the ERGM context).

The sign and significance of the ALAAM parameters θ_I support inferences about the statistical relationship between the corresponding configurations $z_I(y, x, w)$ and the outcome attribute binary vector y, each conditional on all the other effects included in the model.

For example, consider the frequently used contagion effect, using an undirected network for simplicity. The statistic for contagion is the number of pairs of directly connected nodes, *i* and *j* ($i \neq j$) where $x_{ij} = 1$, in which both nodes have the outcome attribute $y_i = y_j = 1$ (see Table 1). If the contagion parameter is found to be positive and significant, this means the contagion configuration (a directly connected pair of nodes both with the outcome attribute) occurs more frequently than expected by chance, given all the other effects included in the model. So there is a statistically significant correlation between a pair of nodes being directly connected, and both having the outcome attribute (conditional on the other effects in the model).

The distinction between the ERGM and the ALAAM arises from the assumptions and hypotheses behind the model. In the ERGM, modeling tie formation, we might hypothesize that having the same attribute value affects (increases, for homophily) the probability of a tie between two nodes, and test for this. In the ALAAM, modeling

¹Although, as noted in Barnes et al. (2020), an ALAAM can be considered as an ERGM for a two-mode network, with the N nodes of one mode representing the actors, and a tie from an actor to the single node of the other mode representing that actor having the outcome attribute, with the observed N node social network as a fixed covariate. And hence this could be implemented as a statnet ergm model, but whether or not it is practical is another question. This conception of an ALAAM could also be a way of implementing a multivariate ALAAM, by having more than one "outcome" node.

Table 1: Configurations used in ALAAMs for undirected networks.

Name	Illustration	Description
Density	\bigcirc	Baseline attribute density (incidence). Also used with directed networks.
Activity		Tendency for actor with the attribute to have ties.
Contagion		Tendency for actor with the attribute to be tied to an actor also with the at- tribute.
Two-star		Tendency of actor with attribute to have additional ties over Activity.
GWActivity		Geometrically weighted activity, described in Stivala (2023). This is used to account for the degree distribution of nodes with the outcome attribute, avoiding problems of near-degeneracy that can occur when using the Activity configuration.
Alter-2Star1		Partner activity two-path; tendency of an actor with the attribute to have a tie to another actor with a tie to a third actor.
Alter-2Star2		Also known as indirect partner attribute. Structural equivalence of actors with the attribute (two-path equivalence); tendency of actors with the attribute to have the same network partner in common.
Partner-Activity		Also known as partner attribute activity. Tendency of the attribute to be present on two directly connected nodes in a two-path.
Partner-Resource		Also known as partner-partner attribute; tendency of the attribute to be present in all three nodes in a two-path.
T1		Actor triangle; tendency of actor with attribute to be involved in a triangle.
T2		Partner attribute triangle; tendency of attribute to be present in actors involved in triangles with another node that also has the attribute.
Т3		Partner-partner attribute triangle; tendency of attribute to be present in all three nodes in a triangle.
attribute_oOc	0	Covariate effect for continuous covariate <i>attribute</i> . The "oOc" notation is from IPNet (Wang et al., 2009), and we may omit this when there is no ambiguity, e.g. "Age_oOc" may also be written simply as "Age". Also used in directed and bipartite networks.
attribute_o_Oc	0	Covariate effect for continuous covariate <i>attribute</i> on partner node (outcome attribute related to continuous attribute on partner node). The "o_Oc" notation is from IPNet (Wang et al., 2009), and we may instead write this as "partner <i>attribute</i> ".
attribute_oOb	0	Covariate effect for binary covariate <i>attribute</i> . The "oOb" notation is from IPNet (Wang et al., 2009), and we may omit this when there is no ambiguity, e.g. "Binary_oOb" may also be written simply as "Binary". Also used in directed and bipartite networks.

Legend:

Node with outcome attribute

O Node irrespective of outcome attribute

Name	Illustration	Description
Sender		Tendency of actors with the attribute to have outgoing ties (activity).
Receiver		Tendency of actors with the attribute to have incoming ties (popularity).
Contagion		Tendency of the attribute to be present in both actors connected by directed tie.
Reciprocity	OM NO	Tendency of the attribute to be present in an actor connected to another by a reciprocated (mutual) tie.
Contagion reciprocity		Also known as mutual contagion. Tendency of the attribute to be present in both actors connected by a reciprocated tie.
Ego in-two-star		Tendency of the attribute to be present in an actor with additional incoming ties over Receiver.
Ego out-two-star		Tendency of the attribute to be present in an actor with additional outgoing ties over Sender.
Mixed-two-star		Tendency of the attribute to be present in an actor in the broker position be- tween two other nodes (local brokerage).
Mixed-two-star source		Tendency of the attribute to be present in an actor in the source position in local brokerage.
Mixed-two-star sink		Tendency of the attribute to be present in an actor in the sink position in local brokerage.
Transitive triangle T1		Tendency of the attribute to be present in an actor in a transitive triangle, the broker position in Mixed-two-star bypassed by a transitive tie.
Transitive triangle T3		Contagion clustering: tendency of the attribute to be present in all three actors in a transitive triangle.
Cyclic triangle C1		Tendency of the attribute to be present in an actor in a cyclic triangle.
Cyclic triangle C3		Contagion cycle: tendency of the attribute to be present in all three actors in a cyclic triangle.

Table 2: Configurations used in ALAAMs for directed networks.

the outcome attribute, we might hypothesize that having a network tie affects (increases, for contagion) the probability that both nodes will have the outcome attribute. Distinguishing homophily and contagion in an observational network study is in general a difficult problem (Shalizi and Thomas, 2011), and ALAAM parameters indicate only (auto-)correlation, not causation.

Once parameters for an ALAAM model of an observed network and outcome binary attribute have been estimated, these can be used to simulate, again using MCMC, a set of outcome binary vectors from the model. These simulated outcomes can be used for goodness-of-fit testing and model evaluation. For further explanation and examples, see Parker et al. (2022).

3 Implementation

ALAAMEE is implemented in Python 3, and uses the NumPy (Harris et al., 2020) package for array data types and linear algebra. The Python code does not require any other packages, simply using a "dictionary of dictionaries" data structure to implement graphs. Just as described in Bianchi et al. (2022), this allows simple and efficient graph construction and implementation of the graph operations required, such as testing for the existence of an edge or arc, and iterating over the neighbours of a node.

ALAAM parameters are usually estimated by stochastic approximation with the Robbins–Monro algorithm (Robbins and Monro, 1951; Snijders, 2002). This is the method used in MPNet, and is also implemented in ALAAMEE. For the stochastic approximation algorithm, all stages of the estimation, including point estimation, estimation of standard errors from the Fisher information matrix (Snijders, 2002), and simulation-based goodness-of-fit testing, are implemented in Python.

For larger networks, on the order of tens of thousands of nodes or more, this method may no longer be practical. For such networks, the EE algorithm can be used, and ALAAMEE also implements this algorithm. The EE algorithm works differently (Stivala et al., 2020a). In this algorithm, a number of estimation processes (each of which is a separate Python task) are run independently. Because these runs are independent, they can be run in parallel to minimize the elapsed time taken.

From the results of these multiple estimation runs, a point estimate and estimated standard error are computed using an R script that uses the mcmcse R package (Flegal et al., 2021) to estimate the Fisher information matrix and the asymptotic covariance matrix for the MCMC standard error with the multivariate batch means method (Dai and Jones, 2017; Flegal and Jones, 2010; Jones et al., 2006; Vats et al., 2018, 2019). The overall estimate and its estimated standard error are then computed from these multiple independent runs as the inverse variance weighted average (Hartung et al., 2008, Ch. 4).

Scripts are provided to run the parallel estimations using either GNU Parallel (Tange, 2018) or, for Linux compute clusters, SLURM (Yoo et al., 2003) job arrays. Scripts for processing network data and converting it between different formats, taking snowball samples from networks, making plots, and computing the Wilson score interval (Wilson, 1927) for the binomial proportion score interval (used to find confidence intervals for Type I and II error rates in the simulation study described in Section 4) are written in R and use the igraph (Csárdi and Nepusz, 2006), ggplot2 (Wickham, 2016), and PropCIs (Scherer, 2018) R packages.

ALAAMEE also implements estimation (and simulation) conditional on snowball sampled network structure, as described in Pattison et al. (2013); Stivala et al. (2016) in the context of ERGM, and in Daraganova (2009); Daraganova and Pattison (2013); Kashima et al. (2013); Stivala et al. (2020b) for ALAAM.

3.1 Change statistics

It is a property of the ALAAM (since it is a variant of the ERGM), that the odds of a node having the outcome attribute, conditional on the values of the outcome for the other nodes, is a function of the change in the vector of statistics associated with switching the outcome attribute value of that node from 0 to 1. It follows that, in implementing the MCMC process for ALAAM simulation and estimation, only these change statistics (Hunter and Handcock, 2006; Snijders et al., 2006; Hunter et al., 2012) need be implemented. That is, rather than writing functions to count each of the configurations in the data, we need only write functions that compute the change statistic value resulting from changing the outcome attribute value of a given node from 0 to 1. The value of the statistics in observed data can be computed by summing the change statistics for each element of the outcome attribute vector that is equal to 1.

```
def changeContagionReciprocity(G, A, i):
1
2
      change statistic for Contagion Reciprocity (mutual contagion)
3
4
      *<->*
5
      ....
6
     delta = 0
7
      for u in G.outIterator(i):
8
          if A[u] == 1 and G.isArc(u, i):
9
              delta += 1
      return delta
```

Figure 1: Example change statistic implementation: the change statistic for "contagion reciprocity" in a directed network.

For example, consider the simplest statistic, attribute Density, sometimes instead called Incidence (Parker et al., 2022) to avoid confusion with graph density. This statistic is simply the number of nodes with the outcome attribute. Its corresponding change statistic is simply the constant 1, since for any node, if its outcome attribute value is switched from 0 to 1, then that increases the Density statistic by 1.

Every change statistic in ALAAMEE is implemented as a function of the form changeStatname(G, A, i) where G is a Graph (or Digraph or BipartiteGraph, as appropriate to the change statistic) object, A is a binary outcome vector, and i is a node identifier. The function returns the change statistic value for switching the node outcome attribute value A[i] from 0 to 1. It is a precondition of the change statistic functions that A[i] == 0. An example is shown in Figure 1. Python "docstrings" are used to document the change statistic function, including an ASCII diagram illustrating the corresponding configuration. This allows the documentation to be viewed at the interactive Python prompt with the built-in help() function.

The code shown in Figure 1 implements the change statistic for the Contagion reciprocity statistic, also known as mutual contagion (see Table 2). This statistic counts the number of pairs of nodes with a reciprocated (mutual) tie between them, in which both nodes have the outcome attribute. Hence the change statistic, computing the change in the statistic when a node *i* has its outcome variable changed from 0 to 1, counts the number of out-neighbours of *i*, i.e. nodes *u* such that there is an arc $i \rightarrow u$, such that *u* has the outcome variable and there is also an arc $u \rightarrow i$.² The ALAAMEE source code repository³ includes unit tests for verifying the correctness of change statistic implementations against known correct values, verifying that alternative implementations give the same results, and comparing their execution speeds.

Some change statistics make use of nodal attribute values. These change statistic functions take also as their first parameter the name of the attribute to use, used as the key in the relevant attribute dictionary in the Graph object. So that these functions have the same signature as the structural statistics, the higher-order function functools.partial () is used to create a function with the (G, A, i) signature. For example, partial (changeoOc, "age") returns a function with the required (G, A, i) signature, implementing the change statistic for outcome related to nodal continuous attribute "age", given the original generic change statistic function changeoOc(attrname, G, A, i). This usage is illustrated in the empirical example in Section 5.1. The same technique is used for statistics that use an auxiliary ("setting") network, a distance matrix, the decay value for geometrically weighted statistics (Stivala, 2023), and for the node type (mode) in two-mode graphs using the BipartiteGraph object.

For some change statistics, computation can be made far more efficient and scalable by using a sparse matrix counting two-paths between each pair of nodes in the network. A similar technique, implementing the sparse matrix as a hash table, has been used for ERGM change statistics (Stivala et al., 2020a). This technique is far simpler and more advantageous for ALAAM estimation and simulation in ALAAMEE, for two reasons, First, in ALAAM the network is exogenous, and hence, once constructed, the two-path lookup sparse matrix need not be modified. Second, the sparse matrix data structure is very easily and efficiently implemented in Python as a "dictionary of dictionaries" data structure, just as the graph data structures are, since dictionaries are a built-in data type in Python.

²Note that the code in Figure 1 can be written less verbosely and more elegantly, and arguably in more idiomatic Python style, in a single line using a list comprehension: return sum([(G.isArc(u, i) and A[u] == 1) for u in G.outIterator(i)]), however this turns out to be slower.

³https://github.com/stivalaa/ALAAMEE

Currently, change statistics for undirected and directed one-mode networks, and undirected two-mode (bipartite) networks are implemented. These statistics include all of those used in the ALAAM models published in Kashima et al. (2013); Letina (2016); Letina et al. (2016); Diviák et al. (2020) for undirected networks, and Gallagher (2019); Parker et al. (2022) for directed networks, for example. ALAAMEE has been used to estimate ALAAM parameters for a director interlock (bipartite) network (Stivala et al., 2023). Change statistics for the new geometrically weighted ALAAM statistics described in Stivala (2023) are also implemented in ALAAMEE.

We hope that the use of Python will facilitate the implementation of further user-defined change statistics, since adding ALAAM change statistics to the Python code, for example as shown in Figure 1, would appear to be considerably easier than the procedure for adding new ERGM change statistics in the statnet ergm package, which requires writing both R and C code (Hunter et al., 2013).

4 Simulation study for estimation using the equilibrium expectation algorithm

To evaluate the performance of the EE algorithm implemented in ALAAMEE for ALAAM parameter estimation and statistical inference, we apply it to estimating parameters for ALAAM outcome vectors with known parameters. These are obtained by generating the outcome vectors by ALAAM simulation from a fixed network (and covariates) with a given set of ALAAM parameters. This is done over a set of 100 simulated ALAAMs, allowing us to measure the point estimate bias and RMSE (root mean square error), as well as the type I (false positive) and type II (false negative) error rates in inference.

This technique was used to evaluate ERGM estimation from snowball sampled network data in Stivala et al. (2016) and for ERGM estimation by the EE algorithm in Stivala et al. (2020a). It was used to evaluate ALAAM estimation from sampled network data in Stivala et al. (2020b).

Here we use the simulated ALAAM outcome values on the "Project 90" network, a sexual contact network of high-risk heterosexuals in Colorado Springs (Potterat et al., 2004; Woodhouse et al., 1994; Klovdahl et al., 1994; Rothenberg et al., 1995). These are exactly the simulations described in Stivala et al. (2020b). The network is the giant component of the Project 90 network, consisting of 4430 nodes, with mean degree 8.31. Binary and continuous attributes are generated for the nodes: the binary attribute is assigned the positive value for 50% of the nodes, chosen at random, and the continuous attribute value v_i at each node i is $v_i \stackrel{iid}{\sim} N(0, 1)$. From this network and nodal attributes, ALAAM outcome vectors are simulated with parameters (Density, Activity, Contagion, Binary, Continuous) = (-15.0, 0.55, 1.00, 1.20, 1.15). As described in Stivala et al. (2020b), these parameters were chosen so that approximately 15% of the nodes have the positive outcome attribute.

Figure 2 and Table 3 show the results for using the EE algorithm implemented in ALAAMEE to estimate parameters from the simulated ALAAMs. For all parameters other than Binary, the type II error rate is less than 5%. For the Binary parameter, however, the type II error rate is estimated to be 59%, with a 95% confidence interval [49%,68%]. When using the stochastic approximation algorithm on the same data, used as the baseline for comparing against results from sampled data in Stivala et al. (2020b), the type II error rate is less than 5% for all parameters, including Binary (Fig. A1). Comparing the results for the EE algorithm (Fig. 2) and the stochastic approximation algorithm (Fig. A1) for the Binary parameter, it seems that the problem is likely not the point estimate, but rather that the estimated standard errors (and hence confidence interval) from the EE algorithm are too large, giving a high type II (false negative) error rate on the Binary parameter. Although this problem only occurs on the Binary parameter, the coverage rate is higher than the nominal 95% on all the parameters: in fact is 100% for the EE algorithm, while for the stochastic approximation algorithm, it is still higher than 95%, but less than 99% (Fig. A1).

Each of these estimation runs, with the default EE algorithm parameters, took on average 49 minutes (sd = 12.7, min. = 44, max. = 216, median = 46, N = 8000) on an Intel Xeon E5-2650 v3 2.30 GHz processor on a Linux cluster.

In order to measure the type I error rate on each parameter, an ALAAM simulation without the corresponding effect (the parameter value is zero) is required. Hence for each of the ALAAM parameters considered (other than Density, which if zero results in almost all nodes have the outcome attribute), another set of 100 ALAAM outcome vectors are simulated, with the parameter set to zero and the other parameters unchanged (apart from Activity, which if zero results in very few nodes having the outcome attribute, and so Density is changed to -7.0 for this case only).

The results for estimating the type I error rate for ALAAM estimation by the EE algorithm are shown in Table 4. In all cases the type I error rate is less than the nominal 5%. Just as for the type II error rate results, however, the coverage rate is higher than the nominal 95%, indicating that the standard error estimates might be too large.



Figure 2: Parameter estimates and estimated standard errors from the EE algorithm for the Project 90 network with simulated attributes. The error bars show the nominal 95% confidence interval. The horizontal line shows the true value of the parameter, and each plot is annotated with the mean bias, root mean square error (RMSE), the percentage of samples for which the true value is inside the confidence interval (coverage rate), and the Type II error rate (False Negative Rate, FNR). N_C is the number of samples (of the total 100) for which a converged estimate was found.

Effect	Bias	RMSE	False negative rate (%)		in C.I.	Total	Mean	Total	
			Estim.	95%	• C.I.	(%)	samples	runs	runs per
				lower	upper		converged	converged	sample
Density	-0.4248	1.1780	0	0	4	100	100	100.00	100
Activity	0.0134	0.0475	0	0	4	100	100	100.00	100
Contagion	0.0338	0.0826	0	0	4	100	100	100.00	100
Binary	0.0249	0.2599	59	49	68	100	100	100.00	100
Continuous	0.0601	0.1724	0	0	4	100	100	100.00	100

Table 3: Type II error rate from estimation of simulated outcomes using the EE algorithm.

The "estim.", "lower", and "upper" columns show the point estimate and lower and upper 95% confidence interval (C.I.), respectively, of the Type II error rate (false negative rate). This C.I. is computed as the Wilson score interval (Wilson, 1927; Scherer, 2018). The "in C.I. (%)" column is the coverage rate for the nominal 95% confidence interval. Results are over 100 simulated ALAAM outcome vectors (samples), each of which is estimated with 100 parallel estimation runs.

Effect	Bias	RMSE	False positive rate (%)		in C.I.	Total	Mean	Total	
			Estim.	95%	C.I.	(%)	samples	runs	runs per
				lower	upper		converged	converged	sample
Activity	0.0050	0.0150	0	0	4	100	100	100.00	100
Contagion	0.0011	0.0386	0	0	4	100	100	100.00	100
Binary	0.0189	0.2924	0	0	4	100	100	99.98	100
Continuous	0.0471	0.1638	0	0	4	100	100	99.99	100

Table 4: Type I error rate from estimation of simulated outcomes using the EE algorithm.

The "estim.", "lower", and "upper" columns show the point estimate and lower and upper 95% confidence interval (C.I.), respectively, of the Type I error rate (false positive rate). This C.I. is computed as the Wilson score interval (Wilson, 1927; Scherer, 2018). The "in C.I. (%)" column is the coverage rate for the nominal 95% confidence interval. Results over 100 simulated ALAAM outcome vectors (samples), each of which is estimated with 100 parallel estimation runs.



Figure 3: Type II error rate (false negative rate) as the number of runs used for each sample is varied.

In the results discussed so far, the point estimates and standard errors are estimated, as described in Section 3, from 100 parallel estimation runs. Figure 3 shows the effect on the type II error rate when the number of runs is varied from 1 up to 100 (the last data point, for 100 runs, therefore corresponding to the results shown in Table 3 and Figure 2). This shows that for all parameters other than Binary, 50 runs (indeed, for the Density, Activity, and Contagion parameters, fewer than 20 runs) are more than sufficient to obtain a type II error rate of less than 5%. For the Binary parameter, however, the type II error rate declines far more slowly, and is still above 50% with 100 runs, as we have seen.

Figure A2 shows the corresponding results for the type I error rate. Although this graph is singularly uninteresting to look at, it shows that it is "safe" to vary the number of runs, in the sense that the type I error rate remains unchanged and less than 5% at all values tested.

The results of these simulation experiments indicate that it is desirable for the purposes of decreasing the type II error rate, without increasing the type I error rate, to use as many runs of the ALAAMEE estimation process as practical. Because these runs are independent, they can be run in parallel to minimize elapsed time, taking advantage of as many processor cores as you have available. The results here indicate that 100 runs is a reasonable number, however for some parameters this might still result in an undesirably high type II error rate.

5 Empirical examples

5.1 Small network

To demonstrate how to use the implementation of the stochastic approximation algorithm for estimating ALAAM parameters, we will use the excerpt of 50 girls from the "Teenage friends and lifestyle study" data (Michell and Amos, 1997; Pearson and Michell, 2000; Pearson and West, 2003; Pearson et al., 2006; Steglich et al., 2006; West and Sweeting, 1996), which is used as an illustrative example for the SIENA software (Ripley et al., 2023) for stochastic actor-oriented models (SAOMs) (Snijders, 2017). The data consists of an excerpt of 50 girls from panel data recording friendship networks and substance use over a three year period from 1995, when the pupils were aged 13, to 1997, in the West of Scotland. The data includes information on smoking (tobacco), alcohol, and cannabis consumption, as well as sporting activities.

This data was also as a tutorial example for the Bayesian ALAAM (Koskinen and Daraganova, 2022) implementation in R.⁴ As noted in the description for this data,⁵ this is not a properly delineated network, and is used only for illustrative purposes.

Unlike SAOMs, we cannot use ALAAMs to model the co-evolution of network and actor covariates based on longitudinal data: we can only model a single binary outcome given a fixed network and other (fixed) covariates, as well as the outcome itself on other nodes. As in the Bayesian ALAAM R tutorial, we will use smoking at the second wave as the outcome variable, and use the network and other covariates from the first wave. Hence the network assumed to diffuse social contagion is observed before the outcome variable, as discussed in Parker et al. (2022).

The categorical variable for smoking is converted to binary by treating any amount of smoking other than completely non-smoking as the positive binary outcome.

Python code to use ALAAMEE to specify an ALAAM model for this data and estimate its parameters using the stochastic approximation algorithm (Snijders, 2002) is shown in Figure 4. It also automatically does a goodness-of-fit test for the converged model (if found). This code took less than two minutes to run on a Windows 10 personal computer with an Intel Core i5-10400 2.90 GHz processor, giving the model shown in Figure 5. The results are consistent (only the contagion and alcohol effects are significant, and positive) with those from estimating the same model using MPNet (Wang et al., 2014). For this small network, MPNet is faster, taking approximately one minute, on the same PC.

The model shown in Figure 5 indicates a significant and positive contagion effect: smokers tend to be directly connected to other smokers. The only other significant effect is for alcohol consumption; this is positive, indicating that drinkers are more likely to smoke.

The goodness-of-fit statistics for this model are shown in Figure 6. The effects in the model are at the top, followed by additional effects which are not included in the model. For effects in the model, the convergence statistic (t-ratio)

⁴https://github.com/johankoskinen/ALAAM

⁵https://www.stats.ox.ac.uk/~snijders/siena/s50_data.htm

```
1 from functools import partial
2 import estimateALAAMSA
3 from changeStatisticsALAAMdirected import *
4 from changeStatisticsALAAM import changeDensity, changeoOc
5
6 model_param_funcs = [changeDensity, changeSender, changeReceiver, changeContagion,
     changeReciprocity, changeContagionReciprocity, changeEgoInTwoStar, changeEgoOutTwoStar,
     changeMixedTwoStar, changeTransitiveTriangleT1, partial(changeoOc, "sport"), partial(
     changeoOc, "alcohol")]
7
8 estimateALAAMSA.run_on_network_attr(
         's50-friendships-directed.net',
9
         model_param_funcs,
10
         [param_func_to_label(f) for f in model_param_funcs],
11
12
          outcome_bin_filename = 's50-outcome.txt',
         binattr_filename = 's50-binattr.txt',
13
          contattr_filename = 's50-contattr.txt',
14
          catattr_filename = 's50-catattr.txt',
15
          directed = True
16
17
      )
```

Figure 4: Python code for estimating parameters of an ALAAM model for the teenage friends and lifestyle data excerpt, with smoking as the outcome variable. After a converged model is found, this will also do a goodness-of-fit test.

	Estimate	Std.Error	t-ratio)
Density	-1.150	2.375	0.021	
Sender	0.340	1.213	-0.022	
Receiver	-0.933	1.403	0.049	
Contagion	1.861	0.910	0.010	*
Reciprocity	1.171	1.465	0.029	
ContagionReciprocity	-2.913	2.054	0.031	
EgoInTwoStar	0.328	0.484	0.049	
EgoOutTwoStar	0.214	0.593	-0.053	
MixedTwoStar	-0.278	0.446	-0.010	
TransitiveTriangleT1	-0.958	0.584	0.065	
sport_oOc	-1.541	1.026	0.001	
alcohol_oOc	0.821	0.398	-0.023	*

Figure 5: Output from using the code in Figure 4 to estimate ALAAM parameters by stochastic approximation for the teenage friends and lifestyle data excerpt, with smoking as the outcome variable. Asterisks indicate statistical significance at p < 0.05.

	t-ratio
Density	0.075
Sender	0.024
Receiver	0.084
Contagion	0.051
Reciprocity	0.075
ContagionReciprocity	0.083
EgoInTwoStar	0.079
EgoOutTwoStar	-0.012
MixedTwoStar	0.030
TransitiveTriangleT1	0.084
sport_oOc	0.066
alcohol_oOc	0.018
MixedTwoStarSource	-0.036
MixedTwoStarSink	-0.372
TransitiveTriangleT3	-0.045
TransitiveTriangleD1	-0.056
TransitiveTriangleU1	-0.050
CyclicTriangleC1	0.053
CyclicTriangleC3	-0.490
AlterInTwoStar2	0.002
AlterOutTwoStar2	-0.539

Figure 6: Goodness-of-fit output for the model in Figure 5, from running the code in Figure 4.

should be less than 0.1 in magnitude (just as they must be for the model to be considered converged by the estimation algorithm). Figure 6 shows that all the effects included in the model meet this criterion.

For effects not included in the model, a rule of thumb is that the t-ratio should be less than 2.0 in magnitude for an acceptable fit (Parker et al., 2022), although some authors have used a stricter threshold of 1.0 (Kashima et al., 2013; Daraganova and Pattison, 2013), or even 0.3 (Diviák et al., 2020). Parker et al. (2022) use 1.645, signifying statistical significance at the 5% level (one-tailed). All of the effects not included in the model, but included in the goodness-of-fit test shown in Figure 6, are less than 1.0 in magnitude, indicating this model has an acceptable fit for all the statistics included in the goodness-of-fit test.

5.2 Large networks

For networks with tens of thousands of nodes or more, estimating ALAAM parameters with the stochastic approximation algorithm may no longer be practical. For such networks, we can instead use the EE algorithm. We will use three such networks as examples for ALAAMEE parameter estimation: undirected online friendship networks for the "Deezer" music streaming service in Croatia, Hungary, and Romania (Rozemberczki et al., 2019). These networks are publicly available from the Stanford large network dataset collection (Leskovec and Krevl, 2014). Descriptive statistics of these networks are shown in Table 5.

Network	Nodes	Mean	Max.	Density	Clustering	Likes	Likes
		degree	degree		coefficient	jazz %	alternative %
Deezer Croatia	54573	18.26	420	0.00033	0.11463	5	38
Deezer Hungary	47538	9.38	112	0.00020	0.09292	5	37
Deezer Romania	41773	6.02	112	0.00014	0.07527	6	36

Table 5: Network descriptive statistics for the Deezer networks.

Each network is a single connected component. Network statistics were computed using the igraph R package (Csárdi and Nepusz, 2006). "Clustering coefficient" is the global clustering coefficient (transitivity).

Each node in these three networks represents a user, and an undirected edge represents friendship in the Deezer online social network. Each node is annotated with a list of genres liked by the user (Rozemberczki et al., 2019). Based on these genre annotations, we created two different binary outcome variables: one for liking jazz, and one for liking "alternative" music. The binary outcome variable for liking jazz is true if the user likes any one or more of the genres in the data that describe jazz music, namely "Jazz", "Instrumental jazz", "Jazz Hip Hop", or "Vocal Jazz". The binary outcome variable for liking alternative music is true if the user likes the genre in the data labelled "Alternative". Consistently across all three networks, approximately 5% of users like jazz, and between 35% and 40% of users like alternative music (Table 5).

Table 6 shows the results of using the EE algorithm implemented in ALAAMEE to estimate parameters for ALAAM models of the three Deezer online social networks, with liking jazz as the outcome variable. The model parameters were selected to test for social contagion of liking jazz on this social network (the Contagion parameter), including specifically in closed triads (the three Triangle parameters), while also accounting for the degree distribution of users who like jazz (the GWActivity parameter), and the number of genres liked by a user and their friends. Degeneracy check plots for these models are shown in Figures A3, A4, and A5.

Table 6: Models estimated using ALAAMEE with the EE algorithm for the Deezer networks, with liking jazz as the outcome variable.

Effect	Croatia	Hungary	Romania
Density	-4.727 (-4.922,-4.533)	-5.054 (-5.271,-4.837)	-4.689 (-4.947, -4.431)
GWActivity [$\alpha = 2.0$]	-2.938 (-8.895,3.018)	5.237 (2.484,7.990)	$\underset{(-1.836, 5.050)}{1.607}$
Contagion	-0.008 (-0.178,0.162)	$\underset{(0.110,0.420)}{0.265}$	$\underset{(0.323,0.903)}{0.613}$
TriangleT1			-0.034
TriangleT2	—		0.004 (-0.254,0.262)
TriangleT3			-0.020 (-1.063,1.023)
num. genres	$\underset{(0.183,0.204)}{\textbf{0.194}}$	$\underset{(0.181,0.204)}{\textbf{0.193}}$	0.194 (0.180,0.207)
partner num. genres	$\underset{(-0.002, 0.001)}{-0.002, 0.001)}$		$\begin{array}{c} -0.006 \\ (-0.013, 0.001) \end{array}$
Converged runs	100	100	100
Total runs	100	100	100

Parameter estimates are shown with 95% confidence interval. Estimates that are statistically significant at the nominal p < 0.05 level are shown in bold.

This model was estimated first on the Romania network (the smallest of the three). Initially the Activity parameter, rather than GWActivity, was used, however the degeneracy check showed that this model was not properly converged, and hence the geometrically weighted activity parameter GWActivity (with decay parameter $\alpha = 2.0$) was used instead of Activity to overcome this problem, as described in Stivala (2023). This model, however, did not converge for the Croatia and Hungary data, but removing the triangle parameters solved this problem, resulting in the models shown in Table 6 (for Hungary, the partner number of genres parameter also had to be removed to find a converged model).

The only parameter (apart from Density, or baseline incidence) that is significant across all three networks is the number of genres liked by a user: rather unsurprisingly, the more genres a user likes, the more likely they are to like jazz. The Contagion parameter is positive and significant for both Hungary and Romania, indicating that (given the assumptions of the model) a liking for jazz is socially contagious in these countries' networks. However this parameter is not significant for Croatia.

Estimating these models (100 parallel estimations) took approximately 22, 11, and 32 minutes, for Croatia, Hungary, and Romania, respectively, on AMD EPYC 7543 2.8 GHz processors on a Linux cluster. We also estimated the same models with ALAAMEE using the stochastic approximation algorithm, and the results are shown in Table B1. These estimations took approximately 32, 14, and 36 hours for Croatia, Hungary, and Romania, respectively, on the same system. The results are consistent with those of the estimation with the EE algorithm. However four parameter estimates are found to be statistically significant by the stochastic approximation algorithm that were not when using the EE algorithm: GWActivity for Croatia, and GWActivity, TriangleT1, and partner number of genres for Romania.

For the Romania network, the negative and significant TriangleT1 parameter indicates that users who like jazz are less likely to be involved in a triangle structure than other users. The negative and significant partner number of genres parameter indicates that users who have friends who like many genres are less likely to like jazz (while the positive and significant number of genres parameter means that a user who likes many genres is more likely to like jazz).

Note that, as discussed in Section 2, by using the ALAAM model, in which the networks ties are fixed (exogenous to the model), we are assuming that only the process of social influence (contagion) is occurring, without the ability to account for the possibility that friends (network neighbours) might both like the same genre of music due to homophily.

Table 7 shows the results of using the EE algorithm to estimate ALAAM parameters for the same three networks, but this time with liking alternative music as the outcome variable. For this data, the full model was able to be estimated for all three countries. Degeneracy check plots for these models are shown in Figures A6, A7, and A8.

Table 7: Models estimated using ALAAMEE with the EE algorithm for the Deezer networks, with liking "alternative" music as the outcome variable.

Effect	Croatia	Hungary	Romania
Density	$\begin{array}{r} -3.276 \\ (-3.399, -3.153) \end{array}$	$\begin{array}{c} -3.019 \\ (-3.148, -2.890) \end{array}$	$\begin{array}{r} -3.157 \\ (-3.310, -3.004) \end{array}$
GWActivity [$\alpha = 2.0$]	-0.348 (-3.666,2.970)	$\underset{(-2.449,2.628)}{0.089}$	-0.380 (-2.754,1.993)
Contagion	$\begin{array}{c} -0.010 \\ (-0.074, 0.053) \end{array}$	$\underset{(\textbf{0.070,0.246})}{\textbf{0.158}}$	$\underset{\left(-0.001,0.219\right)}{0.109}$
TriangleT1	$\underset{\left(-0.010,0.008\right)}{-0.010,0.008)}$	$\begin{array}{c} -0.006 \\ (-0.028, 0.015) \end{array}$	$\begin{array}{c} -0.018 \\ (-0.069, 0.033) \end{array}$
TriangleT2	$\underset{\left(-0.018,0.023\right)}{0.003}$	$\underset{\left(-0.045,0.046\right)}{0.000}$	$\begin{array}{c} -0.005 \\ (-0.100, 0.090) \end{array}$
TriangleT3	$\begin{array}{c} -0.008 \\ (-0.062, 0.046) \end{array}$	$\underset{\left(-0.090,0.146\right)}{0.028}$	$\underset{\left(-0.173,0.262\right)}{0.044}$
num. genres	$\begin{array}{c} 0.448 \\ (0.434, 0.462) \end{array}$	$\underset{(0.404,0.435)}{\textbf{0.419}}$	$\begin{array}{c} 0.405 \\ (0.389, 0.421) \end{array}$
partner num. genres	$\underset{\left(-0.003,0.004\right)}{0.001}$	$\begin{array}{c} -0.010 \\ (-0.016, -0.004) \end{array}$	$\substack{-0.002 \\ (-0.009, 0.005)}$
Converged runs	100	100	100
Total runs	100	100	100

Parameter estimates are shown with 95% confidence interval. Estimates that are statistically significant at the nominal p < 0.05 level are shown in bold.

The results are qualitatively quite similar to the model for jazz, in that the only parameter estimate (other than Density) that is statistically significant across all three networks is number of genres, which is positive. The Contagion parameter is statistically significant only for the Hungary network, and again is positive. None of the Triangle parameters are statistically significant in any of the three countries.

Estimating these models (100 parallel estimations) took approximately 203, 59, and 41 minutes, for Croatia, Hungary, and Romania, respectively (on the same system as the jazz model). We also attempted to estimate the same models using the stochastic approximation algorithm, however for the Croatia and Hungary networks these estimations did not complete within a 48 hour elapsed time limit. The estimation for the Romania network took approximately 30 hours, and the resulting parameter estimates are shown in Table B2. These estimates are consistent with those estimated by the EE algorithm, however the stochastic approximation algorithm finds the Contagion parameter to be statistically significant (and positive) while the EE algorithm does not.

6 Conclusions and future work

ALAAMEE is open-source Python software for the estimation, simulation, and goodness-of-fit testing of the ALAAM social influence model. It currently supports ALAAMs on undirected and directed one-mode networks, and undirected two-mode (bipartite) networks. It also supports estimation from snowball sampled network data.

Models can be estimated using either stochastic approximation with the Robbins–Monro algorithm, or, for large networks, by the EE algorithm. For networks small enough that it is practical — on the order of thousands of nodes, but

also depending on the model parameters and data — we recommend using stochastic approximation, a well-known and widely used method, which is implemented in ALAAMEE just as it is in MPNet for ALAAM parameter estimation. However for larger networks, stochastic approximation is likely to be too slow to be practical, and so the EE algorithm can be used instead. In this work we demonstrated its use on networks on networks of approximately 50 000 nodes, for which stochastic approximation was feasible in some, but not all, cases. The use of the EE algorithm implemented in ALAAMEE to estimate ALAAM parameters for a much larger network, with approximately 1.6 million nodes, for which estimation by stochastic approximation is certainly not feasible, is described in Stivala (2023).

When using the EE algorithm, the results shown in Section 4 indicate that it is always advantageous, and does not result in an increased false positive rate, to use as many runs as practical, and 100 is probably more than sufficient in most cases. Because these runs are entirely independent, elapsed time can be minimized by running them in parallel using as many compute cores and nodes as you have available.

The EE algorithm is fast, scalable to far larger networks, and able to take advantage of multicore and large-scale parallel computing. The simplified EE algorithm (Borisenko et al., 2020) used in ALAAMEE has recently been shown, in the context of ERGMs, to be guaranteed to converge to the MLE, if it exists, when the learning rate (a parameter of the EE algorithm) is sufficiently small (Giacomarra et al., 2023). The proof uses the uncertain energies framework of Ceperley and Dewing (1999), as originally suggested in Borisenko et al. (2020).

However, as shown in this work, using this algorithm can result in very low statistical power on some parameters, due to larger estimated standard errors than the stochastic approximation method on the same data. This has also been observed in using the EE algorithm to estimate parameters for the "citation ERGM" (cERGM) ERGM variant (Schmid et al., 2022), compared with using the default statnet MCMLE algorithm (Stivala and Lomi, 2022).

Because ALAAMEE is written in Python using only the NumPy package, it can easily be run on any system on which Python and NumPy are available. This also facilitates its use in automated scripts, for example for large-scale computational experiments such as those described in Section 4 and Stivala et al. (2020b), which is not practical with a Windows application like MPNet.

The relative ease of Python programming, along with the simple and documented implementations, with unit tests, of a variety of ALAAM change statistics already included in the open-source ALAAMEE software, should facilitate the creation of change statistics for any new configurations required by users of the software.

A demonstration implementation of the EE algorithm for ERGM parameter estimation was written in Python in the same style as ALAAMEE, that is, using NumPy for linear algebra and Python dictionaries for graph data structures. However this was found to be too slow for practical use, and the software⁶ was completely re-written in C (Stivala et al., 2020a). For ALAAM, however, where the MCMC process involves flipping binary variables in a vector rather than edges in a graph, we found that the Python implementation ALAAMEE was sufficiently fast for practical use not only with the EE algorithm, but also with the Robbins–Monro algorithm.

In theory, ALAAMEE could be made considerably faster with little effort by using a Python "just-in-time" (JIT) compiler, such as Numba (Lam et al., 2015) or PyPy (Bolz et al., 2009). However to date we have been unable to accelerate ALAAMEE this way, finding that either the code is not supported, or the "accelerated" version is actually slower than the original.

In Parker et al. (2022), three limitations of ALAAMs are identified. First, the outcome variable is restricted to binary; second, the inherent assumption that the underlying social contagion process is at equilibrium; and third, their inadequacy for very large networks. We suggest that this work, in addition to the use of ALAAM estimation from network snowball samples (Stivala et al., 2020b) effectively addresses the third limitation. The second limitation can be mitigated as suggested in Parker et al. (2022), by applying ALAAM models to data in which the social network is observed at an appropriate time before the outcome behavioural variable is. If longitudinal (panel) data is available, in which the social network ties and actor attributes of a population are observed at multiple time points, the stochastic actor attribute model (SAOM), is a more appropriate choice of model, enabling the estimation of parameters corresponding to the co-evolution of the social network and actor attributes (Snijders, 2017). This leaves the first limitation, that the outcome variable must be binary, to be addressed in future work. We have identified an additional limitation of ALAAMs in this work and in Stivala (2023), namely that, like ERGMs, ALAAMs can suffer from problems of "near-degeneracy" when only simple statistics (such as Activity) are used, particularly on larger networks. The use of the GWActivity parameter can help overcome these problems, but as illustrated by the examples in Section 5.2, it still may not always be possible to fit a model with all the desired parameters. Some avenues for further work on this problem are suggested in Stivala (2023).

⁶https://github.com/stivalaa/EstimNetDirected

One further avenue of further work on ALAAM modeling was suggested in Section 1: the conception of an ALAAM as a bipartite ERGM could be a way of implementing a multivariate ALAAM, that is, an ALAAM with more than one outcome variable.

Funding

This work was funded by the Swiss National Science Foundation project numbers 167326 (NRP 75) and 200778.

Acknowledgements

We used the high performance computing cluster at the Institute of Computing, Università della Svizzera italiana, for the computational experiments described in Section 4. The computational experiments described in Section 5.2 were performed on the OzSTAR national facility at Swinburne University of Technology. The OzSTAR program receives funding in part from the Astronomy National Collaborative Research Infrastructure Strategy (NCRIS) allocation provided by the Australian Government, and from the Victorian Higher Education State Investment Fund (VHESIF) provided by the Victorian Government.

Data availability statement

The "Project 90" data (Potterat et al., 2004; Woodhouse et al., 1994; Klovdahl et al., 1994; Rothenberg et al., 1995; Goel and Salganik, 2010) is available upon registration from https://oprdata.princeton.edu/archive/p90/. The excerpt of 50 girls from the "Teenage friends and lifestyle study" data (Michell and Amos, 1997; Pearson and Michell, 2000; Pearson and West, 2003; Pearson et al., 2006; Steglich et al., 2006; West and Sweeting, 1996) is available from https://www.stats.ox.ac.uk/~snijders/siena/s50_data.htm. The "Deezer" (Rozemberczki et al., 2019) data is available from the Stanford large network dataset collection (Leskovec and Krevl, 2014) at https://snap.stanford.edu/data/gemsec-Deezer.html. All other data, source code, and scripts are freely available from https://github.com/stivalaa/ALAAMEE.

References

- V. Amati, A. Lomi, and A. Mira. Social network modeling. *Annual Review of Statistics and its Application*, 5: 343–369, 2018.
- L. Anselin. Some robust approaches to testing and estimation in spatial econometrics. *Regional Science and Urban Economics*, 20(2):141–163, 1990.
- M. L. Barnes, P. Wang, J. E. Cinner, N. A. Graham, A. M. Guerrero, L. Jasny, J. Lau, S. R. Sutcliffe, and J. Zamborain-Mason. Social determinants of adaptive and transformative responses to climate change. *Nature Climate Change*, 10(9):823–828, 2020.
- F. Bianchi, A. Stivala, and A. Lomi. Multiple clocks in network evolution. *Methodological Innovations*, 15(1):29–41, 2022.
- C. F. Bolz, A. Cuni, M. Fijalkowski, and A. Rigo. Tracing the meta-level: PyPy's tracing JIT compiler. In Proceedings of the 4th Workshop on the Implementation, Compilation, Optimization of Object-Oriented Languages and Programming Systems, ICOOOLPS '09, page 18–25, New York, NY, USA, 2009. Association for Computing Machinery. doi: 10.1145/1565824.1565827.
- A. Borisenko, M. Byshkin, and A. Lomi. A simple algorithm for scalable Monte Carlo inference. *arXiv preprint* arXiv:1901.00533v4, 2020.
- Y. Bramoullé, H. Djebbari, and B. Fortin. Peer effects in networks: A survey. *Annual Review of Economics*, 12: 603–629, 2020.
- M. Byshkin, A. Stivala, A. Mira, R. Krause, G. Robins, and A. Lomi. Auxiliary parameter MCMC for exponential random graph models. *Journal of Statistical Physics*, 165(4):740–754, 2016.
- M. Byshkin, A. Stivala, A. Mira, G. Robins, and A. Lomi. Fast maximum likelihood estimation via equilibrium expectation for large network data. *Scientific Reports*, 8:11509, 2018.
- D. Ceperley and M. Dewing. The penalty method for random walks with uncertain energies. *Journal of Chemical Physics*, 110(20):9812–9820, 1999.
- M. Chakraborty, M. Byshkin, and F. Crestani. Patent citation network analysis: A perspective from descriptive statistics and ERGMs. *PLoS ONE*, 15(12):e0241797, 2020.
- A. D. Cliff and J. K. Ord. Spatial processes: models & applications. Taylor & Francis, 1981.
- G. Csárdi and T. Nepusz. The igraph software package for complex network research. *InterJournal*, Complex Systems:1695, 2006. URL https://igraph.org.
- N. Dai and G. L. Jones. Multivariate initial sequence estimators in Markov chain Monte Carlo. *Journal of Multivariate Analysis*, 159:184–199, 2017.
- G. Daraganova. *Statistical models for social networks and network-mediated social influence processes: Theory and application*. PhD thesis, The University of Melbourne, 2009.
- G. Daraganova and P. Pattison. Autologistic actor attribute model analysis of unemployment: Dual importance of who you know and where you live. In D. Lusher, J. Koskinen, and G. Robins, editors, *Exponential Random Graph Models for Social Networks*, chapter 18, pages 237–247. Cambridge University Press, New York, 2013.
- G. Daraganova and G. Robins. Autologistic actor attribute models. In D. Lusher, J. Koskinen, and G. Robins, editors, *Exponential Random Graph Models for Social Networks*, chapter 9, pages 102–114. Cambridge University Press, New York, 2013.
- T. Diviák, J. A. Coutinho, and A. D. Stivala. A man's world? Comparing the structural positions of men and women in an organized criminal network. *Crime, Law and Social Change*, 74(5):547–569, 2020.

- P. Doreian. Estimating linear models with spatially distributed data. Sociological Methodology, 12:359–388, 1981.
- I. Fellows and M. S. Handcock. Exponential-family random network models. arXiv preprint arXiv:1208.0121, 2012.
- I. E. Fellows and M. S. Handcock. Analysis of partially observed networks via exponential-family random network models. *arXiv preprint arXiv:1303.1219*, 2013.
- J. M. Flegal and G. L. Jones. Batch means and spectral variance estimators in Markov chain Monte Carlo. *The Annals of Statistics*, 38(2):1034–1070, 2010.
- J. M. Flegal, J. Hughes, D. Vats, N. Dai, K. Gupta, and U. Maji. *mcmcse: Monte Carlo Standard Errors for MCMC*. Riverside, CA, and Kanpur, India, 2021. R package version 1.5-0.
- N. E. Friedkin. Social networks in structural equation models. Social Psychology Quarterly, 53(4):316–328, 1990.
- H. C. Gallagher. Social networks and the willingness to communicate: Reciprocity and brokerage. *Journal of Language and Social Psychology*, 38(2):194–214, 2019.
- F. Giacomarra, G. Bet, and A. Zocca. Generating synthetic power grids using exponential random graphs models. *arXiv preprint arXiv:2310.19662v1*, 2023.
- S. Goel and M. J. Salganik. Assessing respondent-driven sampling. *Proceedings of the National Academy of Sciences of the USA*, 107(15):6743–6747, 2010.
- M. S. Handcock, D. R. Hunter, C. T. Butts, S. M. Goodreau, Morris, and Martina. statnet: Software tools for the representation, visualization, analysis and simulation of network data. *Journal of Statistical Software*, 24(1):1–11, 2008. URL http://www.jstatsoft.org/v24/i01.
- M. S. Handcock, D. R. Hunter, C. T. Butts, S. M. Goodreau, P. N. Krivitsky, and M. Morris. *ergm: Fit, Simulate and Diagnose Exponential-Family Models for Networks*. The Statnet Project (http://www.statnet.org), 2022. URL http://CRAN.R-project.org/package=ergm. R package version 4.3.2.
- C. R. Harris, K. J. Millman, S. J. van der Walt, R. Gommers, P. Virtanen, D. Cournapeau, E. Wieser, J. Taylor, S. Berg, N. J. Smith, R. Kern, M. Picus, S. Hoyer, M. H. van Kerkwijk, M. Brett, A. Haldane, J. F. del Río, M. Wiebe, P. Peterson, P. Gérard-Marchant, K. Sheppard, T. Reddy, W. Weckesser, H. Abbasi, C. Gohlke, and T. E. Oliphant. Array programming with NumPy. *Nature*, 585(7825):357–362, 2020. doi: 10.1038/s41586-020-2649-2.
- J. Hartung, G. Knapp, and B. K. Sinha. *Statistical meta-analysis with applications*. John Wiley & Sons, Hoboken, NJ, 2008.
- R. M. Hummel, D. R. Hunter, and M. S. Handcock. Improving simulation-based algorithms for fitting ERGMs. *Journal of Computational and Graphical Statistics*, 21(4):920–939, 2012.
- D. R. Hunter and M. S. Handcock. Inference in curved exponential family models for networks. *Journal of Computational and Graphical Statistics*, 15(3):565–583, 2006.
- D. R. Hunter, M. S. Handcock, C. T. Butts, S. M. Goodreau, and M. Morris. ergm: A package to fit, simulate and diagnose exponential-family models for networks. *Journal of Statistical Software*, 24(3):1–29, 2008. URL https://www.jstatsoft.org/v024/i03.
- D. R. Hunter, P. N. Krivitsky, and M. Schweinberger. Computational statistical methods for social network models. *Journal of Computational and Graphical Statistics*, 21(4):856–882, 2012.
- D. R. Hunter, S. M. Goodreau, and M. S. Handcock. ergm.userterms: A template package for extending statnet. *Journal of Statistical Software*, 52(2):1–25, 2013. doi: 10.18637/jss.v052.i02.
- G. L. Jones, M. Haran, B. S. Caffo, and R. Neath. Fixed-width output analysis for Markov chain Monte Carlo. *Journal of the American Statistical Association*, 101(476):1537–1547, 2006.
- Y. Kashima, S. Wilson, D. Lusher, L. J. Pearson, and C. Pearson. The acquisition of perceived descriptive norms as social category learning in social networks. *Social Networks*, 35(4):711–719, 2013.

- A. S. Klovdahl, J. J. Potterat, D. E. Woodhouse, J. B. Muth, S. Q. Muth, and W. W. Darrow. Social networks and infectious disease: The Colorado Springs study. *Social Science & Medicine*, 38(1):79–88, 1994.
- J. Koskinen. Exponential random graph modelling. In P. Atkinson, S. Delamont, A. Cernat, J. Sakshaug, and R. Williams, editors, *SAGE Research Methods Foundations*. SAGE, London, 2020. doi: 10.4135/9781526421036888175.
- J. Koskinen. Exponential random graph models. In J. McLevey, J. Scott, and P. J. Carrington, editors, *The Sage Handbook of Social Network Analysis*, chapter 33, pages 474–500. Sage, second edition, 2023.
- J. Koskinen and G. Daraganova. Bayesian analysis of social influence. *Journal of the Royal Statistical Society Series* A: Statistics in Society, 185(4):1855–1881, 2022.
- P. N. Krivitsky, D. R. Hunter, M. Morris, and C. Klumb. ergm 4: New features for analyzing exponential-family random graph models. *Journal of Statistical Software*, 105(1):1–44, 2023. doi: 10.18637/jss.v105.i06.
- S. K. Lam, A. Pitrou, and S. Seibert. Numba: A LLVM-based Python JIT compiler. In *Proceedings of the Second Workshop on the LLVM Compiler Infrastructure in HPC*, LLVM '15, New York, NY, USA, 2015. Association for Computing Machinery. doi: 10.1145/2833157.2833162.
- R. T. A. Leenders. Modeling social influence through network autocorrelation: constructing the weight matrix. *Social Networks*, 24(1):21–47, 2002.
- J. Leskovec and A. Krevl. SNAP Datasets: Stanford large network dataset collection. http://snap.stanford.edu/data, June 2014.
- S. Letina. Network and actor attribute effects on the performance of researchers in two fields of social science in a small peripheral community. *Journal of Informetrics*, 10(2):571–595, 2016.
- S. Letina, G. Robins, and D. Maslić Seršić. Reaching out from a small scientific community: the social influence models of collaboration across national and disciplinary boundaries for scientists in three fields of social sciences. *Revija za sociologiju*, 46(2):103–139, 2016.
- D. Lusher, J. Koskinen, and G. Robins, editors. *Exponential Random Graph Models for Social Networks*. Structural Analysis in the Social Sciences. Cambridge University Press, New York, 2013.
- L. Michell and A. Amos. Girls, pecking order and smoking. Social Science & Medicine, 44(12):1861–1869, 1997.
- K. Ord. Estimation methods for models of spatial interaction. *Journal of the American Statistical Association*, 70 (349):120–126, 1975.
- A. Parker, F. Pallotti, and A. Lomi. New network models for the analysis of social contagion in organizations: an introduction to autologistic actor attribute models. *Organizational Research Methods*, 25(3):513–540, 2022.
- P. E. Pattison, G. L. Robins, T. A. B. Snijders, and P. Wang. Conditional estimation of exponential random graph models from snowball sampling designs. *Journal of Mathematical Psychology*, 57(6):284–296, 2013.
- M. Pearson and L. Michell. Smoke rings: social network analysis of friendship groups, smoking and drug-taking. *Drugs: Education, Prevention and Policy*, 7(1):21–37, 2000. doi: 10.1080/dep.7.1.21.37.
- M. Pearson and P. West. Drifting smoke rings. Connections, 25(2):59-76, 2003.
- M. Pearson, C. Steglich, and T. A. B. Snijders. Homophily and assimilation among sport-active adolescent substance users. *Connections*, 27(1):47–63, 2006.
- J. Potterat, D. E. Woodhouse, S. Q. Muth, R. B. Rothenbueg, W. W. Darrow, A. S. Klovdahl, J. B. Muth, et al. Network dynamism: history and lessons of the Colorado Springs study. In M. Morris, editor, *Network epidemiology: A handbook for survey design and data collection*, pages 87–114. Oxford University Press, 2004.
- R. M. Ripley, T. A. B. Snijders, Z. Boda, A. Vörös, and P. Preciado. *Manual for RSiena*. University of Oxford, Department of Statistics; Nuffield College, 2023. Version February 6, 2023.

- H. Robbins and S. Monro. A stochastic approximation method. *The Annals of Mathematical Statistics*, 22(3):400–407, 1951.
- G. Robins, P. Elliott, and P. Pattison. Network models for social selection processes. *Social Networks*, 23(1):1–30, 2001a.
- G. Robins, P. Pattison, and P. Elliott. Network models for social influence processes. *Psychometrika*, 66(2):161–189, 2001b.
- R. B. Rothenberg, D. E. Woodhouse, J. J. Potterat, S. Q. Muth, W. W. Darrow, and A. S. Klovdahl. Social networks in disease transmission: the Colorado Springs study. In R. H. Needle, S. L. Coyle, S. G. Genser, and R. T. Trotter, editors, *Social Networks, Drug Abuse, and HIV Transmission*, volume 151, pages 3–19. National Institute on Drug Abuse, 1995.
- B. Rozemberczki, R. Davies, R. Sarkar, and C. Sutton. GEMSEC: Graph embedding with self clustering. In *Proceedings of the 2019 IEEE/ACM International Conference on Advances in Social Networks Analysis and Mining (ASONAM 2019)*, pages 65–72, New York, NY, USA, 2019. Association for Computing Machinery.
- R. Scherer. *PropCIs: Various confidence interval methods for proportions*, 2018. URL https://CRAN. R-project.org/package=PropCIs. R package version 0.3-0.
- C. S. Schmid, T. H. Y. Chen, and B. A. Desmarais. Generative dynamics of supreme court citations: Analysis with a new statistical network model. *Political Analysis*, 30(4):515–534, 2022. doi: 10.1017/pan.2021.20.
- C. R. Shalizi and A. C. Thomas. Homophily and contagion are generically confounded in observational social network studies. *Sociological Methods & Research*, 40(2):211–239, 2011.
- T. A. B. Snijders. Markov chain Monte Carlo estimation of exponential random graph models. *Journal of Social Structure*, 3(2):1–40, 2002.
- T. A. B. Snijders. Stochastic actor-oriented models for network dynamics. *Annual Review of Statistics and its Application*, 4:343–363, 2017.
- T. A. B. Snijders, P. E. Pattison, G. L. Robins, and M. S. Handcock. New specifications for exponential random graph models. *Sociological Methodology*, 36(1):99–153, 2006.
- C. Steglich, T. A. B. Snijders, and P. West. Applying SIENA. Methodology, 2(1):48-56, 2006.
- A. Stivala. Overcoming near-degeneracy in the autologistic actor attribute model. *arXiv preprint arXiv:2309.07338v2*, 2023.
- A. Stivala and A. Lomi. A new scalable implementation of the citation exponential random graph model (cERGM) and its application to a large patent citation network. Talk presented at INSNA Sunbelt XLII conference, July 2022. URL https://doi.org/10.5281/zenodo.7951927.
- A. Stivala, A. Palangkaraya, D. Lusher, G. Robins, and A. Lomi. ERGM parameter estimation of very large directed networks: implementation, example, and application to the geography of knowledge spillovers. Talk presented at INSNA Sunbelt XXXIX Conference, June 2019. URL https://doi.org/10.5281/zenodo.7952037.
- A. Stivala, G. Robins, and A. Lomi. Exponential random graph model parameter estimation for very large directed networks. *PLoS ONE*, 15(1):e0227804, 2020a.
- A. Stivala, P. Wang, and A. Lomi. Numbers and structural positions of women in a national director interlock network. Talk presented at INSNA Sunbelt XLIII Conference, June 2023. URL https://doi.org/10.5281/ zenodo.8092829.
- A. D. Stivala, J. H. Koskinen, D. A. Rolls, P. Wang, and G. L. Robins. Snowball sampling for estimating exponential random graph models for large networks. *Social Networks*, 47:167–188, 2016.

- A. D. Stivala, H. C. Gallagher, D. A. Rolls, P. Wang, and G. L. Robins. Using sampled network data with the autologistic actor attribute model. *arXiv preprint arXiv:2002.00849*, 2020b.
- O. Tange. GNU Parallel 2018. Ole Tange, Mar. 2018. doi: 10.5281/zenodo.1146014.
- D. Vats, J. M. Flegal, and G. L. Jones. Strong consistency of multivariate spectral variance estimators in Markov chain Monte Carlo. *Bernoulli*, 24(3):1860 – 1909, 2018. doi: 10.3150/16-BEJ914.
- D. Vats, J. M. Flegal, and G. L. Jones. Multivariate output analysis for Markov chain Monte Carlo. *Biometrika*, 106 (2):321–337, 2019.
- P. Wang, G. Robins, and P. Pattison. *PNet: A program for the simulation and estimation of exponential random graph models*. Melbourne School of Psychological Sciences, The University of Melbourne, 2009. URL http://www.melnet.org.au/s/PNetManual.pdf.
- P. Wang, G. Robins, P. Pattison, and J. Koskinen. *MPNet: Program for the simulation and estimation of (p*) exponential random graph models for multilevel networks*. Melbourne School of Psychological Sciences, The University of Melbourne, 2014. URL http://www.melnet.org.au/s/MPNetManual.pdf.
- P. Wang, A. Stivala, G. Robins, P. Pattison, J. Koskinen, and A. Lomi. *PNet: Program for the simulation and estimation of (p*) exponential random graph models for multilevel networks*, 2022. URL http://www.melnet. org.au/s/MPNetManual2022.pdf.
- Z. Wang, I. E. Fellows, and M. S. Handcock. Understanding networks with exponential-family random network models. *Social Networks*, 78:81–91, 2024. doi: 10.1016/j.socnet.2023.07.003.
- P. West and H. Sweeting. Background, rationale and design of the West of Scotland 11 to 16 study. MRC Medical Sociology Unit Working Paper Number 52, 1996.
- H. Wickham. ggplot2: Elegant Graphics for Data Analysis. Springer-Verlag New York, 2016. ISBN 978-3-319-24277-4. URL https://ggplot2.tidyverse.org.
- E. B. Wilson. Probable inference, the law of succession, and statistical inference. *Journal of the American Statistical Association*, 22(158):209–212, 1927.
- D. E. Woodhouse, R. B. Rothenberg, J. J. Potterat, W. W. Darrow, S. Q. Muth, A. S. Klovdahl, H. P. Zimmerman, H. L. Rogers, T. S. Maldonado, J. B. Muth, et al. Mapping a social network of heterosexuals at high risk for HIV infection. *AIDS*, 8(9):1331–1336, 1994.
- A. B. Yoo, M. A. Jette, and M. Grondona. SLURM: Simple linux utility for resource management. In D. Feitelson, L. Rudolph, and U. Schwiegelshohn, editors, *Job Scheduling Strategies for Parallel Processing*, volume 2862 of *Lecture Notes in Computer Science*, pages 44–60, Berlin, Heidelberg, 2003. Springer Berlin Heidelberg. doi: 10.1007/10968987_3.

Appendix A Supplementary figures



Figure A1: Stochastic approximation parameter estimates and estimated standard errors for the Project 90 network with simulated attributes. This is the baseline result for the Project 90 example in a study of the effect of network sampling on ALAAM estimation (Stivala et al., 2020b). The error bars show the nominal 95% confidence interval. The horizontal line shows the true value of the parameter, and each plot is annotated with the mean bias, root mean square error (RMSE), the percentage of samples for which the true value is inside the confidence interval (coverage rate), and the Type II error rate (False Negative Rate, FNR). A converged estimate was found for 99 of the total 100 samples.



Figure A2: Type I error rate (false positive rate) as the number of runs used for each sample is varied.



Figure A3: Degeneracy check for the Deezer Croatia network with liking jazz as the outcome variable (Table 6). Trace plots and histograms show statistics of 100 networks simulated from the model. The blue lines on the histograms show mean and 95% confidence interval, and red lines show the observed values.



Figure A4: Degeneracy check for the Deezer Hungary network with liking jazz as the outcome variable (Table 6). Trace plots and histograms show statistics of 100 networks simulated from the model. The blue lines on the histograms show mean and 95% confidence interval, and red lines show the observed values.



Figure A5: Degeneracy check for the Deezer Romania network with liking jazz as the outcome variable (Table 6). Trace plots and histograms show statistics of 100 networks simulated from the model. The blue lines on the histograms show mean and 95% confidence interval, and red lines show the observed values.



Figure A6: Degeneracy check for the Deezer Croatia network with liking "alternative" music as the outcome variable (Table 7). Trace plots and histograms show statistics of 100 networks simulated from the model. The blue lines on the histograms show mean and 95% confidence interval, and red lines show the observed values.



Figure A7: Degeneracy check for the Deezer Hungary network with liking "alternative" music as the outcome variable (Table 7). Trace plots and histograms show statistics of 100 networks simulated from the model. The blue lines on the histograms show mean and 95% confidence interval, and red lines show the observed values.



Figure A8: Degeneracy check for the Deezer Romania network with liking "alternative" music as the outcome variable (Table 7). Trace plots and histograms show statistics of 100 networks simulated from the model. The blue lines on the histograms show mean and 95% confidence interval, and red lines show the observed values.

Appendix B Supplementary tables

Effect	Croatia	Hungary	Romania
Density	-4.706	-5.022	-4.659
GWActivity [$\alpha = 2.0$]	(0.000) -2.813 (0.861)	5.266 (0.681)	1.666 (0.584)
Contagion	-0.009 (0.032)	0.266 (0.030)	$\underset{(0.057)}{0.610}$
TriangleT1			-0.033 (0.009)
TriangleT2	—	—	0.009 (0.049)
TriangleT3	—		-0.068 (0.201)
num. genres	$\underset{(0.003)}{0.193}$	0.192 (0.003)	0.192 (0.003)
partner num. genres	-0.000 (0.000)		

Table B1: Models estimated using ALAAMEE with the stochastic approximation algorithm for the Deezer networks, with liking jazz as the outcome variable.

Parameter estimates are shown with their estimated standard errors. Parameter estimates that are statistically significant at the nominal p < 0.05 level are shown in bold.

Table B2: Model estimated using ALAAMEE with the stochastic approximation algorithm for the Deezer Romania network, with liking "alternative" music as the outcome variable.

Effect	Estimate	Std. error	t-ratio	
Density	-3.136	0.032	0.015	*
GWActivity [$\alpha = 2.0$]	-0.352	0.334	0.016	
Contagion	0.110	0.019	0.031	*
TriangleT1	-0.019	0.010	-0.016	
TriangleT2	-0.004	0.021	0.018	
TriangleT3	0.042	0.046	0.024	
num. genres	0.401	0.004	-0.032	*
partner num. genres	-0.002	0.001	0.009	

Asterisks indicate statistical significance at the nominal p < 0.05 level. Only the results for Romania are shown, as estimation for the other two networks (Croatia and Hungary) did not complete within the 48 hour elapsed time limit.