AN INVESTIGATION OF FIT MEASURES FOR LONGITUDINAL NETWORK AND ATTRIBUTE CO-EVOLUTION MODELS

BY

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DISSERTATION

Submitted in partial fulfillment of the requirements
for the degree of Doctor of Philosophy in Psychology
in the Graduate College of the
University of Illinois at Urbana-Champaign, 2010

Urbana, Illinois

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Abstract

Modeling the processes underlying social network and attribute change allows researchers to better identify and understand dependencies present among actors — people, places, or things. The connections that exist among these actors change over time, depend on the presence or absence of other connections, and depend on the characteristics of the actors present. Advanced modeling techniques have been proposed that are designed to capture changes in structure and actor attributes.

Fit measures have been developed for actor-based models of network structural evolution (Schweinberger, 2007; Snijders, 1996). Snijders et al. (2006) extended the actor-based structural evolution model to an actor-based *co-evolutionary* model that includes actor attributes. Despite recent methodological advances in the estimation of co-evolution models, measures have neither been developed nor evaluated to assess how the inclusion of actor attributes contributes to the model.

Four measures are developed in this paper, including an extension of Snijders' t-test to a Pseudo-Wald test statistic, an extension of Schweinberger's score test for use in a co-evolution model, an entropy-based goodness-of-fit measure, and an R^2 goodness-of-fit measure for actor-based co-evolution models.

Following the theoretical development of each measure, the behavior and performance of each are compared in a large simulation study. Results from this simulation show that each proposed measure displays expected behavior, especially as the number of actors increases, and shows promise for future use as fit measures in co-evolution models.

Acknowledgments

Completing this project would not have been possible without the encouragement of many people. Many thanks to my adviser, Carolyn J. Anderson, who read my numerous revisions and helped make some sense of the confusion. Also thanks to my committee members, Shin-Kap Han, Sungjin Hong, Larry Hubert, and especially Hank Green, who offered their time, guidance, and support.

Thanks to Tom Snijders and Ruth Ripley for their constant suggestions. This has been a great learning experience for me, mostly because of how wonderful Tom and Ruth were at answering my endless emails.

I am blessed with a job that I love, working with an amazing group of people. The people who are responsible when I mess up - Steve Wunder and Randy Overton - have been wonderfully supportive as I completed my degree. A special thanks to my "focus group" - Andrea Schnell, Lisa Thomas, Sue Young, and Carolyn Drayton - you have given me sanity throughout the crazy. Thanks to my family and friends who endured this long process with me.

Last but not least, thank you to my husband, Frank. Your ability to tackle any obstacle has inspired me to take the time and put in the effort needed to fulfill my dreams. Thank you for giving me everything I ever could have wanted. You are a wonderful man, husband, and father. I'm so lucky to have you in my life...

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List of Notation

Table 1: Notation Summary

Variable	**Size**	**Definition**
n		number of actors
M		number of observed time periods
$\boldsymbol{X}(t_m)$	$n \times n$	matrix of tie variables (network matrix) at time t_m
$\boldsymbol{x}(t_m)$	$n \times n$	observed network at time t_m
x_{ij}	1×1	observed network tie from actor i to actor j
$\boldsymbol{x}(i\Delta j)$	$n \times n$	observed network where actor i changes the tie to actor j while all other ties remain the same
h		specifies a particular attribute Z_h
$\boldsymbol{Z}_h^*$	$n \times 1$	vector of constant actor attributes on attribute h
$\boldsymbol{z}_h^*$	$n \times 1$	observed vector of constant actor attributes on attribute h
$\boldsymbol{Z}_h(t_m)$	$n \times 1$	vector of changing actor attributes on attribute h at time t_m
$\boldsymbol{z}_h(t_m)$	$n \times 1$	observed vector of changing actor attributes on attribute h at time t_m
$\boldsymbol{z}(i \updownarrow_h \delta)$	$n \times 1$	observed vector of actor attributes when actor i's attribute changes by $\delta = 1$ on attribute h, while all other attributes levels remain the same
$\boldsymbol{Y}(t_m)$	$n \times (n+M)$	$[\boldsymbol{X}(t_m), \boldsymbol{Z}_h(t_m)]$ at time t_m
$\boldsymbol{y}(t_m)$	$n \times (n+M)$	observed network and attributes $[\boldsymbol{x}(t_m), \boldsymbol{z}_h(t_m)]$ at time t_m
$s_{ik}^{[\boldsymbol{X}]}$	$P \times 1$	network statistic k for actor i
$s_{ik}^{[\boldsymbol{Z}_h]}$	$Q \times 1$	attribute statistic k for actor i on attribute h
$\boldsymbol{\beta}^{[\boldsymbol{X}]}$	$P \times 1$	vector of network parameters
$\boldsymbol{\beta}^{[\boldsymbol{Z}_h]}$	$Q \times 1$	vector of attribute parameters
K	$P+Q$	length of vector with both network and attribute parameters
$\boldsymbol{\beta}_k$	$K \times 1$	vector of both network and attribute parameters
$\boldsymbol{\rho}_m$	$(M-1) \times 1$	vector of time dependence parameters
$\alpha_k^{[\boldsymbol{X}]}$	$K \times 1$	captures the dependence between the rate function and actor-dependent statistics
$\alpha_k^{[\boldsymbol{Z}_h]}$	$K \times 1$	captures the dependence between the rate function and actor-dependent statistics

Continued on the following page

Variable	**Size**	**Definition**
$a\left[\boldsymbol{X}\right]_{ki}\left(\boldsymbol{Y}(t)\right)$	$K \times 1$	the vector of actor-dependent statistics
$a\left[\boldsymbol{Z}_h\right]_{ki}\left(\boldsymbol{Y}(t)\right)$	$K \times 1$	the vector of actor-dependent statistics
$\boldsymbol{\theta}$	$L \times 1$	vector of parameters, $(\boldsymbol{\rho}, \boldsymbol{\beta}_k)$
$\boldsymbol{\theta}_1$	$(L-R) \times 1$	vector of unrestricted parameters
$\boldsymbol{\theta}_2$	$R \times 1$	vector of parameters in hypothesis H_0, set equal to $\mathbf{0}$
$\boldsymbol{\theta}_0$	$L \times 1$	vector of parameters under H_0, $\boldsymbol{\theta}_0' = [\boldsymbol{\theta}_1', \boldsymbol{\theta}_2']$
$\boldsymbol{\Sigma}$	$L \times L$	covariance matrix of $\boldsymbol{\theta}$
$g_n(\boldsymbol{y}_n, \boldsymbol{\theta})$	$L \times 1$	estimating function of $\boldsymbol{\theta}$
$\boldsymbol{\Delta}(\boldsymbol{\theta})$	$L \times L$	partial derivative matrix of g_n with respect to $\boldsymbol{\theta}$
$\Gamma(\boldsymbol{\theta}_0)$	$R \times (L-R)$	$\boldsymbol{\Delta}_{21}\boldsymbol{\Delta}_{11}^{-1}$
$b_n(\boldsymbol{y}_n, (\boldsymbol{\theta}_1, \mathbf{0}))$		$g_{2n}(\boldsymbol{z}_n, (\boldsymbol{\theta}_1, \mathbf{0})) - \Gamma(\boldsymbol{\theta}_0) g_{1n}(\boldsymbol{z}_n, (\boldsymbol{\theta}_1, \mathbf{0}))$
Σ		covariance matrix of b_n
$\lambda^{[X]}(\boldsymbol{Y}, m)$	$n \times 1$	network rate function
$\lambda^{[Z_h]}(\boldsymbol{Y}, m)$	$n \times 1$	attribute rate function
$f^{[\boldsymbol{X}]}(\boldsymbol{\beta}^{[\boldsymbol{X}]}, \boldsymbol{y})$	$n \times 1$	network evaluation function
$f^{[\boldsymbol{Z}_h]}(\boldsymbol{\beta}^{[\boldsymbol{Z}_h]}, \boldsymbol{y})$	$n \times 1$	attribute evaluation function
$\xrightarrow{d}$		converges in distribution to
z_i	$n \times 1$	vector of actor levels on attribute
sim_{ij}^{z}		the similarity between actors i and j on attribute $\boldsymbol{z}$ where $sim_{ij}^{z} = 1 - (\lvert z_i - z_j \rvert / \max_{i,j} \lvert z_i - z_j \rvert)$
$I\{z_i = z_j\}$		an indicator that equals 1 if actor i has the same covariate value as actor j, equals 0 if not

1 Introduction

Statistical models of social networks represent dependencies among actors. Difficulties in network modeling are largely due to the amount of dependency present in the data. Ties depend on actors present in the network and on other existing ties. Networks depend on previous network structures. Actor attributes affect the presence of ties and the attributes of other actors. Changes over time in network structure and of actor attributes depend on one another. Simple longitudinal network models quickly become complex, exponentially increasing the difficulty of modeling these dependent structures. In these models, three main components — network structure, attributes of actors, and attributes of the ties among actors (dyadic covariates) —allow for the development of complex hypotheses across different areas of interest.

Statistical social network analysis gained popularity following the research of Holland and Leinhardt (1970, 1971, 1977). Holland and Leinhardt (1977) developed the idea of using continuous time sociometric Markov chain models for dynamic network models, proposing that changes from a current network to a future network were determined by a continuous time Markov process. Using the assumption that network dynamics can be thought of as a Markov chain, this research allowed for a network evolution model where the probability distribution of future states, given the present state, does not depend on past states.[1]

Wasserman (1979, 1980), Wasserman and Iacobucci (1988), and Leenders (1995, 1996) extended the work of Holland and Leinhardt (1977) and developed several continuous-time Markov chain models, though the models were limited in that they only accounted for reciprocity among pairs of actors. These dynamic statistical models assume conditional dyad independence. When con-

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[1] The stochastic process proposed may not be appropriate in all applications, including models with third level and higher dependencies, but does allow for a first approximation.

ditioning on the observation immediately prior, the ties among two actors are stochastically independent of all other dyads. The assumption that dyads evolve as independent Markov chains ignores more complex network structures. Advances in network co-evolution models allow for the inclusion of actor attributes (Snijders, Steglich & Schweinberger, 2006). Co-evolution models evaluate and estimate changes in network structure and changes in actor attributes, also called covariates. One example of how attributes affect network change can be seen in *homophily* behaviors, often described by the phrase ‘birds of a feather flock together’. According to theories of homophily, actors are more likely to have ties with similar others and actors who are similar are more likely to have ties. Two mechanisms included in the co-evolution model describe how structure and attributes affect each other: social selection and social influence. Social selection explains how actor attributes influence the underlying processes that drive network change over time. Research has shown that during elementary school, friendship ties remain mostly within boys or girls, with few ties crossing among genders. The gender of each actor drives friendship tie formation. Gender is considered an exogenous attribute; it is constant and cannot be influenced by network structure. Social influence explains how network ties influence actor attributes. Actors become like the others who they share ties with. For example, expertise spreads among actors who communicate. Expertise levels change over time and must be measured at each observation, making expertise an endogenous attribute. Allowing additional dependencies and more complex parameters, the actor-based modeling approach adopted in this paper allows for higher order effects (such as transitivity among groups of three actors) and inclusion of actor attributes (such as how expertise levels of actors change over time).

Alternative models for dynamic networks have been developed by several research efforts (see Snijders, van de Bunt, & Steglich (2009) and Doreian & Stokman (1997) for lists of additional references). Actor-based models rely on simulations to explain probabilities of future behaviors. Actor-based simulation models have not been explored with estimation theory. If done, they would allow one to estimate and test effect inclusion or to test the theory supporting a statistical model. These simulation models allow for general simulation of network evolution, without relying on underlying theoretical statistical models. Alternative estimation techniques have been considered, however given the current research available, the actor-based modeling approach dominates network co-evolution modeling.[2]

Longitudinal network data are essentially panel data, where time is considered to be continuous between discrete observation points, suggesting the use of continuous time Markov models (Norris, 1997). The research presented here focuses on an actor-based modeling approach documented by Snijders (1996, 2001, 2005). Snijders' approach provides a great deal of flexibility, allowing for higher order parameters that include dependencies among multiple actors. This approach also has the ability to test statistical theories, including hypothesis testing for effect inclusion. Snijders proposed stochastic, actor-based models where non-deterministic rules guide the decisions of actors within a probabilistic framework called the actor-based model that uses method of moments to estimate a vector of parameters. Using method of moments allows estimation that is otherwise problematic due, in part, to an intractable likelihood function. The actor-based model will be discussed in greater detail in the following sections on model specification and estimation.

The goodness-of-fit of a model measures how well a statistical model represents the observed data. After a statistical model is fit to the data, the model generates a set of expected values for observations. Goodness-of-fit measures compare observed and expected data. The method of comparison often depends on the technique used to estimate the model. There are challenges involved in estimation and testing goodness-of-fit in these complicated modeling techniques. As the number of actors increases, the universe of possible combinations of ties becomes very large very quickly. An intractable likelihood function and lack of a saturated model make modeling network change a challenge, and make the usual goodness-of-fit measures impossible. Until alternative estimation methods are found, options for goodness-of-fit measures are limited. To help with

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[2] The DEDICOM model also provides an alternative way to approach square tables that describe asymmetric relationships among a number of actors (Harshman, 1978, 1981; Kiers, 1989; Kiers & Takane, 1993; Kiers, ten Berge, Takane, & de Leeuw, 1990; ten Berge & Kiers, 1989).

the interpretation of statistical co-evolution models, a measure of how well the model fits the observed data is needed. Measures of unexplained variance in regression models are common in standard statistical techniques but none exist for co-evolution models.

Currently there are only two available measures to assess inclusion of effects, both appropriate for estimation by method of moments. Snijders (1996) suggested dividing parameter estimates by their estimated standard errors. When the test statistic indicates that a parameter estimate is large compared to its standard error, this is evidence that inclusion of the parameter significantly improves the overall fit of the model. The test statistic is assumed to have a t-distribution; however, this test is more of a guideline since the behavior of these estimated t-statistics is still not fully understood. The standard errors are most likely underestimated. This t-test can only test one parameter at a time. Chapter 4.1 generalizes this statistic to a Pseudo-Wald statistic that can test multivariate hypotheses.

Recently, Schweinberger (2007) developed a generalized Neyman-Rao score test for testing parameters in a network evolution model, though not in a co-evolution model. However, generalization of the available measure to co-evolution modeling is reasonable and desirable. The score test has been implemented for the co-evolution model; however, the use of score tests in co-evolution models remains unsupported by either theory or empirical study. Theory must support the use of the score test for a co-evolution model to fully understand its properties. This dissertation uses Schweinberger's previous work on the score test to address the lack of theory behind its use to determine effect inclusion for the co-evolution model. The score test will be extended to the co-evolution model in Chapter 5.

The need to understand stochastic actor-based models has been brought to attention by the researchers who developed the actor-based co-evolution models. As Snijders, van de Bunt and Steglich (2010) state

> *Especially important will be the further development of ways to assess the goodness-of-fit of these models and to diagnose what in the data-model combination may be mainly responsible for a possible lack of fit. (p.37)*

In the following chapters, I present background information on modeling changes in network structure and actor attributes. Chapter 2 on model specification provides a summary of the rate and objective functions of the actor-based co-evolution model using recent notation and discusses assumptions and important effects. Following this summary, Chapter 3 covers model estimation using a method of moments approach. Previous work on fit measures is presented in Chapter 4, including an extension of Snijders' t-test to a multivariate case and an extension of the score test to the co-evolution model. Chapter 5 proposes two new measures of overall goodness-of-fit, followed by a simulation study in Chapters 6 and 7 that evaluates the performance of the proposed entropy-based measure, along with the proposed Pseudo-Wald test statistic and the generalization of Schweinberger's score test to the network co-evolution model.

2 Specification of Co-evolution Models

Modeling co-evolution of networks and actor attributes requires an extension of the methods for modeling network dynamics. Background information on this modeling framework comes from several sources (Snijders, 1996; Snijders, 2001; Snijders, 2005; Snijders, Steglich & Schweinberger, 2006; Steglich, Snijders & Pearson, 2009; Steglich, Snijders & Pearson, 2010).

The goal of a co-evolution model is to capture changes in the ties among actors, the attributes of actors, or the attributes of the ties among actors (dyadic covariates) that occur over time. The co-evolution model consists of rate functions and objective functions. These are described in the two sections following the presentation of useful notation and simplifying assumptions.

2.1 Notation

Let $\boldsymbol{X}(t_m)$ be a stochastic $n \times n$ matrix of ties at time t_m, where n is the number of actors present. The matrix $\boldsymbol{x}(t_m)$ is the observed network at time t_m, where element x_{ij} has a value of 1 if a tie exists from actor i (an ego) to actor j (an alter), and a value of 0 if the tie does not exist. Note that this is a directed, binary network. Thus, tie x_{ij} may be different than x_{ji} and ties may only have values of 1 (tie present) or 0 (tie not present). The network is also assumed to be nonreflexive, forcing the diagonal $x_{ii}(t_m)$ to be undefined. The observations are panel data; that is, observed networks are snapshots of a continuous underlying Markov process. Although time is assumed to be continuous, the network is only observed at two or more discrete, ordered time points ($t_1 < t_2 < ... < t_M$).

Actor attributes may also change over time. Exogenous, constant actor attributes (such as gender) comprise an $n \times 1$ vector of values and denoted by $\boldsymbol{Z}_h^*$. Endogenous, time-varying actor attributes comprise an $n \times M$ matrix of values on attribute h for each time point and denoted by $\boldsymbol{Z}_h(t_m)$. This matrix consists of rows of actors with columns capturing the attribute level at each observed time point. To simplify notation, the network matrix and one time varying attribute is represented as $\boldsymbol{Y}(t_M) = [\boldsymbol{X}(t_M), \boldsymbol{Z}_h(t_M)]$ and has dimension $n \times (n + M)$ for a time varying attribute. For a constant actor attribute (e.g., gender), $M = 1$ and the dimension of $\boldsymbol{Y}(t_M) = [\boldsymbol{X}(t_M), \boldsymbol{Z}_h^*)]$ is $n \times (n + 1)$. Matrix $\boldsymbol{Y}(t_M)$ combines all the information on an attribute and network at each time point. All available observed data are represented by the series of matrices, $\boldsymbol{y}(t_1), ..., \boldsymbol{y}(t_M)$.

For the purposes of this work, a model with one network relation and one time varying actor attribute ($h = 1$) is considered. Further generalizations to additional actor attributes, multiple relations, and to valued or undirected networks are possible, but not considered here. The actor-based modeling approach is not appropriate for coordination networks where tie creation is determined by a coordinated action among actors. Coordination networks (such as actors entering into agreements with one another) can be modeled using undirected or alternative directed network modeling approaches that do not have the assumptions of the actor-based model.

2.2 Background

Statistical social network analysis gained popularity following the research of Holland and Leinhardt (1970, 1971, 1977). Holland and Leinhardt (1977) developed the idea of using continuous time sociometric Markov chain models for dynamic network models, proposing that changes from a current network to a future network were determined by a continuous time Markov process. The Markov process has a transition matrix that determines the rate that changes occur. The transition matrix is defined as

$$q_{\boldsymbol{x},\boldsymbol{x}(i\Delta j)}(t) = \left\{ \begin{array}{ll} \lambda_{ij}(\boldsymbol{x}, t) & \text{if } \boldsymbol{x} \text{ and } \boldsymbol{x}(i\Delta j) \text{ differ in one element} \\ 0 & \text{if } \boldsymbol{x} \text{ and } \boldsymbol{x}(i\Delta j) \text{ differ in more than one element} \end{array} \right\}.$$

Using the assumption that network dynamics can be thought of in this way as a Markov chain, this research allowed for a network evolution model where the probability distribution of future states, given the present state, does not depend on past states. The Markov process proceeds in small micro-steps, changing one tie at a time. This framework was later extended to co-evolution models and the Markov process generalizes to small micro-steps where an actor can change one tie or a level of attribute at a time. A method of moments approach to estimation was proposed to estimate the stochastic process. The stochastic process proposed in Holland and Leinhardt (1977) may not be appropriate in all applications, including models with third level and higher dependencies, but it does allow for a first approximation.

Snijders (1996, 2001) extended Holland and Leinhardt's continuous time Markov chain models and introduced random utility models (McFadden, 1974; Maddala, 1983) to longitudinal network modeling. Snijders also proposed estimation methods that allowed for dependencies beyond dyads, better capturing structural changes in a network. Snijders assumed that the rate of changes follow the transition matrix proposed in Holland and Leinhardt (1977), but separated the rate function into two parts $\lambda_{ij}(\boldsymbol{y}, t) = \lambda_i^*(\boldsymbol{y}, t) p_i(j|\boldsymbol{y})$, where $\lambda_i^*(\boldsymbol{y}, t)$ captures the rate that actor i changes one of his ties, and $p_i(j|\boldsymbol{y})$ is the conditional probability that actor i changes the tie with actor j from x_{ij} to $x_{ij}^* = 1 - x_{ij}$. $p_i(j|\boldsymbol{y})$ can be modeled as having multinomial logit form.

$$p_i(j|\boldsymbol{x}(t), \boldsymbol{z}(t)) = \frac{\exp(f_i(\boldsymbol{\beta}, \boldsymbol{x}(i\Delta j)(t), \boldsymbol{z}(t)))}{\sum_h \exp(f_i(\boldsymbol{\beta}, \boldsymbol{x}(i\Delta h)(t), \boldsymbol{z}(t)))}$$

Taking this multinomial logit form, the conditional probability equates to assuming that actor i selects the other actor that maximizes the value of actor i's objective function plus a random element, $f_{\boldsymbol{X},i}(j|\boldsymbol{x}) + \epsilon_i^{[\boldsymbol{X}]}(\boldsymbol{y})$, where $\epsilon_i^{[\boldsymbol{X}]}(\boldsymbol{y})$ is distributed Gumbel $(0, 1)$. Snijders (2001) allowed for third and higher order dependencies and signifies a huge step forward in longitudinal network modeling.

2.3 Assumptions

Dependencies among ties and attributes can be difficult to formulate mathematically. The following simplifying assumptions make co-evolution processes estimable and interpretable.

1. Each actor has control over their out-degree $\boldsymbol{X}_{ij}(j = 1, ...n, i \neq j)$ and over changing attributes $Z_{hi}(h = 1, ..., H)$. A directed relation allows us to assume that an actor who initiates the tie, controls the tie. Self-ties $\boldsymbol{X}_{ii}$ are ignored.

2. Data are observed and measured at discrete time points. Changes are occurring throughout the evolution of a network, but not all changes are directly measured. Differences between two consecutive measured time points are the sum of many simple, unobserved changes that occur between time points.

3. Either a tie will be created, maintained, or dissolved; or an attribute will increase or decrease by one unit or stay the same. During each small, unobserved segment of continuous time between measured time points, only one tie or attribute change can be made. Complex changes in structure or attribute level are the result of many small, simple changes.

4. The observed network and attributes at the first time period ($\boldsymbol{Y}(t_1)$) are assumed and are conditioned upon for modeling future states. Given network and attribute levels at time t_m (i.e., $\boldsymbol{X}(t_m)$ and $\boldsymbol{Z}_h(t_m)$), the distribution of the future state of the network and attributes (i.e., $\boldsymbol{X}(t_{m+1})$ and $\boldsymbol{Z}_h(t_{m+1})$) is independent (lag 1) of what occurred before time t_m. The distribution of future states depends only on the state immediately preceding it.

2.4 Timing Of Decisions: The Rate Functions

The Markov property of the actor-based model leads to the decomposition of changes in ties among actors and in attributes into very small actor decisions. Large changes are the result of many small changes. Between each measured time point, many small changes are made that dissolve, maintain, or form network ties; or that change behavior or attitude.

The rate functions capture how much and how quickly network and attribute change occur. When the series of opportunities to make decisions satisfy the

Poisson processes with a rate of λ, the interval between consecutive events (random variable C) follows an exponential distribution:

$$f_C(c) = \lambda e^{-\lambda c}.$$

The rate parameters capture how frequently these choices are made between observed time points. A rate parameter for actors over each time interval is hypothesized for both network and attribute change. Therefore, there are two types of parameters: network rate parameters and attribute rate parameters.

The network rate parameter $\lambda^{[\boldsymbol{X}]}(\boldsymbol{Y}, m)$ captures the rate actors make decisions to change or maintain the presence of a tie. By ignoring the endowment component of the objective function as described in the following section, it is assumed that all actors share the same rate function. Thus, a rate parameter will be estimated for each time interval for both network and attribute change. A high value for a network rate parameter means that actors are making frequent changes their outgoing ties, while a low value means that the actors tend not to change their outgoing ties. The behavioral rate parameter $\lambda^{[\boldsymbol{Z}_h]}(\boldsymbol{Y}, m)$ describes how quickly actors change attribute levels by one unit. A high value for an attribute rate parameter means that actors' attribute levels are frequently updated. A low value means that actors' attribute levels remain rather constant.

The network rate parameter captures the opportunities for actor i to make changes to outgoing ties. The network rate parameter is randomly distributed and follows a Poisson process where times between changes are modeled by an exponential distribution with a parameter given by the rate function $\lambda_i^{[\boldsymbol{X}]}$.

The network rate function for each actor in the time period (t) between times t_m and t_{m+1} is given by

$$\lambda_i^{[\boldsymbol{X}]}(\boldsymbol{Y}, m) = \rho_m^{[\boldsymbol{X}]} \exp\Big(\sum_k \alpha_k^{[\boldsymbol{X}]} a\,[\boldsymbol{X}]_{ki}\,(\boldsymbol{Y}(t_m))\Big),$$

where $\rho_m^{[\boldsymbol{X}]}$ is the vector of time dependent parameters for network structure, $\alpha_k^{[\boldsymbol{X}]}$ captures the dependence between the rate function and actor-dependent statistics (such as the degree distribution and covariates), and $a\left[\boldsymbol{X}\right]_{ki}(\boldsymbol{Y}(t_m)$, is the vector of actor-dependent statistics.

The attribute rate parameter captures the opportunity for an actor to make changes to the level of an attribute. The attribute rate parameter is randomly distributed and follows a Poisson process where the time between changes is modeled by an exponential distribution, with parameters given by the rate function $\lambda_i^{[\boldsymbol{Z}_h]}$. The attribute rate function is given by

$$\lambda_i^{[\boldsymbol{Z}_h]}(\boldsymbol{Y}, m) = \rho_m^{[\boldsymbol{Z}_h]} \exp\Big(\sum_k \alpha_k^{[\boldsymbol{Z}_h]} a\left[\boldsymbol{Z}_h\right]_{ki}(\boldsymbol{Y}(t_m))\Big),$$

where $\rho_m^{[\boldsymbol{Z}_h]}$ is the vector of time dependency parameters for actor attributes, $\alpha_k^{[\boldsymbol{Z}_h]}$ captures the dependence between the rate function and actor-dependent statistics (such as the degree distribution and covariates), and $a\left[\boldsymbol{Z}_h\right]_{ki}(\boldsymbol{Y}(t_m)$, is the vector of actor-dependent statistics. The actor dependent statistics in the network and attribute rate functions may differ. For example, if the statistic does not take into account network structure but does represent attribute levels, it will appear in the attribute rate function but not the network rate function.

A critical property of the exponential distribution associated with the rate function is the ‘forgetfulness property’. Unequal durations between observed times become meaningless since the time scale is absorbed into the ρ_m parameters. The forgetfulness of this distribution also justifies the use of the Markov property for the stochastic process, $\boldsymbol{Y}(t_m)$.

2.5 Actors’ Decisions To Form Or Dissolve Ties: The Objective Functions

The objective function works with the rate functions. The rate functions determine the rate that actors’ make changes, and the objective function captures what changes are made. The objective function can be broken down into three main components: the evaluation function f, the endowment function, and a random component ϵ. Each part of the objective function has an important job.

The evaluation function f captures the overall structure of the network. The probability that a tie will change depends on the different structures present in the network. For example, a network with a high transitive triplet structure would show that ties would have a higher probability of forming if they close a transitive triple, or a higher probability of a tie among actors i and k if actor i chooses j and actor j chooses k.

The endowment function attempts to capture differences in the value between forming and dissolving ties. This component allows for different costs for making or dissolving a tie. An example provided in Snijders, Steglich and Schweinberger (2006) states that the cost of losing a reciprocal tie may be greater than the cost of forming a reciprocal tie. Although theoretically important, including the endowment function in practice adds little to a co-evolution model. It is important to look at how forming a tie and dissolving a tie differ in strength, but in practice, including this function increases model complexity and makes the estimation process more difficult. In this paper, the endowment function is ignored and explanations focus on the evaluation function associated with forming, dissolving or maintaining a tie.

The random component, ϵ, of the objective function represents residual noise and is a function of the intermediate state of the network. The random residuals are assumed to be independent and to follow a standard Gumbel (or extreme value) distribution. This assumption for residuals implies a logistic model (i.e. a logit link function).

The objective function captures the probability that a tie will be maintained, formed or dissolved among two actors. The objective function for network change optimized by actor i is the weighted sum of parameters $\beta_k^{[\boldsymbol{X}]}$ and variables $s_{ik}^{[\boldsymbol{X}]}$ that are statistics computed from observed data (see table 2.1 for a reference of possible effects).

Recall that the matrix $\boldsymbol{Y}$ is the observed network and attribute, $(\boldsymbol{X}, \boldsymbol{Z}_h)$. The objective function for network change optimized by actor i is the weighted sum of parameters $\beta_k^{[\boldsymbol{X}]}$ and variables $s_{ik}^{[\boldsymbol{X}]}$, such that

$$f_i^{[\boldsymbol{X}]}(\boldsymbol{\beta}^{[\boldsymbol{X}]}, \boldsymbol{y}) + \epsilon_i^{[\boldsymbol{X}]}(\boldsymbol{y}) = \sum_k \beta_k^{[\boldsymbol{X}]} s_{ik}^{[\boldsymbol{X}]}(\boldsymbol{y}) + \epsilon_i^{[\boldsymbol{X}]}(\boldsymbol{y}).$$

The objective function for attribute or behavior change is the weighted sum of parameters $\boldsymbol{\beta}^{[\boldsymbol{Z}_h]}$ and variables $s_{ik}^{[\boldsymbol{Z}_h]}$ that are statistics computed from observed data (see table 2.1 for a reference of possible effects).

$$f_i^{[\boldsymbol{Z}_h]}(\boldsymbol{\beta}^{[\boldsymbol{Z}_h]}, \boldsymbol{y}) + \epsilon_i^{[\boldsymbol{Z}_h]}(\boldsymbol{y}) = \sum_k \beta_k^{[\boldsymbol{Z}_h]} s_{ik}^{[\boldsymbol{Z}_h]}(\boldsymbol{y}) + \epsilon_i^{[\boldsymbol{Z}_h]}(\boldsymbol{y}).$$

The most intuitive formulation of this modeling technique has to do with the probability that actor i will change the tie variable to actor j represented as a function of the current state of the network. The matrix $\boldsymbol{x}(i\Delta j)$ for $i \neq j$ describes the network configuration where actor i changes the tie variable to actor j, but all other ties remain the same. With fixed attribute levels at time t and where l is the set of all other actors, excluding actors i and j, the resulting choice probability for network ties is

$$P(\boldsymbol{x}(i\Delta j)|\boldsymbol{x}(t), \boldsymbol{z}(t)) = \frac{\exp(f_i^{[\boldsymbol{X}]}(\beta^{[\boldsymbol{X}]}, \boldsymbol{x}(i\Delta j)(t), \boldsymbol{z}(t)))}{\sum_l \exp(f_i^{[\boldsymbol{X}]}(\beta^{[\boldsymbol{X}]}, \boldsymbol{x}(i\Delta l)(t), \boldsymbol{z}(t)))}.$$

The inclusion of the matrix $\boldsymbol{x}(i\Delta j)$ compares the matrix only excluding actor j in the numerator with the matrices that result from leaving out each of the present actors in the denominator.

With fixed network ties at time t, the probability of attribute change is

$$P(\boldsymbol{z}(i \updownarrow_h \delta)|\boldsymbol{x}(t), \boldsymbol{z}(t)) = \frac{\exp(f_i^{[\boldsymbol{Z}_h]}(\beta^{[\boldsymbol{Z}_h]}, \boldsymbol{x}(t), \boldsymbol{z}(i \updownarrow_h \delta)(t)))}{\sum_{\tau \in \{-1,0,1\}} \exp(f_i^{[\boldsymbol{Z}_h]}(\beta^{[\boldsymbol{Z}_h]}, \boldsymbol{x}(t), \boldsymbol{z}(i \updownarrow_h \tau)(t)))}, \tag{2.1}$$

where $\boldsymbol{z}(i \updownarrow_h \delta)$ is the vector when actor i changing his or her level by $\delta = 1$ on attribute h. The summation in the denominator of Equation (2.1) looks at attribute level changes for the actor, when each actor can maintain, decrease by one unit or increase by one unit his or her attribute level. The summation also ensures that probabilities sum to 1. The inclusion of the vector $\boldsymbol{z}(i \updownarrow_h \delta)$ compares the vector when actor i changes his level on attribute h by 1 in the numerator with the vectors that result from other attribute level changes in the denominator.

2.6 Effects

Networks and attributes can be explanatory and dependent variables, either in separate models or simultaneously in the co-evolution model. For example, in social selection models the attribute is the explanatory variable and the network is the dependent variable. The model of how network structure changes over time depends on an actors' likelihood of establishing, maintaining, or dissolving a tie and the rate that decisions about ties are made.

The evaluation function in the model includes effects that describe structure and actor attributes. A small subset of possible network effects $s_{ik}^{[\boldsymbol{X}]}$ are presented in the upper part of table 2.1 and a small subset of possible attribute effects $s_{ik}^{[\boldsymbol{Z}_h]}$ are presented in the lower part of table 2.1. As more co-evolution theories and applications develop, the number of effects can be expected to expand. The list of possible attribute effects contain some additional notation. The vector $\boldsymbol{z}_i$ is a vector of attributes, and sim^z_{ij} is defined as the similarity between actors i and j on covariate v, where $sim^z_{ij} = 1-(|z_i-z_j|/\max_{i,j}|z_i-z_j|)$.As an example, the transitivity network effect considers the ties present among a group of three actors. Three actors exhibit transitive structure if actor i has a tie with actor j, actor j has a tie with actor h, and actor i has a tie with actor h. The covariate-related similarity x reciprocity interaction parameter compares the attribute level of actors that have reciprocal ties. The total similarity effect measures how similar actor i is with each actor on the attribute.

Table 2.1: Possible Effects

Parameter	**Network Statistic**
Density (or out-degree)	$x_{i+} = \sum_j x_{ij}$
Reciprocity	$\sum_j x_{ij}x_{ji}$
Transitive Triplets	$\sum_{j,h} x_{ij}x_{ih}x_{jh}$
Transitive Ties	$\sum_h x_{ih}\mathrm{max}_j(x_{ij}x_{jh}$
Number of 3-cycles	$\sum_{j,h} x_{ij}x_{jh}x_{hi}$
Balance	$\frac{1}{n-2}\sum_{j=1} x_{ij} \sum_{h=1,h\neq i,j}(b_o - \mid x_{ih} - x_{jh})$
	where b_o is the mean of $\lvert x_{ih} - x_{jh}\rvert$
Betweenness	$\sum_{j,h} x_{hi}x_{ij}(1 - x_{hj})$
In-degree Popularity (Square Root)	$\sum_i x_{ij}\sqrt{x_{+j}}$
Out-degree Popularity (Square Root)	$\sum_i x_{ij}\sqrt{x_{j+}}$
Activity	$(1/n)\sum_j x_{ij}\sum_h x_{jh}$
Covariate similarity	$m_j x_{ij}(sim^z_{ij} - \widehat{sim}^z_{ij})$
Covariate-alter	$\sum_j x_{ij}z_j$
Same Covariate	$\sum_j x_{ij}I\{z_i = z_j\}$
	where $I\{z_i = z_j\} = 1$ if $z_i = z_j$ and 0 otherwise
Covariate-related similarity x reciprocity	$\sum_j x_{ij}x_{ji}(sim^z_{ij} - \widehat{sim}^z_{ij})$
Covariate-ego	$\sum_j x_{ij}z_i = z_i x_{i+}$
Covariate-ego x alter	$\sum_j x_{ij}z_i z_j$
Behavioral tendency (linear shape)	z_i
Behavioral quadratic shape	z_i^2
Behavioral total similarity	$\sum_j x_{ij}(sim^z_{ij} - \overline{sim^z})$
Behavioral in-degree	$z_i\sum_j x_{ji}$
Behavioral out-degree	$z_i\sum_j x_{ij}$
Behavioral average alter	$z_i\frac{(\sum_j x_{ij}z_j)}{\sum_j x_{ij}}$
Average Similarity	$x_{i+}^{-1}\sum_{j=1}^{n} x_{ij}(\mathrm{sim}^z_{ij}) - \widehat{\mathrm{sim}}^z_{ij})$

3 Estimation of Co-evolution Models - Method of Moments

The likelihood function for this model cannot be computed explicitly; therefore, maximum likelihood estimation is difficult. Using the general framework of Markov Chain Monte Carlo (Besag, 2001; Schweinberger & Snijders, 2007), method of moments estimation procedures can be specified for network and attribute co-evolution. Method of moments makes estimation easier, since there is no need for a likelihood function. It also serves as the basis for using a generalized Neyman-Rao score test as a measure of fit. The method of moments estimation algorithm compares the observed network to hypothetical networks generated in the simulations, generally yielding consistent estimates. However, because the estimation uses a stochastic algorithm, results vary from one model run to the next. In addition, estimates are often not efficient, where efficiency depends on the choice of statistics.

In the general case (for data $\boldsymbol{Y}$ and vector of parameters $\boldsymbol{\theta}$), the method of moments estimator is based on the statistic $u(\boldsymbol{Y})$, where $u(\boldsymbol{y})$ is the observed value of $u(\boldsymbol{Y})$. The moment equation gives the value $\widehat{\boldsymbol{\theta}}$ where the expected value of $u(\boldsymbol{Y})$ equals the observed value, $u(\boldsymbol{y})$; that is,

$$E_{\widehat{\boldsymbol{\theta}}}(u(\boldsymbol{Y})) = u(\boldsymbol{y}). \tag{3.1}$$

Equation (3.1) gives a locally unique (and often globally unique) moment equation solution. The delta method and implicit function theorem provide an asymptotic covariance matrix for the estimated vector of parameters. Under regularity conditions, if $\hat{\boldsymbol{\theta}}$ is a consistent solution to the moment equation, the asymptotic covariance matrix for $\hat{\boldsymbol{\theta}}$ is given by the equation:

$$\text{cov}_{\boldsymbol{\theta}}(\hat{\boldsymbol{\theta}}) \approx D_{\boldsymbol{\theta}} \text{cov}_{\boldsymbol{\theta}}(u(\boldsymbol{Y})) D'_{\boldsymbol{\theta}}, \tag{3.2}$$

where $D_{\boldsymbol{\theta}}$ is inverse of the vector of first partial derivatives,

$$D_{\boldsymbol{\theta}} = \Big(\frac{\partial E_{\boldsymbol{\theta}}(u(\boldsymbol{Y}))}{\partial \boldsymbol{\theta}}\Big)^{-1}.$$

The moment estimate parameters ($\hat{\boldsymbol{\theta}}$) provide the solution to the following equation (note: this equation shows that given the network and attributes at time t_m, the sum of the expected values at time t_{m+1} minus the observed values at time t_{m+1} will equal zero):

$$g_n(\boldsymbol{y}_n, \boldsymbol{\theta}) = \sum_{m=1}^{M-1} E_{\boldsymbol{\theta}}[u_m(\boldsymbol{Y}(t_{m+1}))|\boldsymbol{Y}(t_m) = \boldsymbol{y}(t_m)] - u_m(\boldsymbol{y}(t_{m+1})) = \mathbf{0}. \tag{3.3}$$

The function g_n is an unbiased estimating function for all n and all $\boldsymbol{\theta}$ such that

$$E_{\boldsymbol{\theta}}[g_n(\boldsymbol{Y}_n, \theta) \mid Y(t_1) = \boldsymbol{y}(t_1)] = 0$$

with covariance Σ. Additionally, the diagonal matrix $\Delta_n(\boldsymbol{\theta})$ is the partial derivative matrix of g_n with respect to $\boldsymbol{\theta}$,

$$\Delta_n(\boldsymbol{\theta}) = \frac{\partial g_n(\boldsymbol{y}_n, \boldsymbol{\theta})}{\partial \boldsymbol{\theta}'} = \frac{\partial}{\partial \boldsymbol{\theta}'} E_{\boldsymbol{\theta}}[u(\boldsymbol{Y}(t_2)) \mid \boldsymbol{Y}(t_1) = \boldsymbol{y}(t_1)]. \tag{3.4}$$

Within this general framework, four main components must be estimated: rate functions for network and attribute change, and evaluation functions for network and attribute change.

The natural statistic to estimate $\rho_m^{[\boldsymbol{X}]}$, $u(\rho_m^{[\boldsymbol{X}]})$, for the network rate function is

$$u(\rho_m^{[\boldsymbol{X}]}) = \sum_{i,j} a_{ki}^{[\boldsymbol{X}]}(\boldsymbol{Y}(t_{m-1}))|X(t_m) - X(t_{m-1})|.$$

The natural statistic to estimate $\rho_m^{[\boldsymbol{Z}_h]}$ for the attribute rate function is

$$u(\rho_m^{[\boldsymbol{Z}_h]}) = \sum_{i} a_{ki}^{[\boldsymbol{Z}_h]}(\boldsymbol{Y}(t_{m-1}))|Z_{hi}(t_m) - Z_{hi}(t_{m-1})|.$$

The statistic used to estimate $\boldsymbol{\beta}_k^{[\boldsymbol{X}]}$, the vector of network change parameters, is

$$u_m(\boldsymbol{Y}(t_{m-1}), \boldsymbol{Y}(t_m)) = \sum_{i} s_{ik}^{[\boldsymbol{X}]}(\boldsymbol{X}(t_m), \boldsymbol{Z}(t_{m-1})).$$

The statistic used to estimate $\boldsymbol{\beta}_k^{[\boldsymbol{Z}_h]}$, the vector of attribute change parameters, is

$$u_m(\boldsymbol{Y}(t_{m-1}), \boldsymbol{Y}(t_m)) = \sum_{i} s_{ik}^{[\boldsymbol{Z}_h]}(\boldsymbol{X}(t_{m-1}), \boldsymbol{Z}(t_{m-1}), \boldsymbol{Z}(t_m)).$$

The stochastic processes of the moment equations (3.3) can be easily simulated using approximation methods such as the one proposed in Robbins and Monro (1951) described in Snijders (2001, 2002). Using the delta method and the implicit function theorem within the method of moments framework, the covariance matrix of $\hat{\boldsymbol{\theta}}$ can be derived in Equation (3.2). Monte Carlo methods can estimate the covariance matrix $\Sigma_{\boldsymbol{\theta}}$ and the partial derivative matrix, $D_{\boldsymbol{\theta}}$.

The estimation algorithm is implemented in three phases in the RSiena package.

1. In phase 1, the parameter vector is held constant at its initial value and is used to obtain an initial estimate of the derivative matrix.

2. In phase 2, parameter values vary between runs, reflecting deviations between generated and observed values of the statistics.
3. In phase 3, the parameter vector is held constant at its final value and is used to estimate the covariance matrix and the derivative matrix used for computing standard errors.

The estimation of standard errors of the MoM estimates requires the estimation of derivatives that indicate how sensitive the expected values of the statistics are with respect to the parameters. The chosen method to estimate derivatives in the RSiena package uses the score function. This methods avoids a bias-variance dilemma present in finite differences methods, is unbiased, requires less computation time, and is consistent. Using the estimation approach detailed in this chapter, the following chapter outlines currently available and proposed measures used to test for inclusion of effects.

4 Tests For Effect Inclusion

Four main goals drive the research presented in the remainder of this document.

1. Extend Snijders' t-test to a Pseudo-Wald statistic to accommodate multivariate hypotheses, including
    (a) determining a suitable estimate for $\widehat{\Sigma}_{\widehat{\boldsymbol{\beta}}}$,
    (b) studying the distribution of the Pseudo-Wald statistic, and
    (c) comparing the performance of the Pseudo-Wald statistic to the performance of the generalized score test.
2. Extend Schweinberger's network score test to a co-evolution model.
3. Develop an entropy-based goodness-of-fit measure.
4. Propose the framework for a generalized R^2 goodness-of-fit measure.
5. Conduct a simulation to compare model selection procedures, including
    (a) comparing the distribution and behavior of the Pseudo-Wald test, the generalized score test, and the proposed entropy goodness-of-fit measure, and
    (b) comparing results of effect inclusion using the Pseudo-Wald test, the score test, and the entropy goodness-of-fit measure.

4.1 Snijders' t-Test Extended To A Pseudo-Wald for Multivariate Tests

Snijders (1996) proposed a statistic for assessing the significance of a parameter. With a null hypothesis for testing whether a parameter is significantly different than 0, this statistic consists of dividing a parameter estimate by its estimated standard error. The sampling distribution of this statistic is assumed (based on simulation studies) to be approximately standard Gaussian. The distributional assumption gives a suggested cut-off value of $|2|$ corresponding to a $p < 0.05$. Values greater than $|2|$ are considered large and signify that associated parameters should be included in a model.

The Pseudo-Wald test approximates a likelihood ratio test in that it works by testing the null hypothesis that a set of parameters is equal to some value (in this case, equal to zero). Unlike the t-test, the Pseudo-Wald test can be used to test multiple parameters and linear combinations of them simultaneously.

If $\widehat{\boldsymbol{\beta}} \approx$ Multivariate Normal$(\boldsymbol{\beta}, \Sigma_{\boldsymbol{\beta}})$ and the null hypothesis, for example, is specified as $H_0 : \boldsymbol{\beta}_k - \boldsymbol{\beta}_k^\star = \boldsymbol{\beta}_{k+1} - \boldsymbol{\beta}_{k+1}^\star = 0$ when testing for 2 parameters equal to one another. This test equals

$$H_0 : \begin{pmatrix} 1 & 0 \\ 0 & 1 \end{pmatrix} \left[\begin{pmatrix} \boldsymbol{\beta}_k \\ \boldsymbol{\beta}_{k+1} \end{pmatrix} - \begin{pmatrix} \boldsymbol{\beta}_k^\star \\ \boldsymbol{\beta}_{k+1}^\star \end{pmatrix} \right] = \begin{pmatrix} 0 \\ 0 \end{pmatrix},$$

$$L\,(\boldsymbol{\beta}_k - \boldsymbol{\beta}_k^\star) = \mathbf{0},$$

where $\boldsymbol{\beta}_k^\star$ and $\boldsymbol{\beta}_{k+1}^\star$ are some specified values. When testing for inclusion of effects, $\boldsymbol{\beta}^\star$ equals the vector $\mathbf{0}$, simplifying the equation above to $H_0 : \boldsymbol{L}\boldsymbol{\beta} = \mathbf{0}$. The Pseudo-Wald test statistic can be computed by

$$\widehat{\boldsymbol{\beta}}' \boldsymbol{L}' (\boldsymbol{L} \widehat{\Sigma}_{\widehat{\boldsymbol{\beta}}} \boldsymbol{L}')^{-1} \boldsymbol{L} \widehat{\boldsymbol{\beta}} \sim \chi^2_{\text{number of rows in } \boldsymbol{L}}.$$

During the simulation study, the global hypothesis was broken down and the Pseudo-Wald test was used to look at all possible combinations of parameters, ranging from testing if all parameters are equal to the equality of each pair of parameters. A subset of all possible Pseudo-Wald tests was included in the analysis. The covariance matrix, $\widehat{\Sigma}_{\widehat{\boldsymbol{\beta}}}$, is already estimated by the algorithm used to find parameter estimates as part of the RSiena package. Type 1 errors may be inflated by the break down of the global hypothesis. For the purpose of this study, no correction is made, though in practice, an appropriate correction should be used.

4.2 Schweinberger's Score Test Extended To The Co-evolution Model

Recall, obstacles inherent to longitudinal social network co-evolution modeling include an intractable likelihood function, functions that are difficult to estimate, problems with model convergence, and the absence of a saturated model. Schweinberger (2007) developed a score-type test for measuring inclusion of effects (i.e. parameters equal to zero) that overcomes these obstacles and provides a tool for model evaluation that can be used in forward model selection. The theory presented only considered for network evolution, not network and attribute co-evolution; Schweinberger did not extend the statistic for both network and attribute parameters. However, the SIENA program allows for its use while developing co-evolution models. Further theoretical generalization is needed to ensure testing accuracy.

Schweinberger's test is similar to a Rao score test. It is found by generalizing the C(α) test (Neyman and Pearson, 1928 parts i and ii) and replacing the Fisher score function with regular estimating functions (Basawa, 1991). This test has several appealing features, notably that the restricted model of the null hypothesis is the only model that must be estimated and that it relies on method of moment estimators. These features allow for faster estimation and overcome the obstacles associated with an unavailable likelihood function.

This derivation follows Schweinberger's assumption of two time points, $M = 2$. This is done only for ease of presentation, as underlying Markov processes allow for generalization to a larger M.

The vector of parameters $\boldsymbol{\theta}$ can be partitioned into two parts $\boldsymbol{\theta}' = (\boldsymbol{\theta}_1', \boldsymbol{\theta}_2')$. The vector $\boldsymbol{\theta}_1$ is composed of all unrestricted parameters included in the model, both structural and behavioral. The parameters in $\boldsymbol{\theta}_1$ are both included in H_0 and H_1. The vector $\boldsymbol{\theta}_2$ is composed of the parameters to be tested (of length R and with all parameters set equal to zero). The null hypothesis is H_0: $\boldsymbol{\theta}_2 = \mathbf{0}$, versus the alternative hypothesis $H_1 : \boldsymbol{\theta}_2 \neq \mathbf{0}$. These hypotheses can also be generalized to have nonzero values. In this argument, the vector $\boldsymbol{\theta}$ contains network and attribute parameters (i.e. the $\beta_k^{[\boldsymbol{X}]}$ and $\beta_k^{[\boldsymbol{Z}_h]}$ parameters). For this case, where the null hypothesis is that $\boldsymbol{\theta}_2 = 0$, the vector $\boldsymbol{\theta}_0' = (\boldsymbol{\theta}_1', \mathbf{0}')$. The values in the vector $\boldsymbol{w}_n$ are appropriate normalizing constants. To take a closer look at the partitioned $\boldsymbol{\theta}_0$ vector, it is important to divide other quantities with respect to $\boldsymbol{\theta}' = (\boldsymbol{\theta}_1', \boldsymbol{\theta}_2')$:

$$\boldsymbol{\Sigma} = \begin{pmatrix} \boldsymbol{\Sigma}_{11} & \boldsymbol{\Sigma}_{12} \\ \boldsymbol{\Sigma}_{12}' & \boldsymbol{\Sigma}_{22} \end{pmatrix},$$

$$g_n(\boldsymbol{y}_n, \boldsymbol{\theta}) = \begin{pmatrix} g_{1n}(\boldsymbol{y}_n, \boldsymbol{\theta}) \\ g_{2n}(\boldsymbol{y}_n, \boldsymbol{\theta}) \end{pmatrix},$$

$$\boldsymbol{\Delta}(\boldsymbol{\theta}) = \begin{pmatrix} \boldsymbol{\Delta}_{11}(\boldsymbol{\theta}) & \boldsymbol{\Delta}_{12}(\boldsymbol{\theta}) \\ \boldsymbol{\Delta}_{12}'(\boldsymbol{\theta}) & \boldsymbol{\Delta}_{22}(\boldsymbol{\theta}) \end{pmatrix},$$

where $g_n(\boldsymbol{y}_n, \boldsymbol{\theta})$ is an unbiased estimating function. These vectors and matrices are split to compare distributions of the null and alternative hypotheses. For more description, see equations (3.3) and (3.4), where details of the estimating equation and its covariance structure were presented.

Assume as $n \to \infty$ and where L is the length of g_n,

$$w_n^{1/2} g_n(\boldsymbol{Y}_n, \boldsymbol{\theta}) \quad \xrightarrow{d} \quad MVN_L(\mathbf{0}, \boldsymbol{\Sigma}).$$

Under the null hypothesis $H_0 : \boldsymbol{\theta}_2 = \mathbf{0}$, this assumption implies the following two asymptotic distributions, where $MVN_{(L-R)}$ is $(L-R)$-variate normality and $MVN_{(R)}$ is R-variate multinormal: as $n \to \infty$,

$$w_n^{1/2} g_{1n}(\boldsymbol{Y}_n, (\boldsymbol{\theta}_1, \mathbf{0})) \quad \xrightarrow{d} \quad N_{(L-R)}(\mathbf{0}, \boldsymbol{\Sigma}_{11})$$

and

$$w_n^{1/2} g_{2n}(\boldsymbol{Y}_n, (\boldsymbol{\theta}_1, \mathbf{0})) \quad \xrightarrow{d} \quad N_{(R)}(\mathbf{0}, \boldsymbol{\Sigma}_{22}),$$

where $b_n(\boldsymbol{y}_n, (\boldsymbol{\theta}_1, \mathbf{0})) = g_{2n}(\boldsymbol{z}_n, (\boldsymbol{\theta}_1, \mathbf{0})) - \Gamma(\boldsymbol{\theta}_0) g_{1n}(\boldsymbol{z}_n, (\boldsymbol{\theta}_1, \mathbf{0}))$, $\Gamma = \boldsymbol{\Delta}_{21}\boldsymbol{\Delta}_{11}^{-1}$, and $\boldsymbol{\Delta}_{11}$ is non-singular.

These convergent distributions are based on the assumption that $n \to \infty$. This assumption is examined in the simulation study presented later to determine how large a sample needs to be for this test to perform well. Especially with finite samples of actors (that may mean a small number of actors), the size of n needed for convergence should be studied. (In Schweinberger's simulation study, an $n = 30$ showed good convergence.)

This equation for b_n and the converging distributions of g_{1n} and g_{2n} provide the variance-covariance matrix of b_n. In general form, the covariance matrix of $b_n(\boldsymbol{y}_n, (\boldsymbol{\theta}_1, \mathbf{0}))$, noted by the term Σ, is

$$\operatorname{cov}\left(b_n(\boldsymbol{y}_n, \boldsymbol{\theta}_0)\right) =$$

$$\operatorname{var}(g_{2n}(\boldsymbol{z}_n, \boldsymbol{\theta}_0)) + \operatorname{var}(\Gamma(\boldsymbol{\theta}_0) g_{1n}(\boldsymbol{z}_n, \boldsymbol{\theta}_0)) - 2\operatorname{cov}(g_{2n}(z_n, \boldsymbol{\theta}_0), \Gamma(\boldsymbol{\theta}_0) g_{1n}(z_n, \boldsymbol{\theta}_0)).$$

Substituting in terms for the general form, the covariance matrix becomes

$$\Sigma = \boldsymbol{\Sigma}_{22} + \Gamma(\boldsymbol{\theta}_0)\boldsymbol{\Sigma}_{11}\Gamma(\boldsymbol{\theta}_0)' - (\boldsymbol{\Sigma}_{12}'\Gamma(\boldsymbol{\theta}_0)' + \Gamma(\boldsymbol{\theta}_0)\boldsymbol{\Sigma}_{12}). \tag{4.1}$$

Both g_{1n} and g_{2n} have expected values equal to $\mathbf{0}$, implying that b_n has an expected value of $\mathbf{0}$. Given this expected value and the covariance matrix in Equation (4.1), as $n \to \infty$

$$w_n^{1/2} b_n(\boldsymbol{Y}_n, \boldsymbol{\theta}_0) \quad \xrightarrow{d} \quad N_R(\mathbf{0}, \Sigma).$$

Therefore, as $n \to \infty$

$$w_n b_n'(\boldsymbol{Y}_n, \boldsymbol{\theta}_0)\Sigma^{-1} b_n(\boldsymbol{Y}_n, \boldsymbol{\theta}_0) \quad \xrightarrow{d} \quad \chi^2_R.$$

In summary, the two-tailed proposed multivariate score test (MST) is based on the statistic:

$$MST = w_n b_n'(\boldsymbol{Y}_n, \boldsymbol{\theta}_0)\Sigma^{-1} b_n(\boldsymbol{Y}_n, \boldsymbol{\theta}_0).$$

Under the null hypothesis, given that variables are defined across their entire range and the sample size approaches infinity, the test statistic converges in distribution to an asymptotically central chi-square with R degrees of freedom. Notice that since $b_n(\boldsymbol{Y}_n, (\boldsymbol{\theta}_1, \mathbf{0}))$ contains $\boldsymbol{\theta}_2 = \mathbf{0}$, there is no need to estimate $\boldsymbol{\theta}_2$, making the estimation process more efficient. This test is based on asymptotic properties, although in a finite sample this test approximates a chi-squared distribution with R degrees of freedom, as seen in a simulation study discussed in a following section. The score test compares the expected value of some function (evaluated under some assumed model) to the observed value of the function.

4.3 Remarks About Current Measures

For each of the current measures, various comments should be made about the behavior and interpretation of each measure. Snijders' t-test remains a guideline with an unknown error distribution. This measure provides information when selecting effects that should be investigated further, although the actual properties of the distribution must be further researched. Concerns remain about the theoretical and applied distribution of extending Snijders' t-test to a multivariate null hypothesis.

Because Snijders' t-test and the Pseudo-Wald test statistic have unknown theoretical distributions, these measures of fit are more guidelines than statistical tests. Empirical evidence for the distributions of these statistics is provided in this paper. Combining the Pseudo-Wald test with the extended score test provides a better indication of the contribution effects make to a model's fit and enables better decisions regarding whether particular explanatory variables or effects should be included in the model. Concerns about the score test have been raised within research, though the extent that those concerns apply to the present model remains unknown (Freedman, 2007; Morgan, Palmer & Ridout, 2007; Verbeke & Molenberghs, 2007)

The two tests previously discussed — the Pseudo-Wald test and the score test — approximate the likelihood ratio test, though they only require estimation of one model. Because the co-evolution model has an intractable likelihood function and lacks a saturated model, a likelihood ratio test (Neyman & Pearson, 1928) is not possible; therefore the other two options are relied upon. Both the Pseudo-Wald and score tests are asymptotically equivalent to the likelihood ratio test, and therefore to each other. In general statistical theory, as the number of observations increases, the three test statistics converge to one another. With a finite number of observations, the three test statistics may differ from one another. How close these statistics are to one another provides some evidence about whether the number of observations is large enough, shown by their asymptotic equivalence.

4.4 Previous Simulation Study

The following section describes a simulation study from Schweinberger (2007) that evaluated the behavior of the proposed network score test statistic and Snijders' Pseudo-t-test. The simulation study consisted of two parts: testing for triadic structure and testing for covariate effects. The two parts considered the behavior of test statistics for parameters that capture structural features of the data and the impact of covariates on digraph evolution. The study did not consider the impact of covariates on attributes or the co-evolution of attributes and network structure (although the score test has been applied in these circumstances, this simulation will focus on the impact of covariates).

Table 4.1: Simulation Statistics

Notation	**Mathematical Definition**	**Operational Definition**
$s_{i1}^{[\boldsymbol{X}]}(\boldsymbol{x})$	$\sum_{j=1}^{n} x_{ij}$	the number of arcs (density)
$s_{i2}^{[\boldsymbol{X}]}(\boldsymbol{x})$	$\sum_{j=1}^{n} x_{ij}x_{ji}$	the number of reciprocated arcs
$s_{i3}^{[\boldsymbol{X}]}(\boldsymbol{x})$	$\sum_{j,l=1}^{n} x_{ij}x_{jl}x_{il}$	the number of transitive triplets
$s_{i4}^{[\boldsymbol{X}]}(\boldsymbol{x})$	$\sum_{j,l=1}^{n}(1 - x_{ij})\text{max}_l x_{jl}x_{il}$	the number of indirect connections
$s_{i5}^{[\boldsymbol{X}]}(\boldsymbol{x}, \boldsymbol{c})$	$\sum_{j=1}^{n} x_{ij}c_{ij}$	interaction of arcs and dyadic covariate c_i
$s_{i6}^{[\boldsymbol{X}]}(\boldsymbol{x}, \boldsymbol{d})$	$\sum_{j=1}^{n} x_{ij}d_j$	interaction of arcs and node-bound covariate d

Assuming rate parameters are constant over time and one observed time point, t_0, the following two network observations, t_1 and t_2, were generated from a set of varying distributions, giving multiple sets of networks that can be used to determine the behavior of the two available goodness-of-fit measures. Using the first time point t_0 and the objective function of the null models, the behavior of the score test and Snijders' Pseudo-t-test were compared for t_1 and t_2. Using samples of $n = 30$ and $n = 60$ with 500 replications of each model, Schweinberger tested two separate groups of hypotheses. The first part of the simulation only considered the structural model. In the second part of the simulation study, a dyadic covariate was randomly generated by taking independent draws from a Poisson distribution with $\mu = 1$ and a node-bound covariate was randomly generated by taking independent draws from a Bernoulli distribution with $\pi = 1/2$. Using the first time point t_0, the generated dyadic and node-bound covariates, and the objective functions of the null models, the behavior of the score test and Snijders' Pseudo t-test were compared for t_1 and t_2. The statistics, $s_{ik}^{[\boldsymbol{X}]}(\boldsymbol{x}, j)$, chosen for both parts of the simulation are presented in Table 4.1. As a reminder, given a constant rate parameter (ρ_m for $m = 1$ and $m = 2$), the objective function is given by

$$f_i^{[\boldsymbol{X}]}(\boldsymbol{\beta}^{[\boldsymbol{X}]}, \boldsymbol{x}) = \sum_k \beta_k^{[\boldsymbol{X}]} s_{ik}^{[\boldsymbol{X}]}(\boldsymbol{x}, j).$$

Part 1 of the simulation evaluated the distributions of t-test and score test statistics for $H_0 : \beta_3 = 0$ and $H_0 : \beta_4 = 0$, and score tests for $H_0 : \beta_3 = \beta_4 = 0$. Using two different types of triadic structure - transitive triplets and number of actors at distance two (or number of indirect connections). Setting the rate parameters and the first two network parameters (number of arcs and reciprocated arcs) to constant values, the following vector of parameters was manipulated:

$$\boldsymbol{\theta} = (\rho_1, \rho_2, \beta_1, \beta_2, \beta_3, \beta_4)' = (4, 4, -1, 1, \beta_3, \beta_4)'.$$

To measure the strength and behavior of the test statistics, three levels of each effect were combined. The parameter β_3 had values 0, .2, and .4, and β_4 had values 0, -0.3, and -0.6. Pairwise combinations of these estimates provided nine total models, in a 3×3 factorial design of β_3 and β_4. Schweinberger chose the fixed parameter values based on his experience in fitting models as reasonable initial parameter estimates. The values chosen should not have an effect on the results, though in the proposed simulation study, these values were tested against other initial values.

Part 2 of the simulation evaluated the distributions of t-test and score test statistics for $H_0 : \beta_5 = 0$ and $H_0 : \beta_6 = 0$, and score tests for $H_0 : \beta_5 = \beta_6 = 0$. Setting the rate parameters and three network parameters to constant values, the following vector of parameters was manipulated:

$$\boldsymbol{\theta} = (\rho_1, \rho_2, \beta_1, \beta_2, \beta_3, \beta_5, \beta_6)' = (4, 4, -1, 1, 0.2, \beta_5, \beta_6)'.$$

The parameter β_5 had values 0, .1, and .2, and β_6 had values 0, 0.2, and 0.4. Pairwise combinations of these estimates equal nine total models.

Findings from the two parts of the simulation study support the use of the score test. The score test was shown to have an approximate chi-square distribution. Snijders' Pseudo-t-test appeared conservative, finding fewer significant parameter estimates than expected. The findings also confirm Snijders'

Pseudo-t-test as having a standard normal distribution, even for small sample sizes ($n = 30$). Although an additional simulation study is needed to evaluate performance of the score test for a co-evolution model, the results from Schweinberger's study indicate that the score test has great power and offers a promising tool for co-evolution modeling.

5 Proposed Measures of Goodness-of-fit

5.1 Entropy-based Goodness-of-fit Measure

With the complexities present in co-evolution network models, many measures of explained variation could be proposed to quantify reduction in uncertainty present. It is difficult enough to predict the tendency towards structure within a network without attempting to predict the specific behavior of individual ties or actors. By narrowing the focus to single actors making small changes between time periods, uncertainty can be better accounted for. As the number of actors becomes large, the co-evolution model becomes exponentially more complex. An entropy-based measure for explained variation offers an alternative to traditional goodness-of-fit measures. Borrowing from thermodynamics and information theory, this entropy measure captures how much order can be drawn from the disorder, or how much information can be gathered in the network model.

Entropy is a measure of the uncertainty associated with a random variable (Shannon, 1948). The entropy of a discrete random variable is equal to the expected value of the information of that random variable.

$$\text{Entropy} = H(Y) = -\sum_{i}^{n} p_i \log_2 p_i,$$

where p_i is the probability of actor i creating or dissolving a tie and n is the number of actors. The base of 2 was adopted from Shannon's (1948) equation for uncertainty, based on information theory where 2 refers to bits of information (i.e., 0 or 1). The maximum amount of entropy $\log_2(n)$ is found when all possible events are equally probable, such as with a uniform distribution.

To obtain a goodness-of-fit measure within the range of $(0, 1)$, the entropy measure may be transformed(Vasicek, 1976; Park & Park, 2003; Theil, 1980; Dudewicz & van der Meulen, 1981; Gokhale,1983). This goodness-of-fit measure relies on Jensen's inequality, that shows us

$$Entropy = H(\boldsymbol{Y}) = E\left[\log_2\left(\frac{1}{p_i(\boldsymbol{Y})}\right)\right] \leq \log_2\left[E\left(\frac{1}{p_i(\boldsymbol{Y})}\right)\right] = \log_2(n).$$

This simple measure divides the entropy by the maximum possible entropy to obtain a goodness-of-fit measure; that is,

$$E[R(t)] = 1 - \frac{H(p_i(y))}{\log_2(n)}.$$

This measure has a value of $R = 1$ when events are certain and a $R = 0$ when all events are equiprobable and there is the greatest uncertainty). The entropy goodness-of-fit is measured during the implementation of the Metropolis-Hastings algorithm part of the RSiena estimation process when the final parameter estimates are calculated. Basing this goodness-of-fit measure on an estimation technique that relies on the Metropolis-Hastings algorithm, lays the groundwork for a Bayesian goodness-of-fit measure. Because the Gibbs sampling of Bayesian estimation is a special case of the Metropolis-Hastings algorithm, the adaptation of this proposed entropy-based goodness-of-fit measure can be completed once more research has been completed on the Bayesian estimation technique.

This measure is not constant over time, depending on the rate parameter for each time period. Snijders suggested that an average of measures could be used (2004). Taking the average of this measure seems reasonable for networks where rate parameters are somewhat constant over time. For longitudinal networks with nonconstant rate parameters, this assumption may not make sense. For generality, rate is not assumed to be constant over time. If change does occur at a constant rate, the proposed entropy measure can simply be averaged over time. An entropy measure is reported for each time period, where time period is the difference between two consecutive observations. The entropy measure is an average measure of change within a time period. A separate entropy measure is reported for each time period. When the rate parameter is somewhat constant across time periods, this measure can be averaged to find an overall measure of model fit. For the purposes of this study, rate is not assumed to be constant across time periods. While the entropy measure is reported for each time period, the model should be fit over all available time periods. Modeling each time period separately will lead to degenerate solutions and the model will force important parameters out of the model.

5.2 Generalized R^2 Goodness-of-fit Measure

As an alternative to the entropy-based measure of goodness-of-fit, a generalized R^2 can be found for co-evolution models. The generalized R^2 is traditionally estimated with Maximum Likelihood techniques, where likelihood of the model of interest is bounded by $(0, 1)$ (Cameron & Windmeijer, 1997; Menard, 2000). This proposed goodness-of-fit measure is more appropriate within the Maximum Likelihood framework and with normal response variables. However, the relationship between method of moments and Maximum Likelihood estimation in co-evolution models must be better understood before goodness-of-fit measures can be compared across estimation techniques. The discussion section outlines recent work that explores a Maximum Likelihood estimation method for co-evolution models. This generalized R^2 measure cannot be implemented at this time. When the framework for Maximum Likelihood estimation is better understood, this goodness-of-fit measure should be compared using the intended estimation technique. This dissertation takes a cursory look at this measure, establishing a foundation for comparison in future research. Emphasis is placed on the three other proposed measures: the Pseudo-Wald test, the score test, and the entropy-based goodness-of-fit measure.

The proposed R^2 measure has several appealing characteristics. The generalized R^2 is bounded by $(0, 1)$, should be asymptotically independent of the number of actors, can be interpreted as the proportion of variation explained by the model, is scale-free, and can be maximized using a Maximum Likelihood estimation of the co-evolution model. No additional computation time will be required; All components are gathered during the estimation process. The saturated model is not needed, only an intercept only model and the hypothesized model. Because this measure compares the hypothesized model to the intercept only model, testing for inclusion of effects in a model similar to the other measures described earlier should be based on the difference among two R^2 measures. Thus, this goodness-of-fit measure is a simple calculation using existing statistical results.

The generalized R^2 is defined as

$$R^2 = \frac{1 - \left(\frac{L(0)}{L\left(\widehat{\boldsymbol{\theta}}\right)}\right)^{\frac{2}{n}}}{(1 - L(0))^{\frac{2}{n}}}$$

where $L(0)$ is the likelihood of the model that only contains the intercept (density), $L(\widehat{\boldsymbol{\theta}})$ is the likelihood of the hypothesized estimated model, and n is the number of actors.

6 Simulation Study

6.1 Application

The estimation process applied was originally implemented in the SIENA program, part of the StOCNET package. Recently, an R package has been written that allows for a similar procedure. In this simulation, an early version of this R package was adapted to work from.

The RSiena package (Ripley & Snijders, 2009) provides the basis for the estimation procedures used in this document. The simulation study and development of additional fit measures was completed using altered commands from the RSiena package. Because RSiena is still in development, the general programming will be adapted to include the proposed goodness-of-fit measures. Several important features were missing that necessitated additional programming.

6.2 Simulation Study Outline

The following simulation compares the behavior of Snijders' Pseudo t-test, the proposed Pseudo-Wald statistic for multivariate tests, Schweinberger's score test, and the entropy-based measure. By comparing sensitivity and power, the strengths and weaknesses of each measure can be investigated. Two types of models are considered, a simulation study using a structural model and a simulation study using a co-evolution model, with attributes following two distributions. A general outline of the proposed simulation study extends and supports the previous study by Schweinberger (2007) in his evaluation of the score test for network evolution.

Table 6.1: Statistics Included in Structural Model for Simulation

Operational Definition	**Mathematical Definition**	**Tested/Included**
Density	$\sum_{j=1}^{n} x_{ij}$	included
Reciprocity	$\sum_{j=1}^{n} x_{ij}x_{ji}$	tested
Transitive Triplets	$\sum_{j,h=1}^{n} x_{ij}x_{jh}x_{ih}$	tested
3-cycles	$\sum_{j,h=1}^{n} x_{ij}x_{jh}x_{hi}$	tested
Transitive Ties	$\sum_{h=1}^{n} x_{ih} \max_j(x_{ij}x_{jh})$	tested

Table 6.2: Statistics Included in Co-evolution Model for Simulation

Operational Definition	**Mathematical Definition**	**Tested/Included**
Outdegree-Popularity (Sq Root)	$\sum_{j=1}^{n} x_{ij}\sqrt{x_{j+}}$	tested
Attribute Alter	$\sum_j x_{ij}z_j$	tested
Attribute Ego	$\sum_j x_{ij}z_i = z_i x_{i+}$	tested
Same Attribute	$\sum_j x_{ij}I\{z_i = z_j\}$ where $I\{z_i = z_j\} = 1$ if $z_i = z_j$ and 0 otherwise	tested
Linear Shape	z_i	included
Attribute Average Similarity	$x_{i+}^{-1}\sum_{j=1}^{n} x_{ij}(\mathrm{sim}_{ij}^{z}) - \widehat{\mathrm{sim}_{ij}^{z}})$	tested

1. Randomly generate three 200 by 200 adjacency matrices that have model convergence, some significant structural parameter estimates, and — along with the randomly generated attribute matrix — some significant co-evolution parameter estimates. Parameters of interest for the structural model included structural rate parameters and the parameters listed in Table (6.1). Parameters of interest for the co-evolution model included all parameters from the structural model, attribute rate parameters, and the parameters listed in Table (6.2).

2. Randomly generate a 200 by 3 matrix of attribute levels for actors based on a bernoulli distribution. This matrix had to be manipulated some to allow for significant co-evolution parameter estimates. The attribute levels were randomly generated from a bernoulli ($\pi = 0.3$) distribution for the first time point, a bernoulli ($\pi = 0.4$) distribution for the second time point, and a bernoulli ($\pi = 0.5$) distribution for the third time point.

To ensure significant attribute parameter estimates, the attribute levels within an actor were rearranged to loosely reflect the actor's network activity, measured by outdegree. Without this crucial reordering, none of the parameters emerged as significant when the solution did converge, nor would one expect them to. For example, multiple actors with attribute levels $0, 1, 0$ or $1, 0, 1$ resulted in models that would not converge. For actors with relatively high outdegree over time, attribute levels across time were rearranged to be constant or increasing. For actors with relatively low outdegree over time, levels were rearranged to be constant or decreasing.

3. Randomly generate a 200 by 3 matrix of attribute levels for actors based on a normal distribution ($\mu = 3, \sigma = 1$), to avoid negative attribute levels. Negative attribute levels are not allowed due to how attributes are standardized within the estimation routine. To ensure significant attribute parameter estimates, the attribute levels within an actor were rearranged to reflect the actor's outdegree.

4. Choose a sample of the largest (200 by 200) network and attribute levels for the smaller networks of size 25, 50, and 100. All samples needed to meet the criteria set for the largest network and attribute files (convergence, some significant structural and co-evolution parameter estimates). With the difficulty involved with generating the 200 by 200 network that fit all the criteria and with the relative stability seen in preliminary results, larger networks were not considered.

5. For each number of actors included (25, 50, 100, and 200), 1000 models were simulated for the structural model, 1000 models for the co-evolution model with bernoulli generated attribute levels, and 1000 models for the co-evolution model with normal generated attribute levels.[1]

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[1] To gain some efficiency in estimation and capturing results, the simulation first ran for the score test statistic and then for the entropy and Pseudo-Wald test statistics. The score test statistic models ran quicker because of the restricted parameters but takes much longer to gather results. The programming of the score test does not allow for directly obtaining score test statistics, so the resulting output for each model run must be manually gathered from an output text file. Both one-sided and two-sided score test statistics are provided for each parameter, along with an overall joint score test (see Appendix A). Score test output provides both a two-sided and one-sided test for each parameter estimate. The one-sided test statistic is distributed standard normal. Squaring the one-sided test statistic produces the two-sided test statistic, distributed chi squared. The focus of this analysis is on the one-sided test because of the additional information provided on the sign of the statistic.

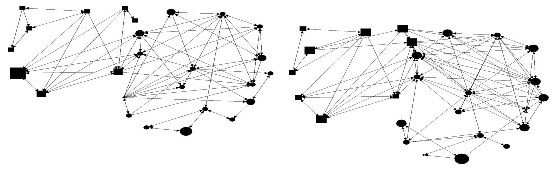
6.3 Andrea Knecht's Friendship Data

To validate simulation results using observed data, a dataset with multiple time points was selected. This dataset is publicly available and was investigated following the simulation to confirm findings on previously collected data.

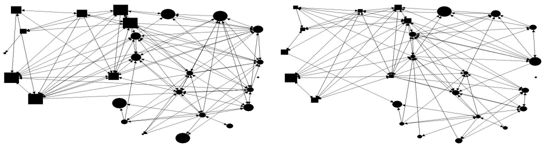
Knecht (2008) collected data on the co-evolution of friendship ties and other attributes among 26 secondary school students. The data were collected at four time points between September 2003 and June 2004. The four time points were three months apart during the students' first year in secondary school. Several attributes (both endogenous and exogenous) were concurrently collected. Attributes included gender, delinquency, alcohol use, age, ethnicity, religion, and attending the same primary school, the first two that are highlighted in this paper.

The observed network captured responses to the question *"Who are your best friends in class?"*. This question was transformed into an adjacency matrix where the 26×26 matrix reports the relation of strong friendship. For a delinquency measure, the researchers asked for frequency (using the categories "never", "once", "two to four times", "five to ten times" and "more than 10 times") of stealing, vandalism, graffiti, and fighting in the last three months. A delinquency scale was created by averaging the four items, with values ranging from 1 (no delinquency) to 5 (very high level of delinquency). Out of the 26 students in the observed classroom, 17 were female and 9 were male. One student left the classroom midway through the year, resulting in structural zeros for the tie strength between this student and all others following her departure.

The four diagrams in Figure 6.1 show how the friendship network and delinquency measure change over the four observed time points. The shape of the nodes reflects the gender of the student (males are squares, females are circles) and the size of the nodes reflects the students' delinquency measure, where larger nodes have higher self-reported delinquency. Table 6.1 contains the parameters tested for inclusion.



(a) Time 1 (b) Time 2



(c) Time 3 (d) Time 4

Figure 6.1: Knecht's Friendship Data

Table 6.3: Statistics Included in Structural and Co-evolution Models for Knecht Data

Parameter	**Network Statistic**
Density (or out-degree)	$x_{i+} = \sum_j x_{ij}$
Reciprocity	$\sum_j x_{ij}x_{ji}$
Transitive Triplets	$\sum_{j,h} x_{ij}x_{ih}x_{jh}$
Number of 3-cycles	$\sum_{j,h} x_{ij}x_{jh}x_{hi}$
Transitive Ties	$\sum_h x_{ih}\text{max}_j(x_{ij}x_{jh}$
Out-degree Popularity (Square Root)	$\sum_i x_{ij}\sqrt{x_{j+}}$
Gender Alter	$\sum_j x_{ij}z_j^*$
Gender Ego	$\sum_j x_{ij}z_i^* = z_i^* x_{i+}$
Same Gender	$\sum_j x_{ij}I\{z_i^* = z_j^*\}$
	where $I\{z_i^* = z_j^*\} = 1$ if $z_i^* = z_j^*$ and 0 otherwise
Similarity on Delinquency	$\sum_j x_{ij}(\text{sim}_{ij} - \overline{\text{sim}})$
Delinquency Linear Shape	z_i
Delinquency Quadratic Shape	z_i^2
Average Similarity on Delinquency	$x_{i+}^{-1}\sum_{j=1}^{n} x_{ij}(\text{sim}_{ij}^z) - \widehat{\text{sim}_{ij}^z})$

7 Simulation Results

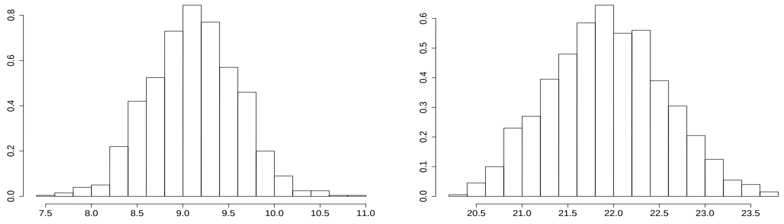
This chapter presents the results from the simulation study. The estimates associated with parameters were allowed to vary with each model and supplemental results are included in Appendices B, C, and D.

7.1 Pseudo-Wald Test for Effect Inclusion

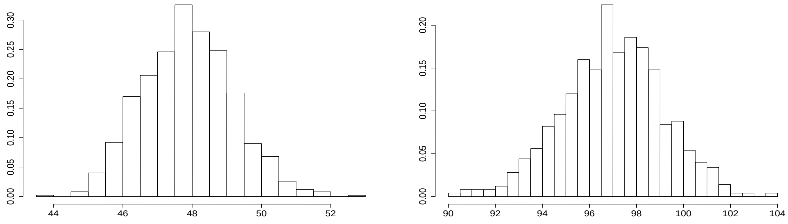
t-tests are included in the following results sections, along with a subset of available Pseudo-Wald test statistics. A complete set of Wald statistics for all possible combinations of parameters was calculated, but a limited number were chosen for inclusion in the following chapters. All model runs included in this analysis had a t-value for convergence less than 0.2 for all non-fixed parameters. Model runs with poor convergence were ignored in this study, though most of these model runs were from networks with a larger number of actors. The important highlights of this section are to understand the shape of the distribution of each parameter t-test and the Wald tests and the direction of the parameter. Significant versus nonsignificant results and the magnitude of scale are worth noting, but are of secondary importance because of the dependence on the data. The shape of distributions should be consistent across different input data and the direction of the parameter estimate should be consistent within models that have the same input data and included parameters.

7.1.1 Structural Model Results

The reciprocity t-test in Figure 7.1 displays consistent behavior for models with 25 and more actors. All reported t-test values are large,



(a) n=25 (b) n=50

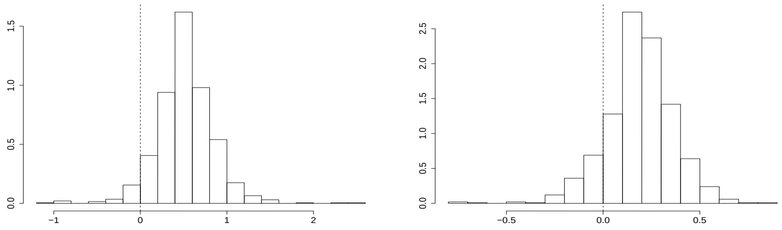


(c) n=100 (d) n=200

Figure 7.1: Structural Model Pseudo-Wald - Reciprocity t-Test

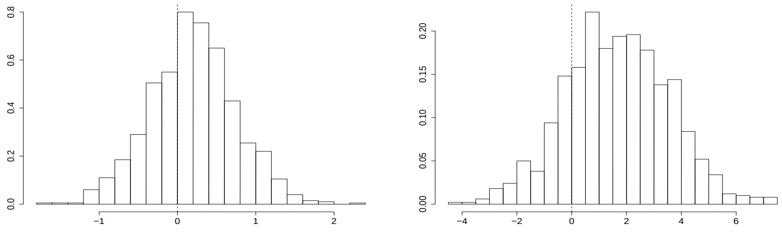
and significantly greater than zero. The reciprocity t-test displays an approximately normal distribution when modeling each number of actors. The values for all t-test statistics are positive, showing that the simulated data display consistent reciprocity behavior, though of differing magnitude, where the size of the t-test increases as the number of actors increases.

The transitive triplet t-test in Figure 7.2 displays similar distributional shape as the reciprocity t-test in Figure 7.1. The transitive triplet t-test does not provide consistent significant values. The most interesting behavior in the transitive triplet t-test distribution is the number of negative t-tests reported. Most t-test values are reported as positive, with a small subset having negative values. This behavior shows that on a number of model runs, the transitive triplet parameter may be reported with the opposite direction than is typically seen. The number of negative t-values reported depends on the number of actors included in the model. Models with 25 and 50 actors had fewer negative transitive triplet t-values reported than models with 100 and 200 actors. While there were relatively few model runs that had negative values, the presence of any negative values reiterates the importance of running models multiple times when



(a) n=25

(b) n=50



(c) n=100

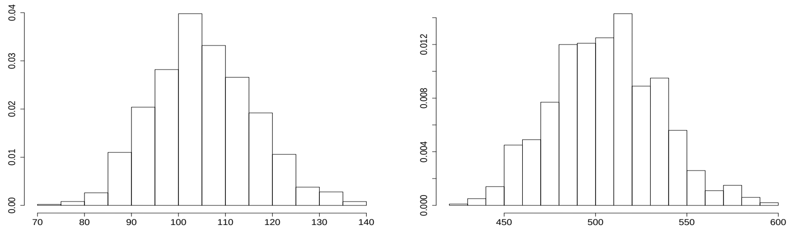
(d) n=200

Figure 7.2: Structural Model Pseudo-Wald - Transitive Triplets t-Test

building a either network or co-evolution model.

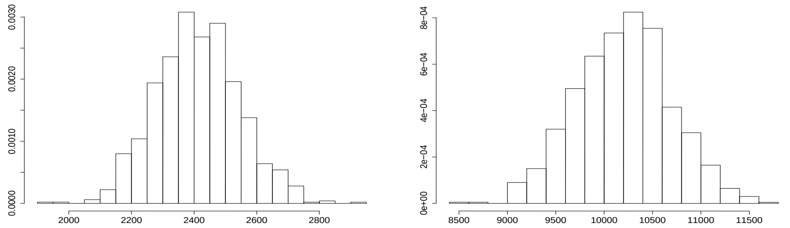
The Pseudo-Wald statistic in Figure 7.3 includes information on all effects tested in the structural model. The normal shape of the distributions confirm that all parameter estimates are consistent and close to one another. All reported Pseudo-Wald values are positive and significant when compared to the critical χ^2 value of 9.49 for four degrees of freedom, calculated by the number of variables included in the test. In this statistic, models appear to have a normal, significant distribution regardless of the number of actors included in the model. By testing the reciprocity, transitive triplets, 3-cycles, and transitive ties parameters concurrently, this Wald test provides evidence that the parameters are statistically different than zero and the effects should be included in the model. The Q-Q plots for this Pseudo-Wald statistic are included in Figure 7.4.

The scale of the reported Pseudo-Wald measures is one cause of concern. As the sample sizes increases, the covariances of parameter estimates become small, resulting in increasingly large Pseudo-Wald test statistics. This behavior is displayed throughout most reported Pseudo-Wald tests. Pseudo-Wald statistics for inclusion of the same parameter values increase



(a) n=25

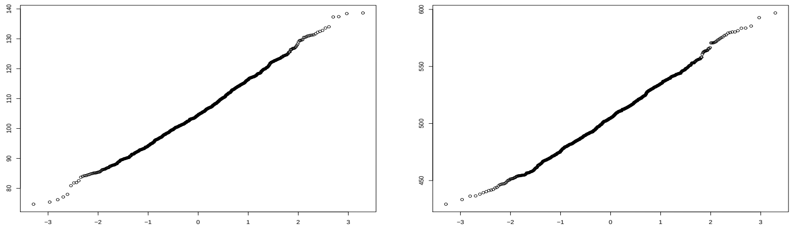
(b) n=50



(c) n=100

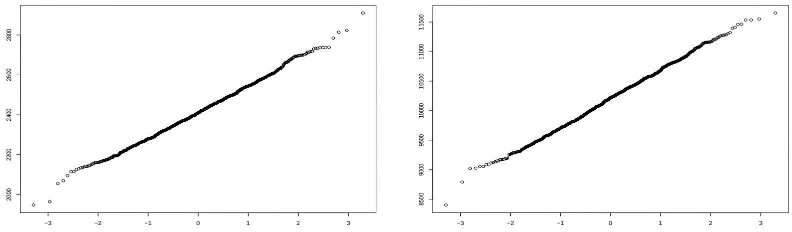
(d) n=200

Figure 7.3: Structural Model Pseudo-Wald - Reciprocity, Transitive Triplets, 3-Cycles, and Transitive Ties



(a) n=25

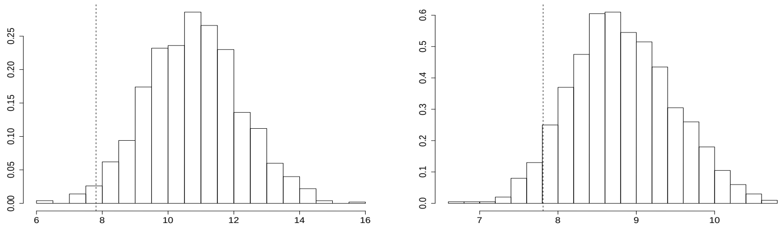
(b) n=50



(c) n=100

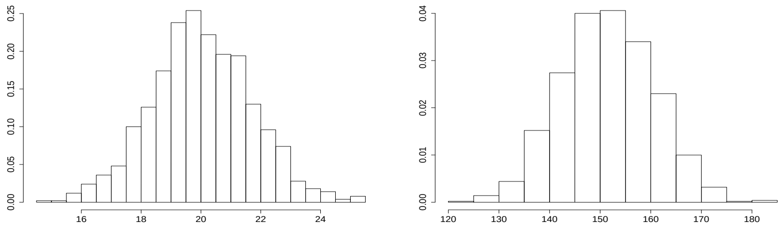
(d) n=200

Figure 7.4: Structural Model Pseudo-Wald - Q-Q plots for Reciprocity, Transitive Triplets, 3-Cycles, and Transitive Ties



(a) n=25

(b) n=50



(c) n=100

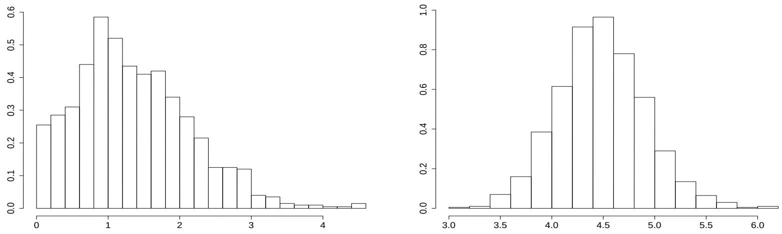
(d) n=200

Figure 7.5: Structural Model Pseudo-Wald - Transitive Triplets, 3-Cycles, and Transitive Ties

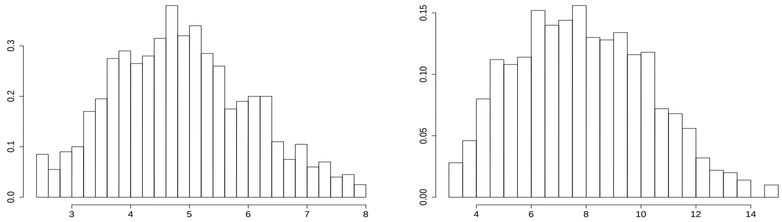
as the sample size increases. The degrees of freedom used in calculating p-values for individual tests controls for only a small part of this relationship.

The Pseudo-Wald statistic in Figure 7.5 tests the transitive triplets, 3-cycles, and transitive ties parameters. When comparing the test statistics in figures 7.3 and 7.5, the inclusion of the reciprocity parameter appears to significantly increase the value of the Pseudo-Wald statistic, seen in the range of reported values at each network size. The scale of the Wald test in Figure 7.3 is much larger (for example, when $n = 25$, the median value is around 105 compared with the median value of around 11 in Figure 7.5) and has an additional degree of freedom. This large increase in magnitude provides evidence of the importance of reciprocity in the model.

The Pseudo-Wald test for 3-cycles and transitive ties also continues the pattern of distributional shape. For illustrative purposes, Figure 7.7 provides the distribution of p-values for the Wald test for 3-cycles and transitive ties in Figure 7.6. Figure 7.8 provides the Q-Q plots for this Wald test. Only models with $n = 200$ display findings consistent with a significant test, though there is a number of reported tests reported as non-



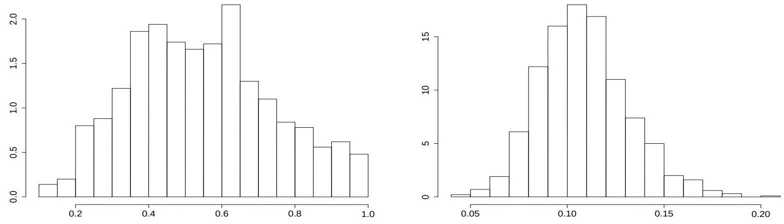
(a) n=25 (b) n=50



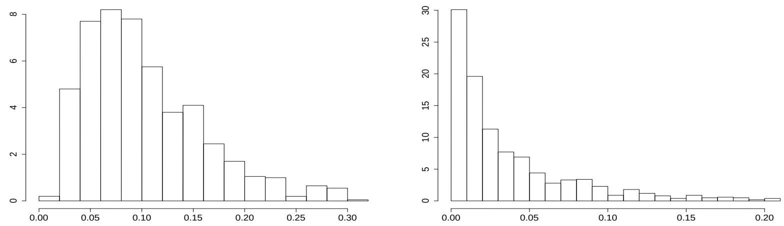
(c) n=100 (d) n=200

Figure 7.6: Structural Model Pseudo-Wald - 3-Cycles and Transitive Ties

significant. The shape of the distribution both for parameter estimates and the associated p-values follow the expected pattern. Additional Pseudo-Wald tests that display similar patterns are included in Appendix C.

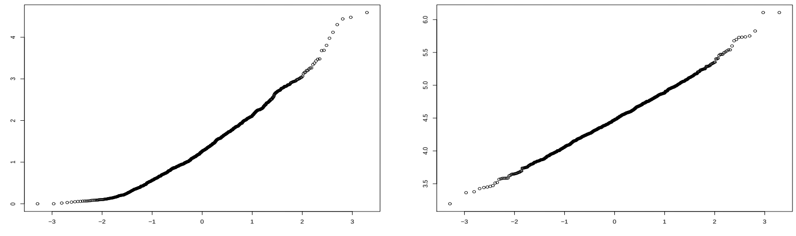


(a) n=25 (b) n=50

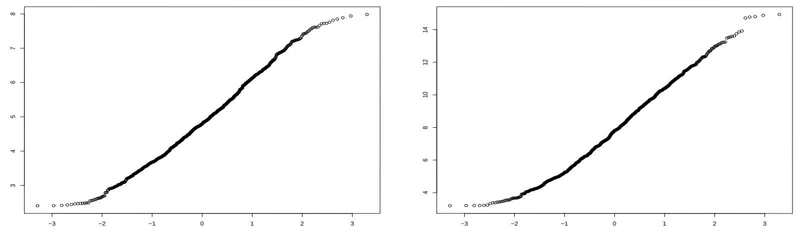


(c) n=100 (d) n=200

Figure 7.7: Structural Model Pseudo-Wald - 3-Cycles and Transitive Ties p-values



(a) n=25 (b) n=50

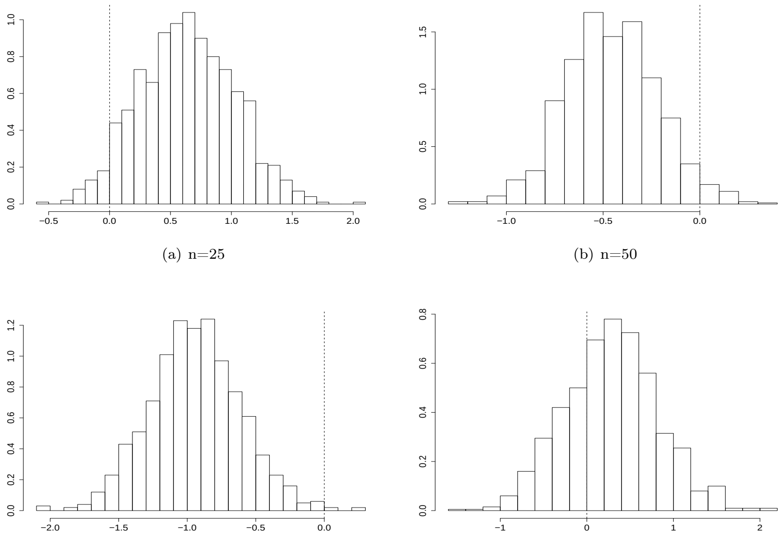


(c) n=100 (d) n=200

Figure 7.8: Structural Model Pseudo-Wald - Q-Q plots for 3-Cycles and Transitive Ties

7.1.2 Co-evolution Model With Bernoulli Attribute Results

The following two figures, Figure 7.9 and 7.10, provide examples of the t-test distributions for parameters in the co-evolution model with a bernoulli distributed attribute. Additional t-test distributions are included in Appendix C. The structural model is assumed as the baseline model, along with the attribute rate parameters for each time period and a linear shape parameter, considered an intercept term for the attribute.



(a) n=25

(b) n=50

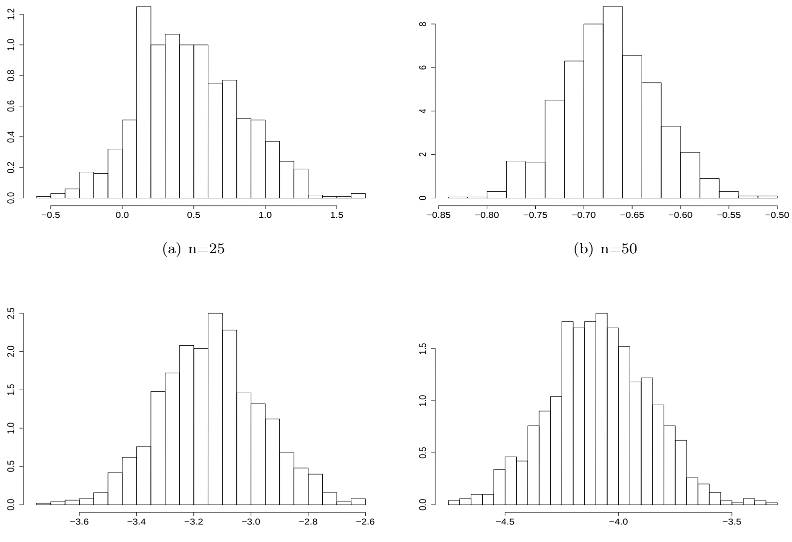
(c) n=100

(d) n=200

Figure 7.9: Co-evolution Model With Bernoulli Attribute Pseudo-Wald - Outdegree-Popularity (Square Root) t-Test

The outdegree-popularity (square root) t-tests in Figure 7.9 signal that model size seems to play a part in the direction of the parameter. For each network size, there are a number of model runs that produced contradictory evidence about the direction of the parameter. For models with varying number of actors, a number of model runs result in parameter estimates with the opposite direction. The shape of the distribution approximates normal as the number of actors increases.

The attribute ego t-test distribution in Figure 7.10 shows non-significant positive values for models with 25 actors, and non-significant negative



(a) n=25

(b) n=50

(c) n=100

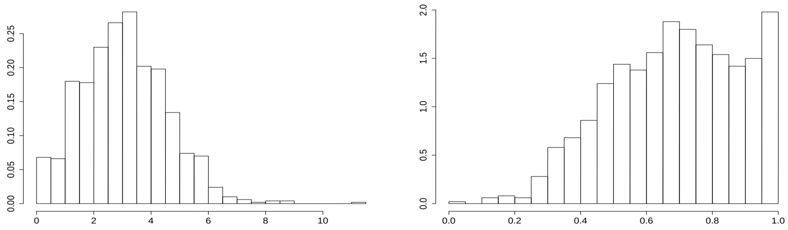
(d) n=200

Figure 7.10: Co-evolution Model With Bernoulli Attribute Pseudo-Wald - Attribute Ego t-Test

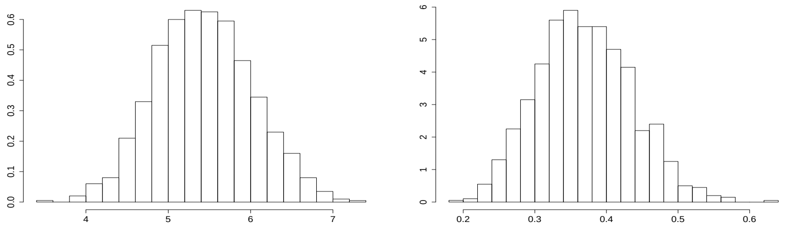
values for models with 50 actors. Models with 100 or more actors have significant negative parameter estimates. The shape of the t-test distribution for models with 25 actors shows some model runs that display the a non-significant negative effect, despite a similar pattern among standard error estimates.

The Pseudo-Wald test statistic for all parameters available to be tested in Figure 7.11 shows results consistent with previous patterns in reported Pseudo-Wald values. The models with 50 or less actors have high p-values corresponding to non-significant Wald statistics. The models with 100 or more actors have low p-values, exceeding the threshold for significance. Based on p-values less than 0.05, models with more actors support including more effects. The distribution of the Wald test statistic that includes all tested co-evolution parameters has more degrees of freedom that any subsequently reported test. The behavior of this overall Wald test confirms that the Wald test statistic statistic behaves as expected.

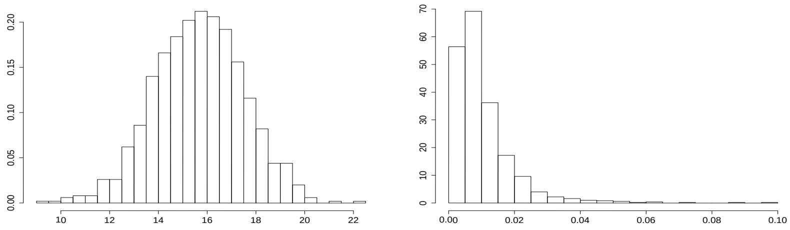
The Pseudo-Wald test statistic for a joint test in Figure 7.12 for attribute alter, attribute ego, attribute same, and average similarity parameters provides conflicting information about inclusion depending on the



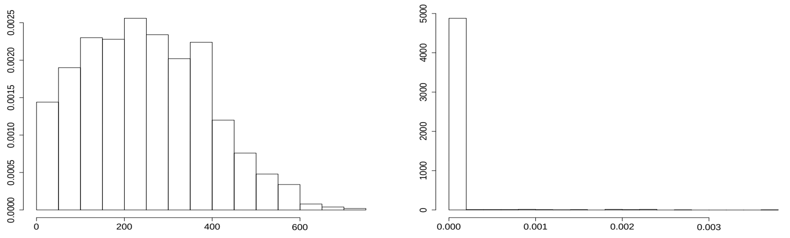
(a) Pseudo-Wald Test Statistic n=25 (b) Pseudo-Wald P-value n=25



(c) Pseudo-Wald Test Statistic n=50 (d) Pseudo-Wald P-value n=50

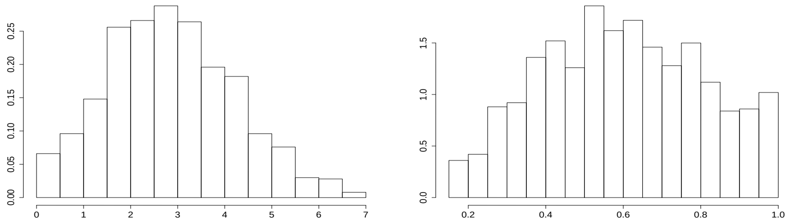


(e) Pseudo-Wald Test Statistic n=100 (f) Pseudo-Wald P-value n=100



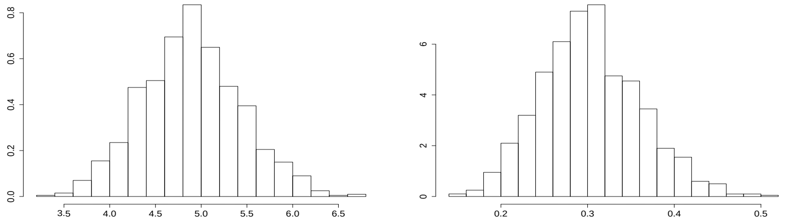
(g) Pseudo-Wald Test Statistic n=200 (h) Pseudo-Wald P-value n=200

Figure 7.11: Co-evolution Model With Bernoulli Attribute - Pseudo-Wald for Outdegree-Popularity (Square Root), Attribute Alter, Attribute Ego, Attribute Same, and Average Similarity



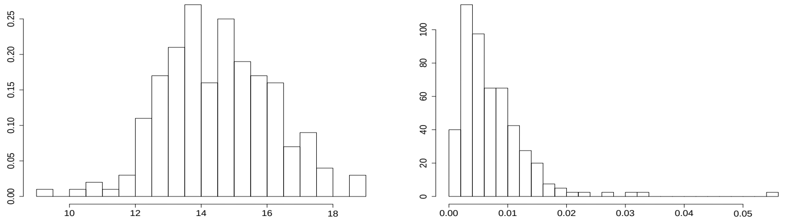
(a) Pseudo-Wald Test Statistic n=25

(b) Pseudo-Wald P-value n=25



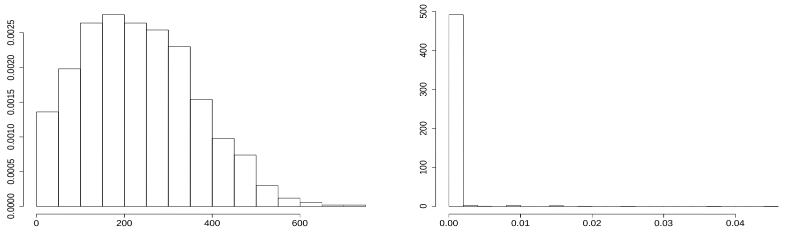
(c) Pseudo-Wald Test Statistic n=50

(d) Pseudo-Wald P-value n=50



(e) Pseudo-Wald Test Statistic n=100

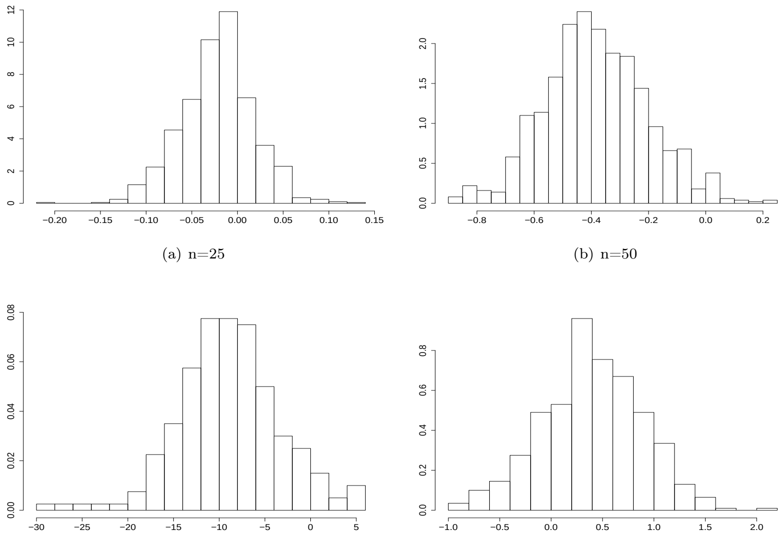
(f) Pseudo-Wald P-value n=100



(g) Pseudo-Wald Test Statistic n=200

(h) Pseudo-Wald P-value n=200

Figure 7.12: Co-evolution Model With Bernoulli Attribute - Pseudo-Wald for Attribute Alter, Attribute Ego, Attribute Same, and Average Similarity



(a) n=25

(b) n=50

(c) n=100

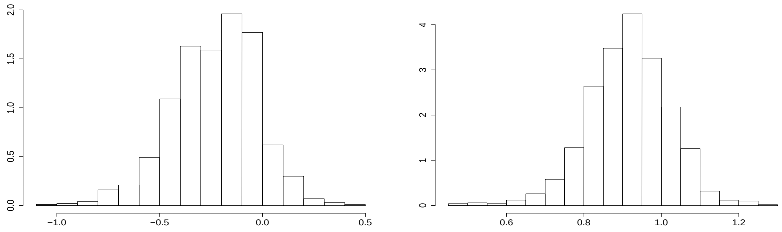
(d) n=200

Figure 7.13: Co-evolution Model With Normal Attribute Pseudo-Wald - Outdegree-Popularity (Square Root) t-Test

size of the network. Smaller networks ($n = 25$ and 50) have nonsignificant Wald test statistics, while larger networks ($n = 100$ and 200) reported significant Wald test statistics. The distribution of the Wald test follows the pattern seen when including other parameters. Additional Pseudo-Wald tests are included in Appendix C that show similar distributional patterns.

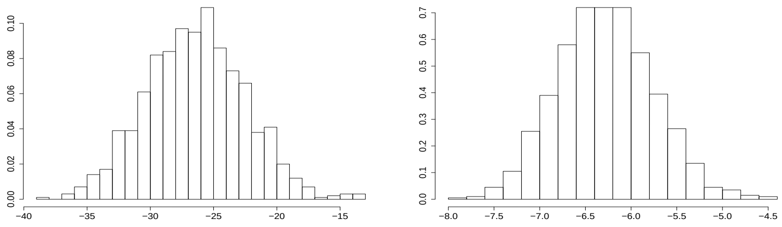
7.1.3 Co-evolution Model With Normal ($\mu = 3, \sigma = 1$) Attribute Results

This section presents the results of the simulation study that looked at the Pseudo-Wald test statistics for a co-evolution model using an matrix of attribute values that was generated from a normal ($\mu = 3, \sigma = 1$) distribution. The same parameters are tested with the normal attribute that were tested with a bernoulli attribute. Pseudo-Wald distributions that follow the same pattern across different attributes may be less sensitive and more immune to attribute change. This may mean that the test is less likely to detect attribute changes.



(a) n=25

(b) n=50



(c) n=100

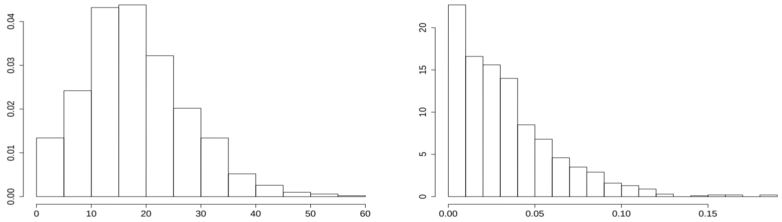
(d) n=200

Figure 7.14: Co-evolution Model With Normal Attribute Pseudo-Wald - Attribute Ego t-Test

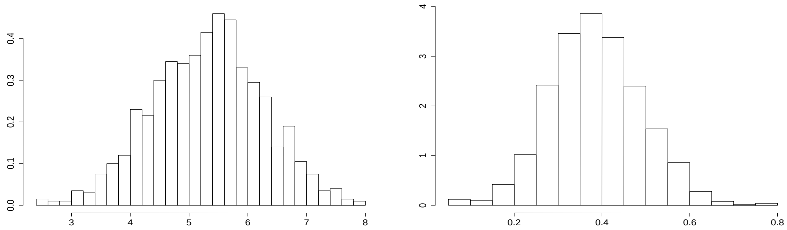
The distribution of the t-test statistic values for the outdegree-popularity (square root) parameter in Figure 7.13 has an expected pattern. The parameter estimates, and respective t-test estimates, provide different information on the direction of the estimate. Each of the different sized models displays a similar behavior. This finding was also seen in the co-evolution models with a bernoulli attribute. A t-test distribution that covers both positive and negative values shows that the results from model runs provide contradictory information.

The distribution of the attribute ego t-test in Figure 7.14 closely approximates a normal distribution, especially as the number of actors increases. An obvious similarity between the t-test distribution for a normal attribute and a bernoulli attribute exists across network sizes. Each network with more than 25 actors results in t-test values that do not span between negative and positive values, a good indication that consecutive model runs will result in consistent results. As the number of actors increases, less contradictory evidence is provided. Additional t-test and Pseudo-Wald distributions are included in Appendix C.

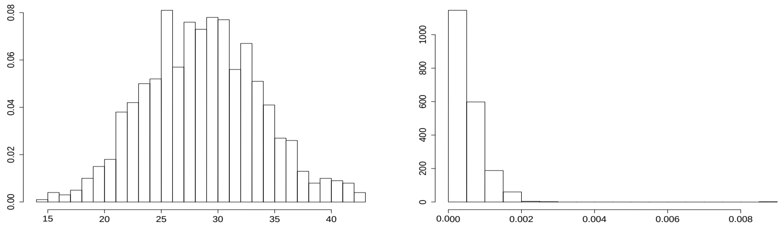
The distribution of the Pseudo-Wald test statistic that includes all



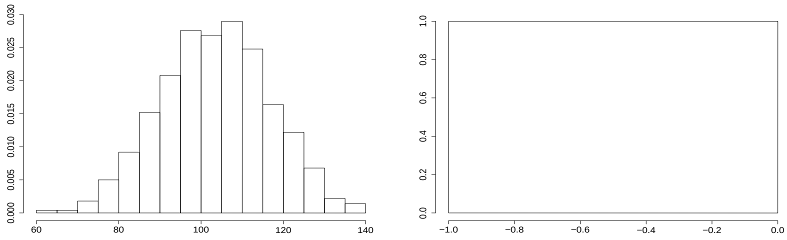
(a) Pseudo-Wald Test Statistic n=25 (b) Pseudo-Wald P-value n=25



(c) Pseudo-Wald Test Statistic n=50 (d) Pseudo-Wald P-value n=50



(e) Pseudo-Wald Test Statistic n=100 (f) Pseudo-Wald P-value n=100



(g) Pseudo-Wald Test Statistic n=200 (h) Pseudo-Wald P-value n=200

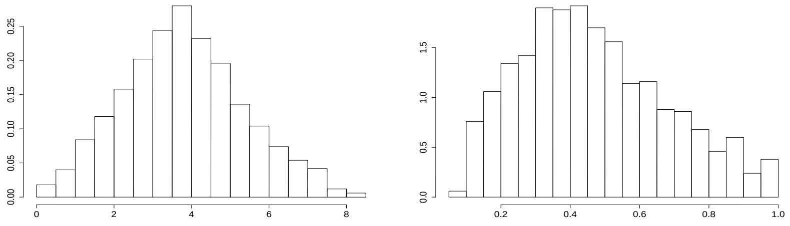
Figure 7.15: Co-evolution Model With Normal Attribute - Pseudo-Wald for Outdegree-Popularity (Square Root), Attribute Alter, Attribute Ego, Attribute Same, and Average Similarity

available parameters in Figure 7.15 displays the expected approximately normal shape. The significance of the Wald test varies between models with different numbers of actors, but the overall shape of the distribution describes the expected behavior. The possibility of a floor effect is apparent when $n = 25$ in this and subsequent Pseudo-Wald test figures. When the model uses data on 25 actors to model behavior, the Wald test seems to have a number of values that are very low, almost at the minimum. When this happens, the shape of the distribution appears to be exponential, but the shape is forced due to the restriction on possible values at the low end.

Figure 7.16 shows the distribution for the Pseudo-Wald test for attribute alter, attribute ego, attribute same, and average similarity that follows a similar pattern of shape across models of increasing size. Models with more actors have a normal shape to the distribution of values, with the shape becoming more normal as the number of actors increases. As the number of actors increases, the Pseudo-Wald test has more significant model runs.

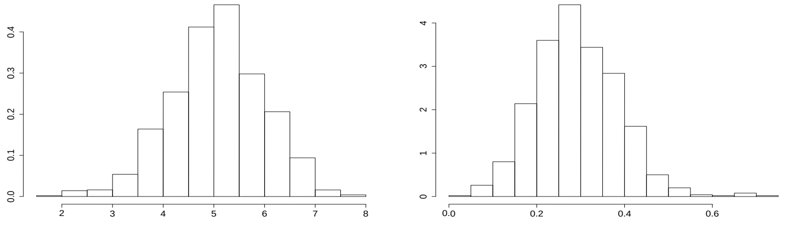
7.2 Score Test for Effect Inclusion

Critical values for score tests vary depending on the available degrees of freedom. Joint score test for structural models have four degrees of freedom, equivalent to a critical χ^2 value of 9.49. Co-evolution models have five degrees of freedom and a critical χ^2 value of 11.07. Score tests for individual parameters have one degree of freedom and critical χ^2 value of 3.84 for two-sided score tests. Transforming from a one-sided test to a two-sided test can be accomplished by squaring the one-sided value. The results provided focus on one-sided score test results for individual parameters. These one-sided values follow a standard normal distribution and have a critical z value of ± 1.96. The one-sided value provides additional information on the direction of the parameter estimates.



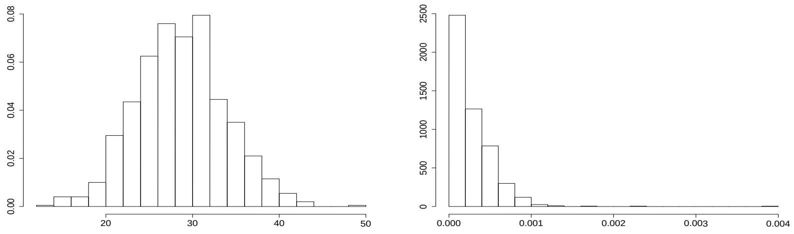
(a) Pseudo-Wald Test Statistic n=25

(b) Pseudo-Wald P-value n=25



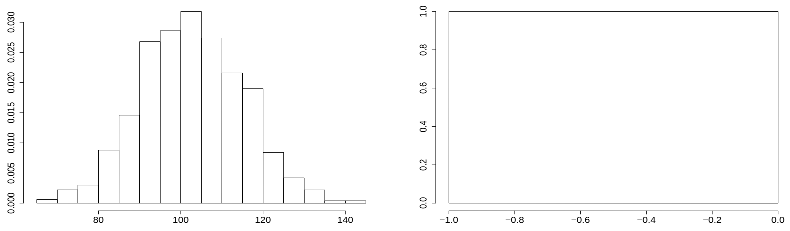
(c) Pseudo-Wald Test Statistic n=50

(d) Pseudo-Wald P-value n=50



(e) Pseudo-Wald Test Statistic n=100

(f) Pseudo-Wald P-value n=100



(g) Pseudo-Wald Test Statistic n=200

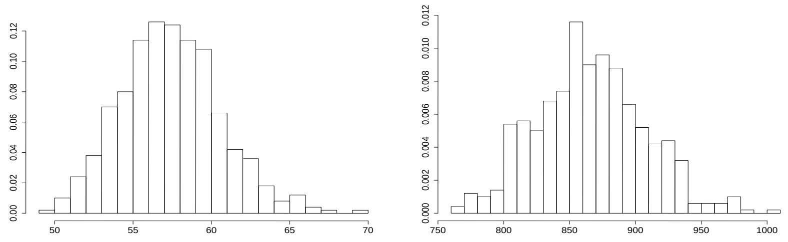
(h) Pseudo-Wald P-value n=200

Figure 7.16: Co-evolution Model With Normal Attribute - Pseudo-Wald for Attribute Alter, Attribute Ego, Attribute Same, and Average Similarity

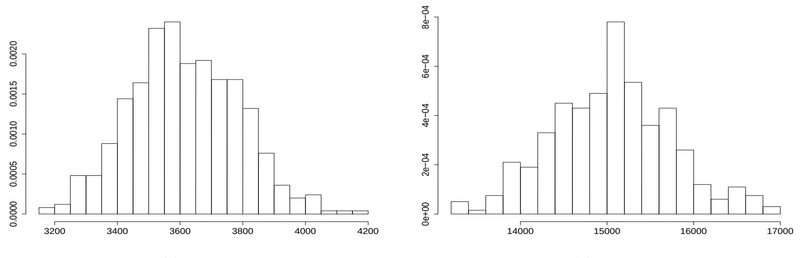
7.2.1 Structural Model Results

Score test results support the theory presented in Schweinberger (2007) for network evolution models. The score test statistics are distributed approximately normal, signaling that the statistic is consistent and reliable across model runs for a structural model. These results support the simulation study summarized in Schweinberger (2007), and support the use of this statistic in models with structural components, not explored in Schweinberger's model. This section with structural model results is included to display the consistency of findings with previous work. The extension of the score test to include attributes does not apply to the structural model, but does provide the basis for comparison later.

Joint score tests were calculated (in Figure 7.17) that include the reciprocity, transitive triplets, 3-cycles, and transitive ties parameters (also all individually tested). All of the individually tested parameters show a nicely behaved normal distribution, with minimal skewness. All parameter estimates have consistent direction within models with a specified number of actors.

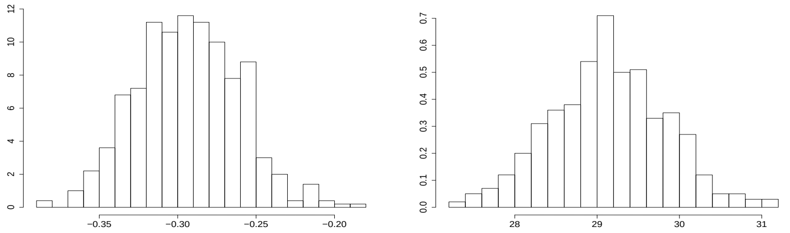


(a) n=25 (b) n=50

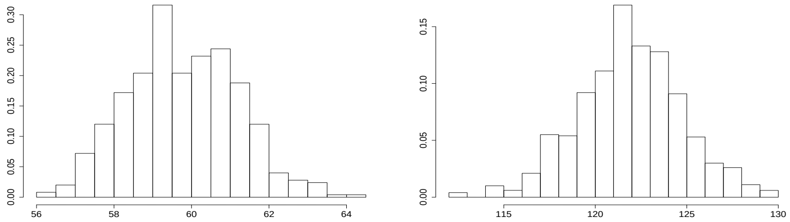


(c) n=100 (d) n=200

Figure 7.17: Structural Model - Joint Score Test

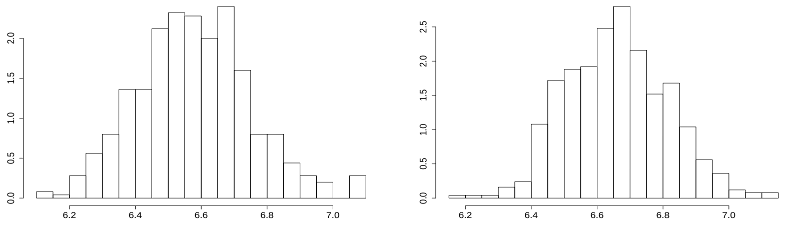


(a) n=25 (b) n=50

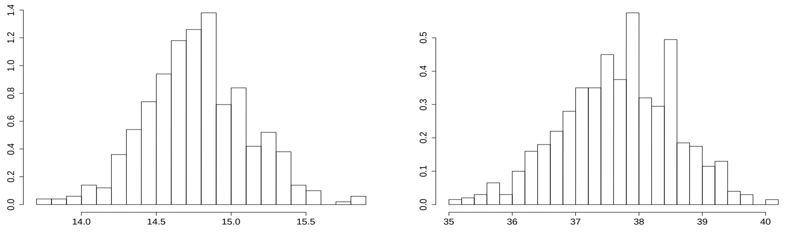


(c) n=100 (d) n=200

Figure 7.18: Structural Model - Reciprocity Score Test - one sided

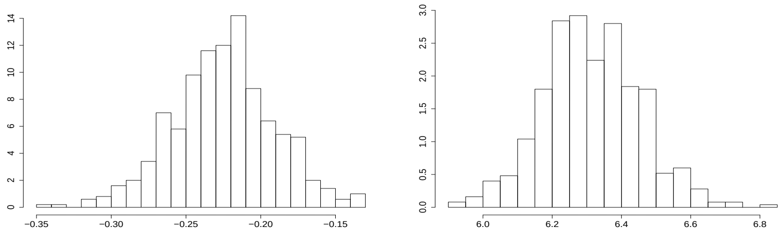


(a) n=25 (b) n=50

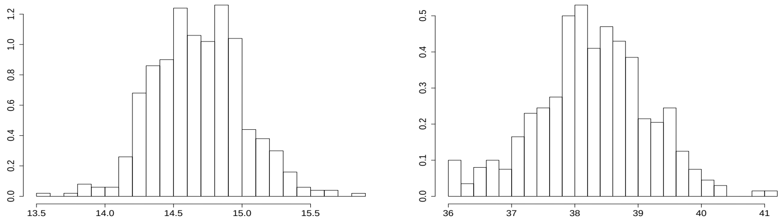


(c) n=100 (d) n=200

Figure 7.19: Structural Model - Transitive Triplet Score Test - one sided

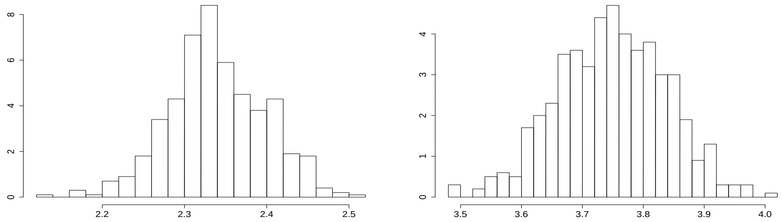


(a) n=25 (b) n=50

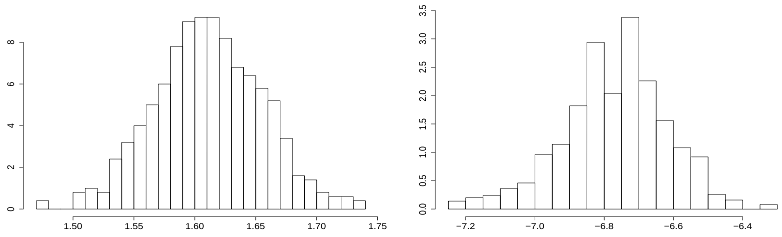


(c) n=100 (d) n=200

Figure 7.20: Structural Model - 3-cycles Score Test - one sided



(a) n=25 (b) n=50



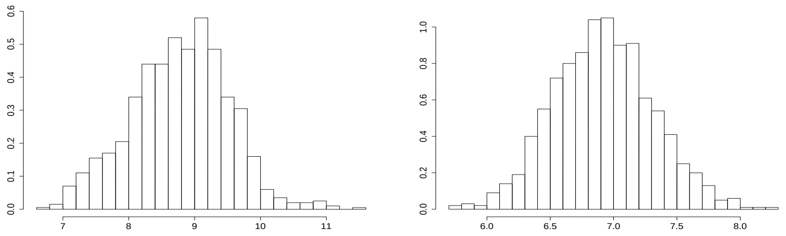
(c) n=100 (d) n=200

Figure 7.21: Structural Model - Transitive Ties Score Test - one sided

7.2.2 Co-evolution Model With Bernoulli Attribute Results

Score test results support the theory presented in Section 4.2 of this paper. The score test statistics are distributed approximately normal, signaling that the statistic is consistent and reliable across model runs. These results support the extension of the score test to co-evolution models, particularly for the inclusion of attribute information. This extension and simulations results provide the theoretical framework for the use of the score test in additional applications beyond structural models.

Joint score tests were calculated that include the alter attribute, ego attribute, outdegree-popularity (square root), same attribute, and average similarity parameters (all also individually tested). The shape of the distributions seen in the Figures 7.22, 7.23 and in Appendix B have a strong relationship with the number of actors. For one-sided tests of individual parameters, the test statistics theoretically follow a standard normal distribution. All score tests for the co-evolution model with a bernoulli attribute follow a normal pattern (histograms provided in Appendix B).



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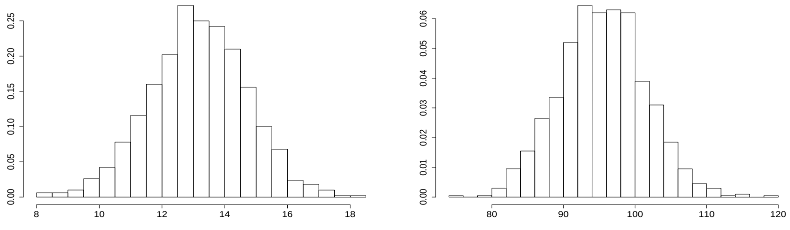
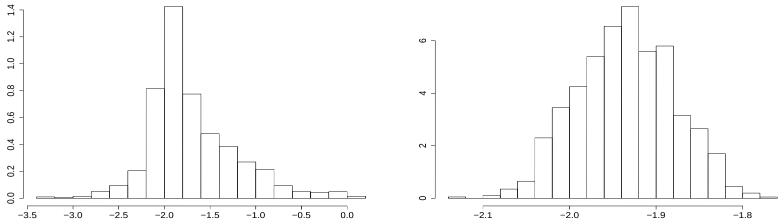
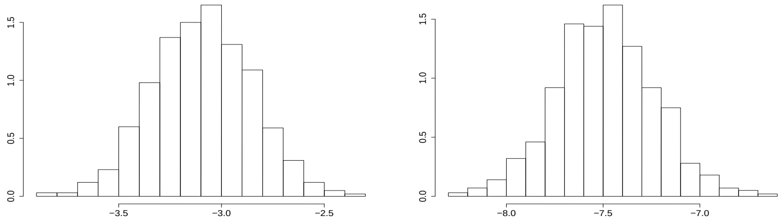


(c) n=100 (d) n=200

Figure 7.22: Co-evolution Model With Bernoulli Attribute - Joint Score Test



(a) n=25 (b) n=50

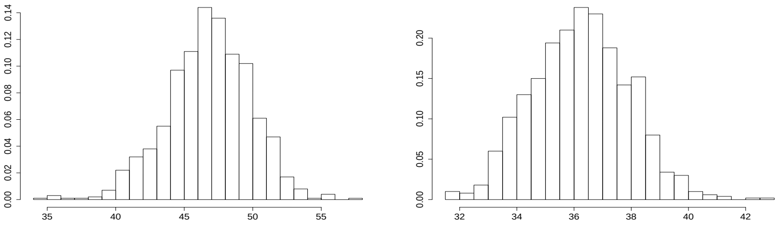


(c) n=100 (d) n=200

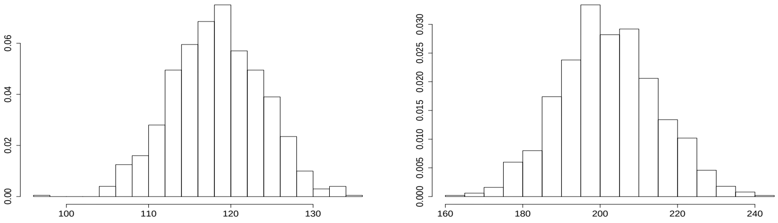
Figure 7.23: Co-evolution Model With Bernoulli Attribute - Attribute Alter Score Test - one sided

7.2.3 Co-evolution Model With Normal $(\mu = 3, \sigma = 1)$ Attribute Results

The results from this section mirror the findings from the previous co-evolution model that used a bernoulli distributed attribute. The results for each size of network cluster together, though some of the distributions display a slight skewness, especially in the scenarios where $n = 25$. Distributions of score test estimates for certain parameters are mirror images of each other across the two attributes. For example, the outdegree-popularity one-sided score test is indistinguishable between the two models (see in Figures $B.28$ and $B.52$). The score test appears to be consistent in the extension to a co-evolution model across attributes with different distributions. These findings support the use of the score test when modeling the co-evolution of network structure and attributes. The joint score test in Figure 7.24 and the attribute alter score test in Figure 7.25 are used to show the shape of the distributions seen in other parameters (included in Appendix B).

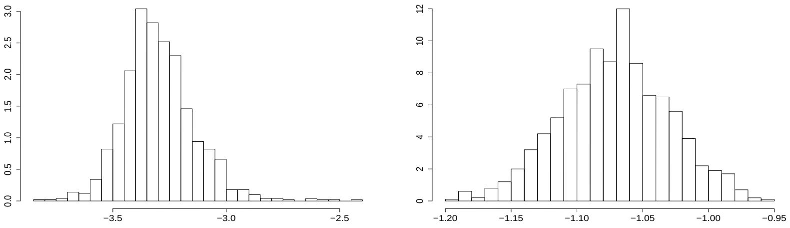


(a) n=25 (b) n=50

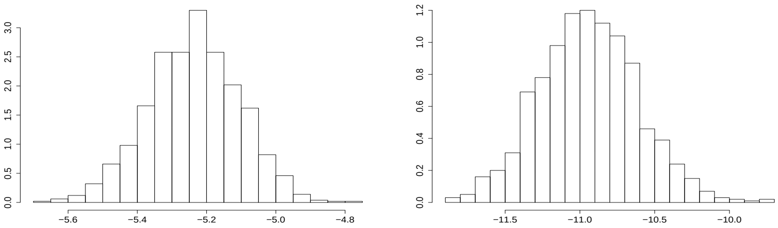


(c) n=100 (d) n=200

Figure 7.24: Co-evolution Model With Normal Attribute - Joint Score Test



(a) n=25 (b) n=50



(c) n=100 (d) n=200

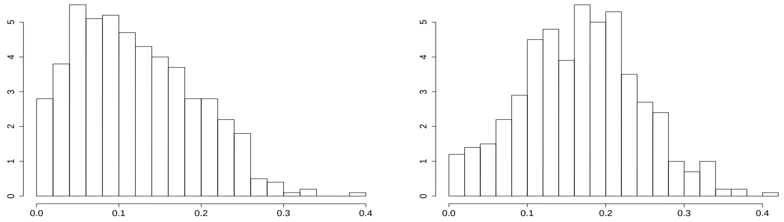
Figure 7.25: Co-evolution Model With Normal Attribute - Attribute Alter Score Test - one sided

7.3 Entropy-based Goodness-of-fit Test

The results of four models are compared in this section. The baseline model includes rate, density, reciprocity, and transitive triplets parameters. The structural model consists of the same parameters included in previous structural analysis - rate, density, reciprocity, transitive triplets, 3-cycles, and transitive ties. Two models consider co-evolution parameters: a model with all parameters from the structural model plus outdegree-popularity (square root), attribute alter, attribute ego, attribute rate, and linear shape, and a full co-evolution model comparable to the previous analysis. Each model has separate entropy measures for each time period, where time period is the difference between two consecutive observations. When the rate parameter is somewhat constant across time periods, this measure can be averaged to find an overall measure of model fit. For the most general case, in this study the rate parameters were not assumed to be constant across time. The entropy-based goodness-of-fit values range from 0 to 1 where a measure of 1 indicates perfect model fit.

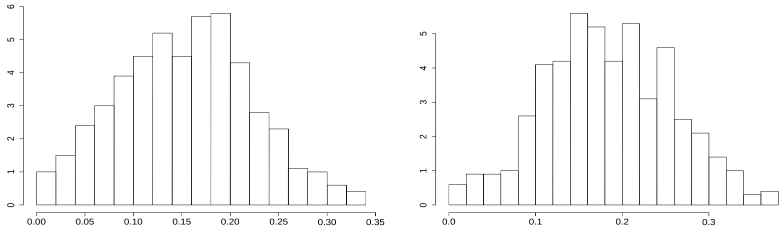
7.3.1 Structural Model Results

For the base model in Figure 7.26, time 1 fit statistics appear rather constant, normally distributed for models with any number of actors. Time 2 fit statistics also appear rather constant and normal, with a slightly higher fit than the time 1 results. For the structural model in Figure 7.27, the shape of the distribution mirrors the shape seen in the base model, but there is a shift in values where structural model fit statistics are higher than the respective base fit statistics.



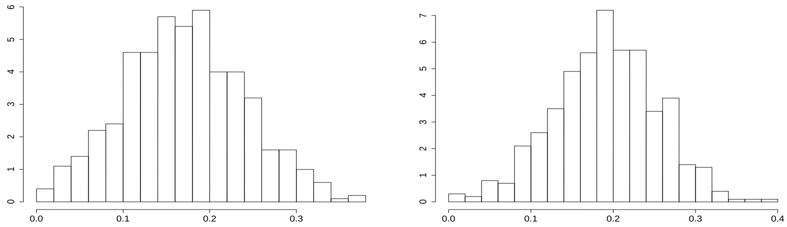
(a) n=25 time 1

(b) n=25 time 2



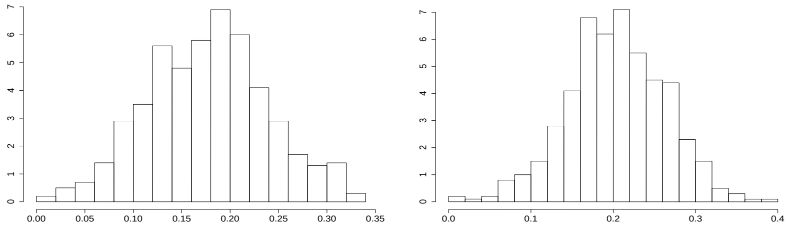
(c) n=50 time 1

(d) n=50 time 2



(e) n=100 time 1

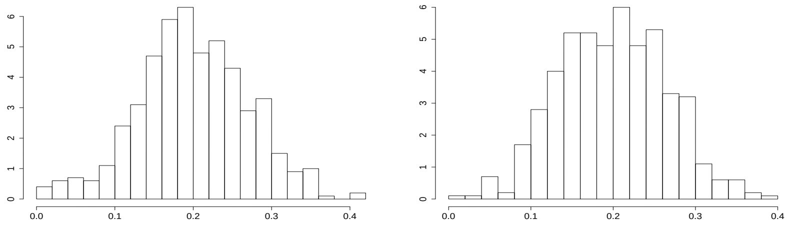
(f) n=100 time 2



(g) n=200 time 1

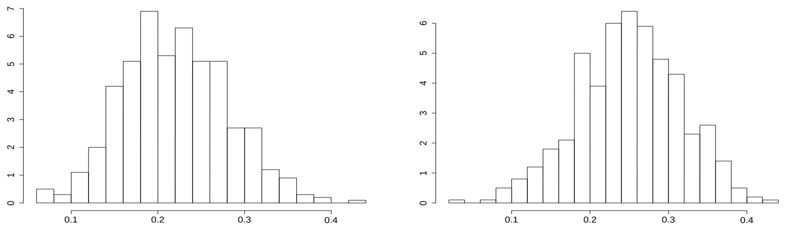
(h) n=200 time 2

Figure 7.26: Entropy Base Model



(a) n=25 time 1

(b) n=25 time 2



(c) n=50 time 1

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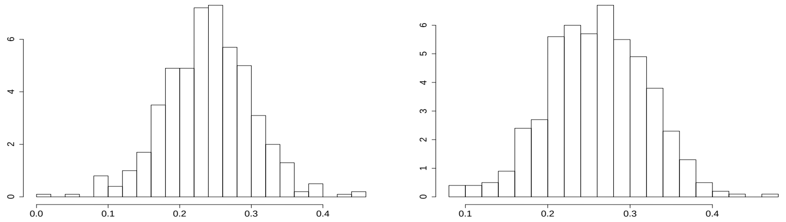
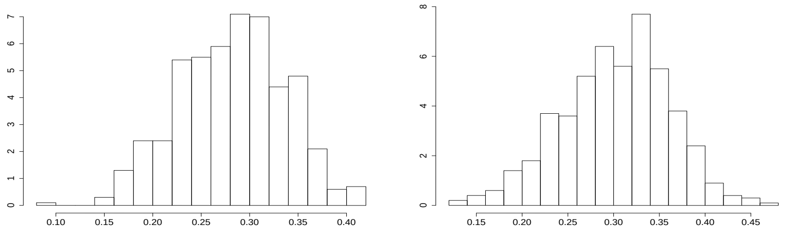


(e) n=100 time 1

(f) n=100 time 2



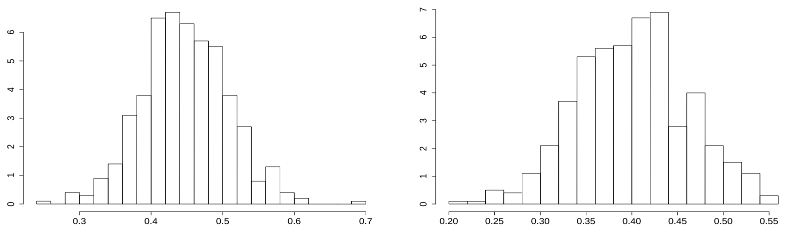
(g) n=200 time 1

(h) n=200 time 2

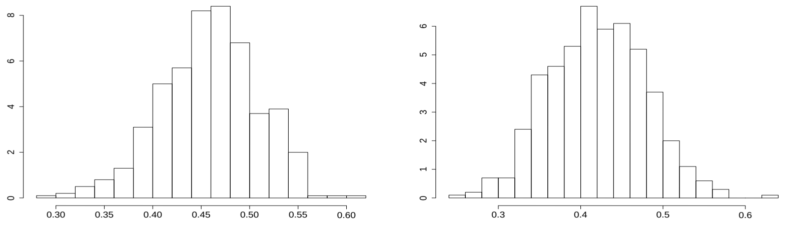
Figure 7.27: Entropy Structural Model

7.3.2 Co-evolution Model Results

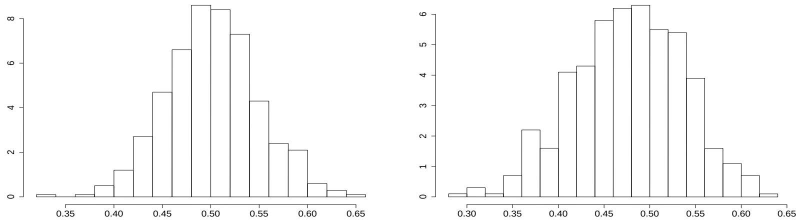
For structural and additional parameters (structural plus), models for both bernoulli attribute in Figure 7.28 and normal attribute in Figure 7.30, fit statistics are higher than the structural model and similar in shape and value. It appears that based on the entropy fit statistics, the structural plus model fits similarly well for both types of attributes. The co-evolution models for both bernoulli attribute in Figure 7.29 and normal attribute in Figure 7.31 have similar shape and values, and show higher values than each respective structural plus model.



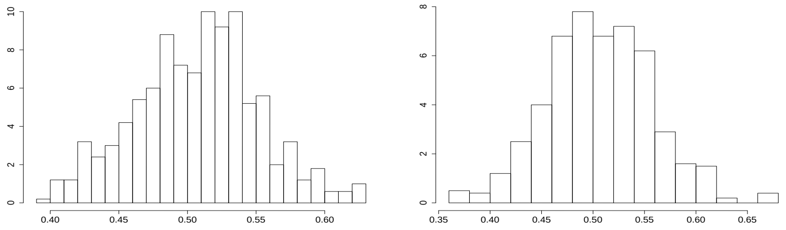
(a) n=25 time 1 (b) n=25 time 2



(c) n=50 time 1 (d) n=50 time 2

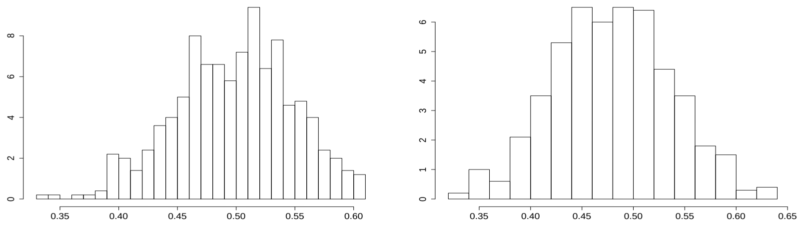


(e) n=100 time 1 (f) n=100 time 2



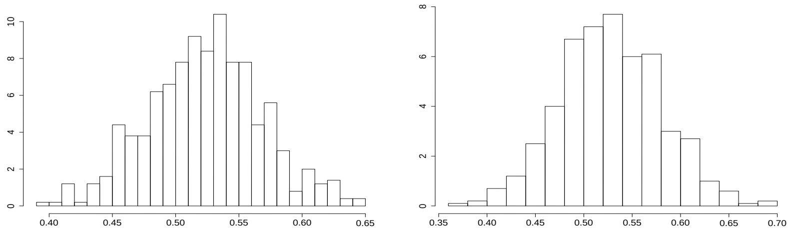
(g) n=200 time 1 (h) n=200 time 2

Figure 7.28: Entropy Structural Plus Model - Bernoulli Attribute



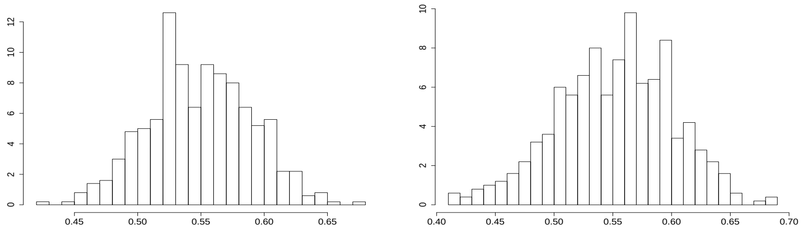
(a) n=25 time 1

(b) n=25 time 2



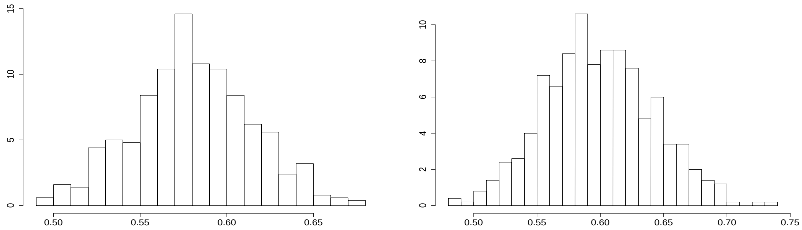
(c) n=50 time 1

(d) n=50 time 2



(e) n=100 time 1

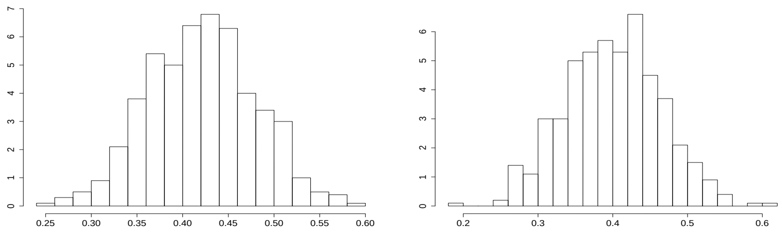
(f) n=100 time 2



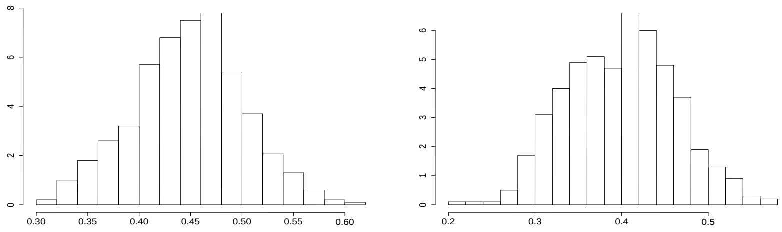
(g) n=200 time 1

(h) n=200 time 2

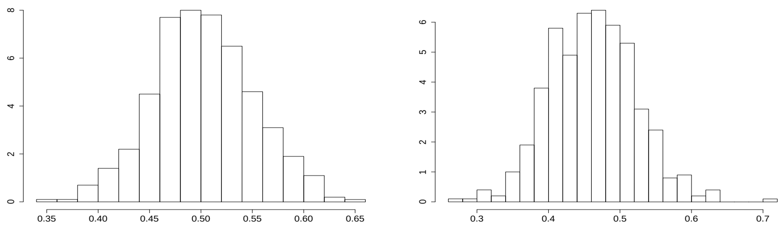
Figure 7.29: Entropy Co-evolution Model - Bernoulli Attribute



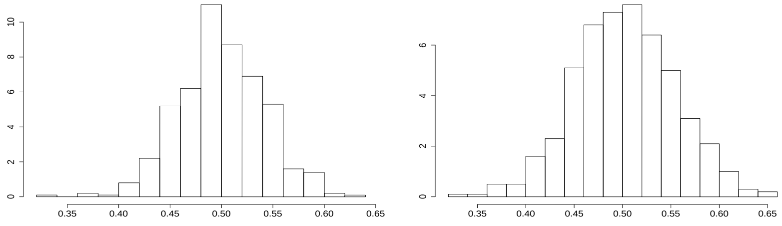
(a) n=25 time 1 (b) n=25 time 2



(c) n=50 time 1 (d) n=50 time 2

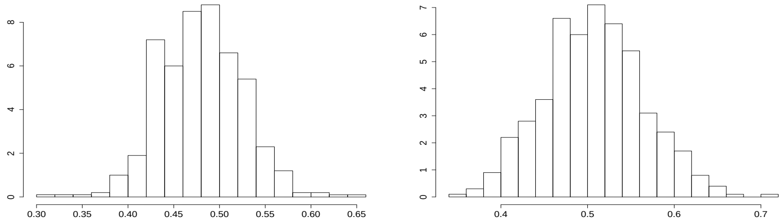


(e) n=100 time 1 (f) n=100 time 2

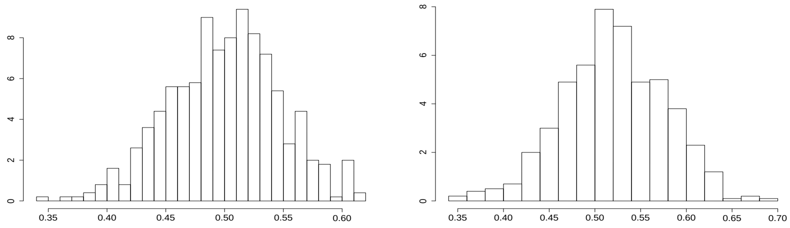


(g) n=200 time 1 (h) n=200 time 2

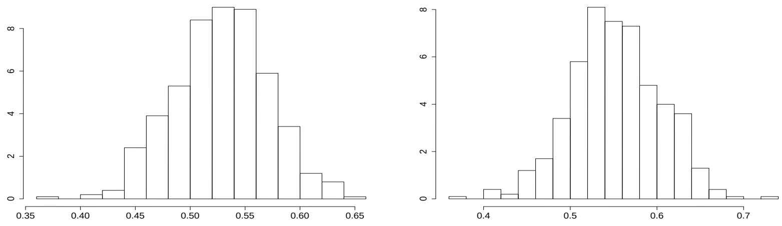
Figure 7.30: Entropy Structural Plus Model - Normal Attribute



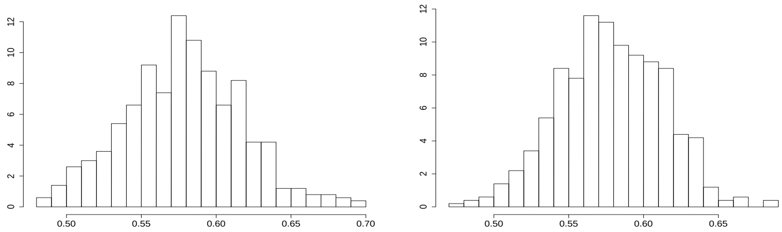
(a) n=25 time 1 (b) n=25 time 2



(c) n=50 time 1 (d) n=50 time 2



(e) n=100 time 1 (f) n=100 time 2



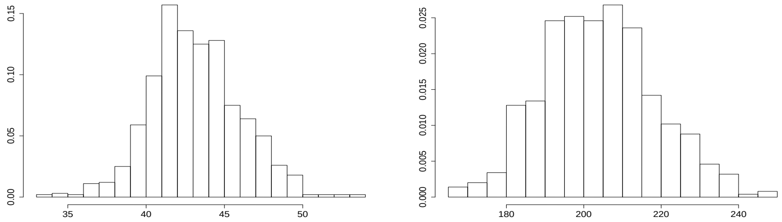
(g) n=200 time 1 (h) n=200 time 2

Figure 7.31: Entropy Co-evolution Model - Normal Attribute

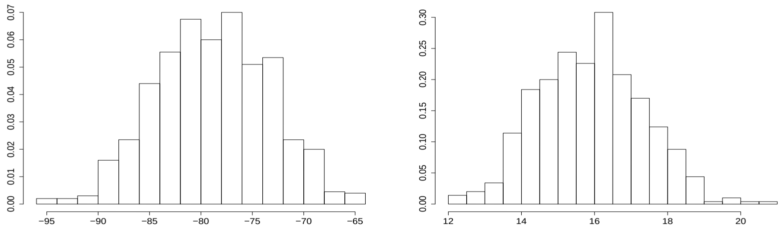
7.4 Knecht's Friendship Data

7.4.1 Pseudo-Wald Test Results

Based on of the t-test and Pseudo-Wald test statistics, a strong case can be made for the inclusion of all tested parameters in the structural model. The distributions of t-test statistics are all positive and significantly different than zero, along with all reported Wald statistics and p-values were well under the guideline of $p < 0.05$

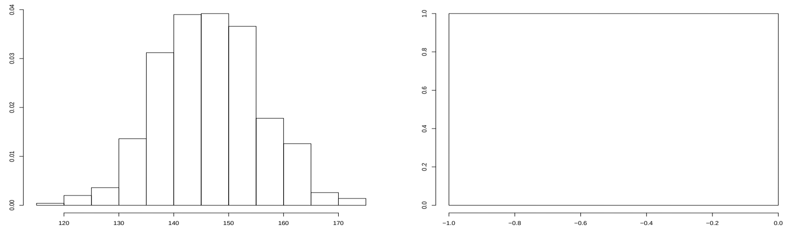


(a) Reciprocity t-Test (b) Transitive Triplets t-Test



(c) 3-cycles t-Test (d) Transitive Ties t-Test

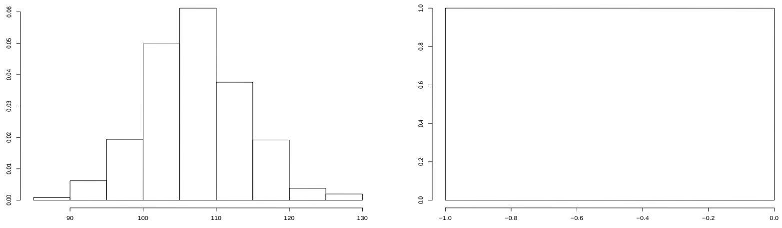
Figure 7.32: Structural Model Pseudo-Wald - Knecht Data - Structural Model t-Tests



(a) Pseudo-Wald Test Statistic (b) Pseudo-Wald P-value

Figure 7.33: Structural Model Pseudo-Wald - Knecht Data - Reciprocity, Transitive Triplets, 3-cycles, and Transitive Ties

Results from the Pseudo-Wald test for the co-evolution model do not support inclusion of all available parameters. Using the structural model

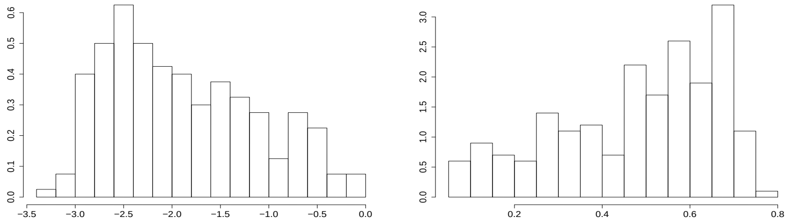


(a) Pseudo-Wald Test Statistic

(b) Pseudo-Wald P-value

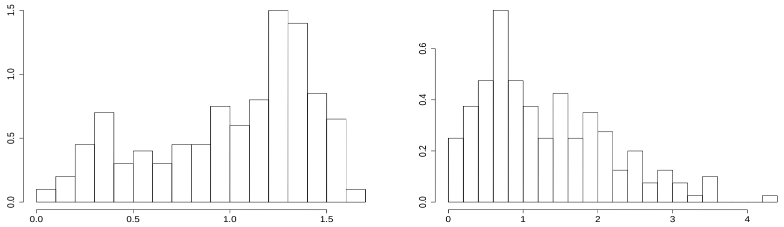
Figure 7.34: Structural Model Pseudo-Wald - Knecht Data - Transitive Triplets, 3-cycles, and Transitive Ties

from above as the baseline model, the t-test statistic distributions suggest the outdegree-popularity parameter is the only t-test that would have strong evidence for inclusion in the model. The p-value distributions from the Wald tests provide quality information about how often a parameter or set of parameters would be included or removed. With p-values both above and below the $p = 0.05$ standard cut-off, the t-test values and Wald statistics vary among model runs, providing somewhat contradictory findings. As an example, the Wald test statistic in Figure 7.36 has a large majority of observations below the $p = 0.05$ cut-off, signaling that overall, all tested parameters should be included in the model. While a large majority are below the cut-off, there are still several model runs that resulted in resulted in non-significant Pseudo-Wald test statistics, and in the case of a few non-significant Pseudo-Wald test statistics, contributing to Type 2 error. This behavior is mirrored in several other reported Pseudo-Wald statistics.



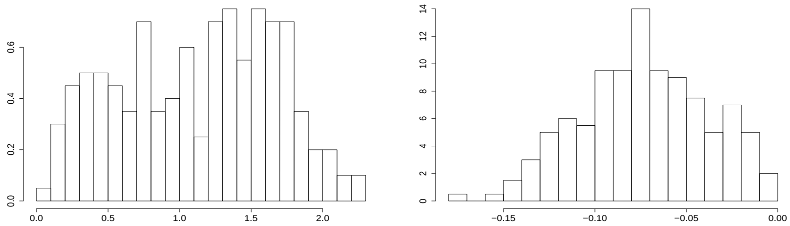
(a) Out-degree Popularity (sqrt) t-Test

(b) Attribute Alter t-Test



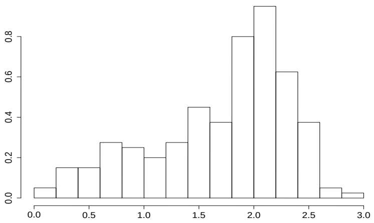
(c) Attribute Ego t-Test

(d) Same Gender t-Test



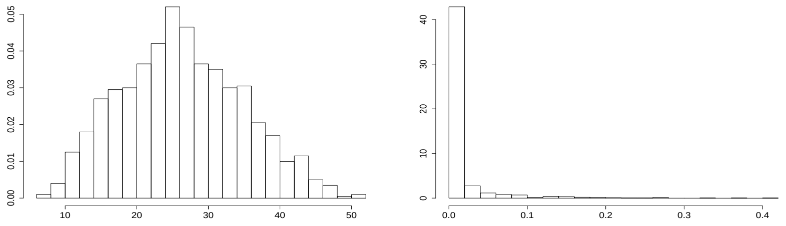
(e) Similarity on Delinquency t-Test

(f) Quadratic Shape t-Test



(g) Average Similarity on Delinquency t-Test

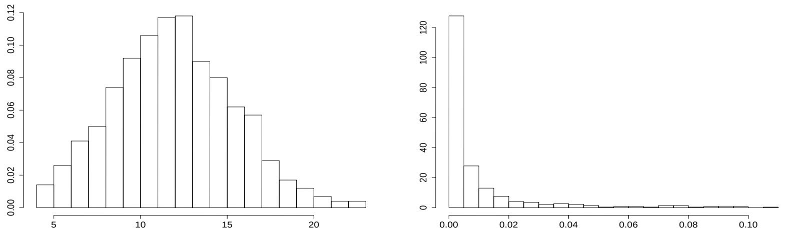
Figure 7.35: Co-evolution Model Pseudo-Wald - Knecht Data - Co-evolution Model t-Tests



(a) Pseudo-Wald Test Statistic

(b) Pseudo-Wald P-value

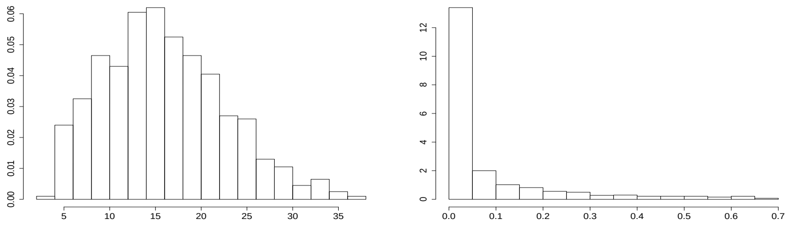
Figure 7.36: Co-evolution Model - Knecht Data - Pseudo-Wald for Outdegree-Popularity, Gender Alter, Gender Ego, Same Gender, Similarity on Delinquency, Quadratic Shape, and Average Similarity on Delinquency



(a) Pseudo-Wald Test Statistic

(b) Pseudo-Wald P-value

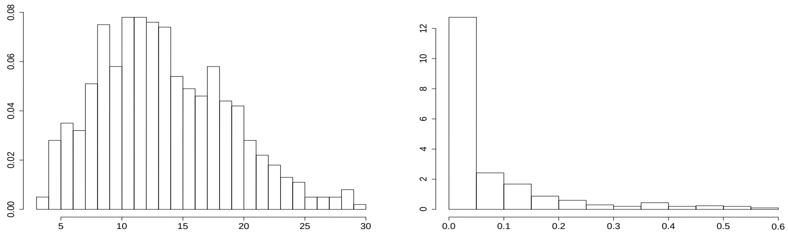
Figure 7.37: Co-evolution Model - Knecht Data - Pseudo-Wald for Outdegree-Popularity and Gender Alter



(a) Pseudo-Wald Test Statistic

(b) Pseudo-Wald P-value

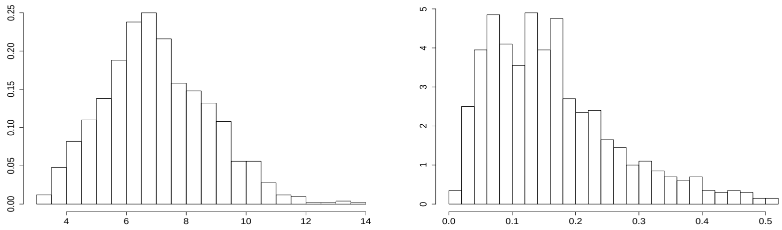
Figure 7.38: Co-evolution Model - Knecht Data - Pseudo-Wald for Gender Alter, Gender Ego, Same Gender, Similarity on Delinquency, Quadratic Shape, and Average Similarity on Delinquency



(a) Pseudo-Wald Test Statistic

(b) Pseudo-Wald P-value

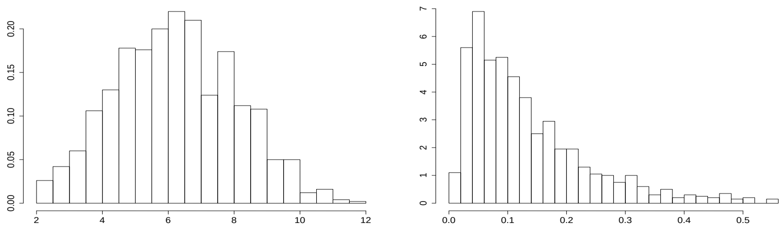
Figure 7.39: Co-evolution Model - Knecht Data - Pseudo-Wald for Gender Alter, Gender Ego, Same Gender, Similarity on Delinquency, and Quadratic Shape



(a) Pseudo-Wald Test Statistic

(b) Pseudo-Wald P-value

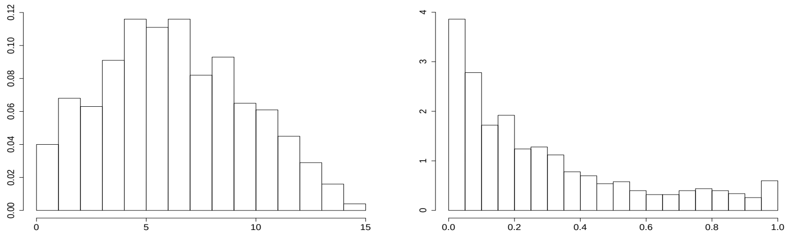
Figure 7.40: Co-evolution Model - Knecht Data - Pseudo-Wald for Gender Alter, Gender Ego, Same Gender, and Similarity on Delinquency



(a) Pseudo-Wald Test Statistic

(b) Pseudo-Wald P-value

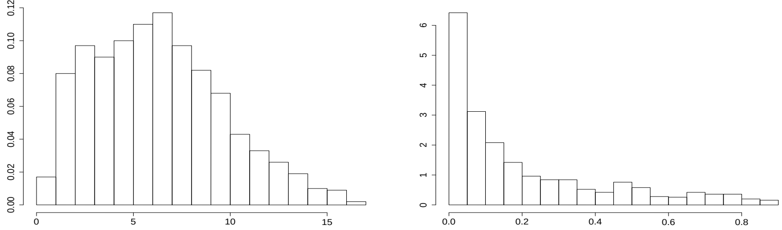
Figure 7.41: Co-evolution Model - Knecht Data - Pseudo-Wald for Gender Alter, Gender Ego, and Same Gender



(a) Pseudo-Wald Test Statistic

(b) Pseudo-Wald P-value

Figure 7.42: Co-evolution Model - Knecht Data - Pseudo-Wald for Same Gender, Similarity on Delinquency, Quadratic Shape, and Average Similarity on Delinquency



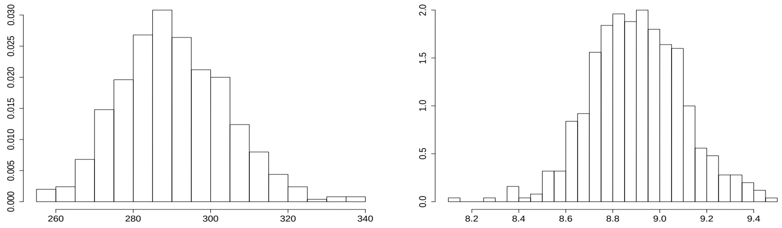
(a) Pseudo-Wald Test Statistic

(b) Pseudo-Wald P-value

Figure 7.43: Co-evolution Model - Knecht Data - Pseudo-Wald for Same Gender, Similarity on Delinquency, and Quadratic Shape

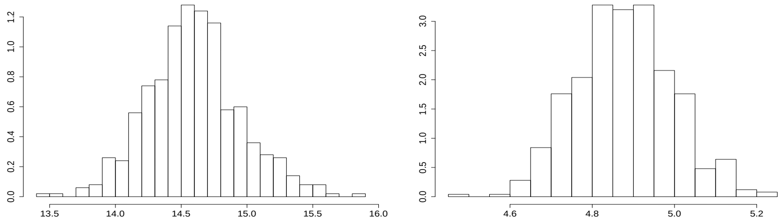
7.4.2 Score Test Results - Structural and Co-evolution Model

The following score test results for the structural and co-evolution models support the findings of Schweinberger (2007), and the extension to a co-evolution model from Section 4.2 of this paper. The score test is well-behaved for the joint test and tests of individual parameters, and reports values that cluster together in a distribution that appears normal. The Knecht data set has a structural model identical to the simulation, but has additional tested parameters in the co-evolution model. The joint score test for the structural model has four degrees of freedom and a critical χ^2 value of 9.49, while the joint score test for the co-evolution model has seven degrees of freedom and a critical χ^2 value of 14.07.



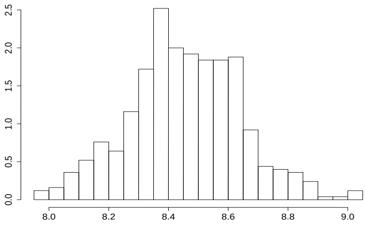
(a) Joint Score Test

(b) Reciprocity Score Test



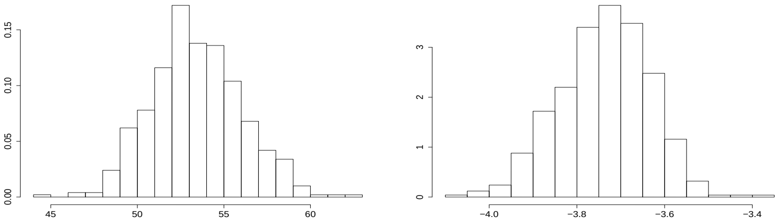
(c) Transitive Triplets Score Test

(d) 3-cycles Score Test

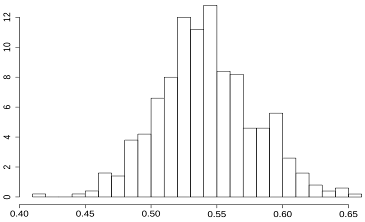


(e) Transitive Ties Score Test

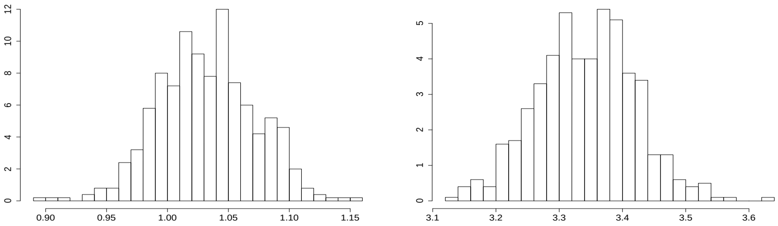
Figure 7.44: Structural Model Score - Knecht Data



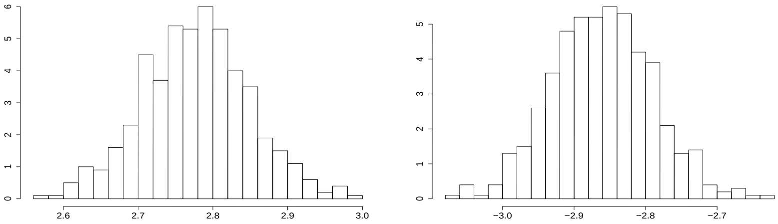
(a) Joint Score Test (b) Outdegree-Popularity (Square Root) Score Test



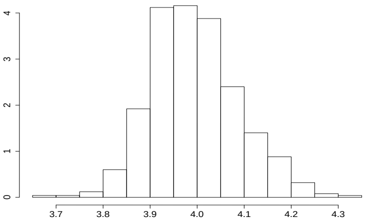
(c) Gender Alter Score Test



(d) Gender Ego Score Test (e) Similarity on Delinquency Score Test



(f) Same Gender Score Test (g) Quadratic Shape Score Test

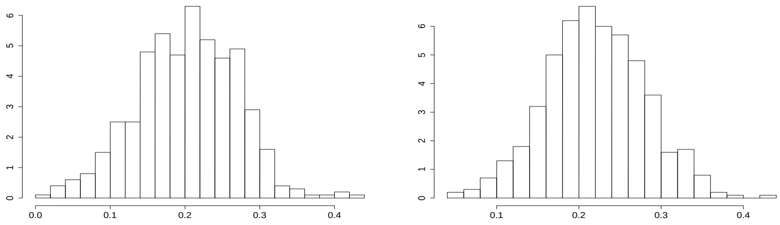


(h) Average Similarity on Delinquency Score Test

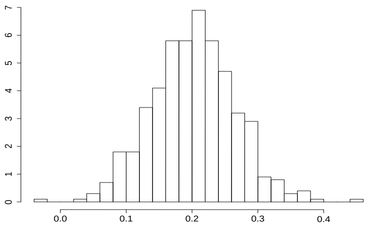
Figure 7.45: Co-evolution Model Score - Knecht Data

7.4.3 Entropy-based Test Results

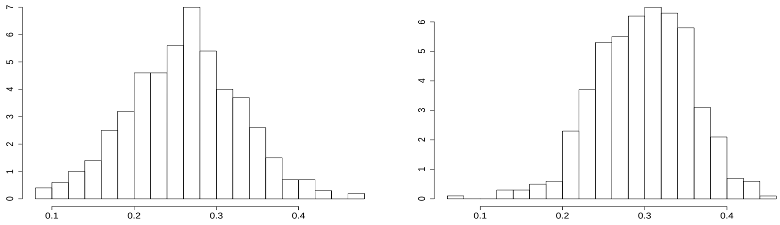
Entropy-based fit statistics presented in the following two sets of figures shows the expected pattern for this fit statistic. Across time, the fit of the model varies to a small degree, providing evidence that averaging the fit measure over time may provided accurate results. Looking at one time point across models, the more parameters that are included in a model, the higher the value of the fit measure. There is a noticeable shift in values between the base and structural models, providing evidence that the structural model fits the data better than the base model. Comparing the structural and structural plus models, there is not a large difference in the fit between these two models, mirroring results from the other measures considered in this paper. Adding parameters to the structural plus model to obtain the full co-evolution model, there is another increase in entropy-based test statistics, again mirroring findings from previous measures. The entropy-based measure shows that when parameters that have evidence for inclusion either from the Pseudo-Wald or score tests are added to the model, the model has increased fit.



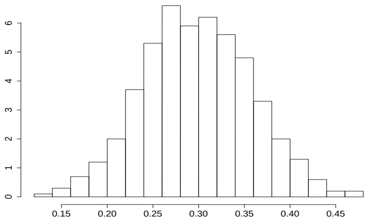
(a) Knecht Base Model Time 1 (b) Knecht Base Model Time 2



(c) Knecht Base Model Time 3

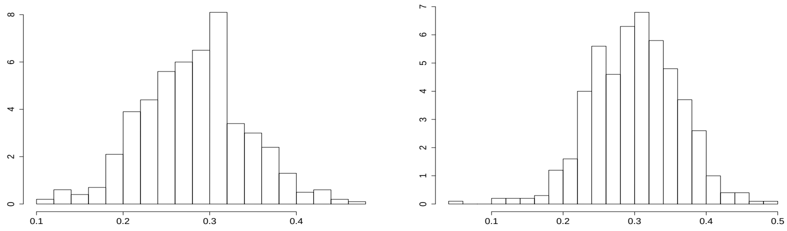


(d) Knecht Structural Model Time 1 (e) Knecht Structural Model Time 2

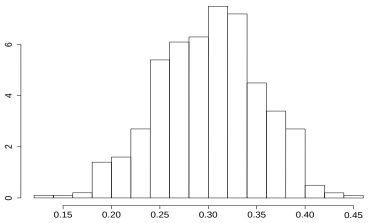


(f) Knecht Structural Model Time 3

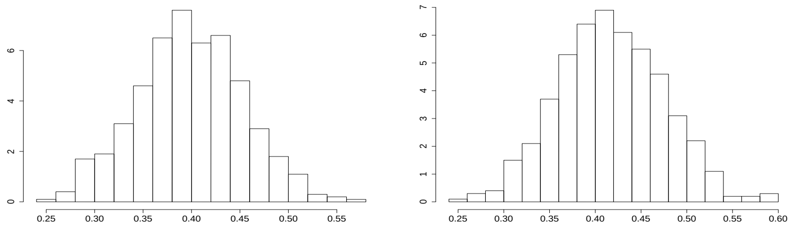
Figure 7.46: Knecht Data - Entropy Base and Structural Models



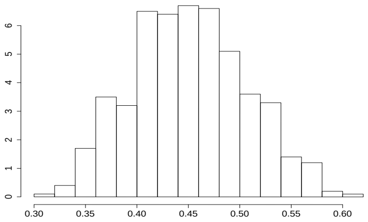
(a) Knecht Structural Plus Model Time 1 (b) Knecht Structural Plus Model Time 2



(c) Knecht Structural Plus Model Time 3



(d) Knecht Co-evolution Model Time 1 (e) Knecht Co-evolution Model Time 2



(f) Knecht Co-evolution Model Time 3

Figure 7.47: Knecht Data - Entropy Structural Plus and Co-evolution Models

7.4.4 Summary of Knecht Results

Table 7.1: Summary of Results for Knecht Data - Structural Model

Operational Definition	**t-Test Significant**	**t-Test Direction**	**Pseudo-Wald Significant**	**Score Test Significant**	**Score Test Direction**	**Entropy Fit**
Reciprocity	Yes	Positive	Yes	Yes	Positive	Yes
Transitive Triplets	Yes	Positive		Yes	Positive	Yes
3-cycles	Yes	Negative	Yes	Yes	Positive	Yes
Transitive Ties	Yes	Positive	Yes	Yes	Positive	Yes

Table 7.2: Summary of Results for Knecht Data - Co-evolution Model

Operational Definition	**t-Test Significant**	**t-Test Direction**	**Pseudo-Wald Significant**	**Score Test Significant**	**Score Test Direction**	**Entropy Fit**
Outdegree-Popularity (Square Root)	Mixed	Negative	Mixed	Yes	Negative	No
Gender Alter	No	Positive	No	Yes	Positive	No
Gender Ego	No	Positive	Mixed	No	Positive	No
Similarity on Delinquency	No	Positive	Yes	Yes	Positive	Yes
Quadratic Shape	No	Negative	Yes	Yes	Negative	Yes
Average Similarity on Delinquency	Mixed	Positive	No	Yes	Positive	Yes
Similarity on Gender	Mixed	Positive	Mixed	Yes	Positive	Yes

8 Discussion

The bell shaped distribution of t-test statistics in models confirms Snijders' (1996) proposal that states the behavior of this Pseudo t-test is approximately normally distributed. The standard errors for models with 25 actors have larger values and a number of outlier observations, a result of limited information and greater variability within the estimation technique. When more information is available, either for additional actors or attributes, modeling consistent behaviors improves. The behavior of t-test distributions show that on a small number of model runs, the parameter estimate may be reported with opposite direction than is typically seen. While there were relatively few model runs that had opposite signs, the presence of any values with unexpected signs reiterates the importance of multiple model runs when building a model. This pattern of unexpected negative values for t-test statistics disappeared in Pseudo-Wald test statistics when considering the same parameters.

The Pseudo-Wald statistic behaves in expected ways as the number of actors increases. Even in the simulation with 100 actors, the standard errors for parameter estimates become so small that most t-values for paramters were significant. When two or more of these parameters are combined into a Pseudo-Wald test, the test statistics become very large, very quickly. For example, in the co-evolution model with a normally distributed attribute Pseudo-Wald test simulation, every model run resulted in a significant Pseudo-Wald joint test statistic. The degrees of freedom used in calculating p-values for individual Pseudo-Wald tests does not account for much of this relationship.

The Pseudo-Wald tests for a variety of subsets of possible parameters were presented in Chapter 7. The Pseudo-Wald test part of the simulation study revealed some interesting and unexpected behaviors. The more parameters included, the less an impact an individual parameter will have, though highly significant parameters will continue to have a large influence on the test.

Future work on transforming the Pseudo-Wald test statistic to better mediate this relationship would increase the proposed measure's usability. The systematic relationship between the magnitude of the Pseudo-Wald and the number of parameters tested should be further researched. The fewer the parameters tested, the less this relationship is apparent. The relationship between the Pseudo-Wald test statistic and the size of the network should be more appropriately controlled. As the number of actors increases, the covariances of and between parameter estimates becomes smaller resulting in Pseudo-Wald test statistics of increasing magnitude. For use in applications, this suggests that testing a small subset of parameters at a time may provide better information for parameter inclusion.

The score test results support the theory presented in Section 4.2 of this paper, for both structural and co-evolution models. This extension provides the theoretical framework for the use of the score test in applications beyond structural models. The score test statistics are distributed approximately normal, signaling that the statistic is consistent and reliable across model runs. These results support the extension of the score test to co-evolution models, for the inclusion of attribute information.

The entropy-based goodness-of-fit measure displayed expected behavior across models of different sizes in the simulation study. Models with fewer actors had fit statistics that were lower and had greater variance. As parameters were added to the model, the model fit increased. The pattern seen in this measure confirm the recommendations of effect inclusion of the Pseudo-Wald and score test results, though in a different manner. The Pseudo-Wald and score tests are measures for effect inclusion, while the entropy-based measure allows for model fit comparisons.

Vexler and Gurevich (2010) warn of applying goodness-of-fit tests based on sample entropy to real data studies. The power of entropy-based tests may be affected by sample entropy estimation, particularly in testing distributional assumptions of normality and uniformity. However, the results from the simulation based on the Knecht data set did not raise concerns when applying this entropy-based goodness-of-fit statistic to real data.

It is interesting to note the connection between a Bayesian approach and the use of an entropy-based goodness-of-fit measure. The principle of maximum entropy in Bayesian probability states that the probability distribution that best represents the current state of knowledge has the largest entropy. The entropy measure proposed in this paper can be adapted to a Bayesian estimation technique, when that approach becomes more widely used for co-evolution network models. The entropy measure is calculated from the Metropolis-Hastings algorithm approach used in the method of moments estimation technique. Because the Gibbs sampling of Bayesian estimation is a special case of the Metropolis-Hastings algorithm, altering this entropy goodness-of-fit measure in future work to use Bayesian estimation would not be difficult. Overall, this proposed entropy-based goodness-of-fit measure provides information about how well a model fits the data. The efficiency and power of this measure need to be further studied, but preliminary results presented here signal the usefulness of the measure.

Because the Pseudo-Wald for all parameters and joint score test are asymptotically equivalent to the likelihood ratio test, the comparison of the two should validate for the asymptotic equivalence of the two measures. The Pseudo-Wald test in Figure 7.3 and joint score test in Figure 7.17 for the structural model both have similar shape, though the relationship of the values depends on the number of actors in the model. For models with 25 actors, the score test has lower values than the Pseudo-Wald test (a mean of about 58 versus 105), but has higher values for models with more than 25 actors. The values of the tests allow a decision to be made about effect inclusion, though at a certain point the difference between p-values is so small that values are indistinguishable. A similar relationship between the Pseudo-Wald and score test can also be seen in both of the co-evolution models. The entropy-based goodness-of-fit measure provides one source of information about how well the overall model fits the data, a different test than those for effect inclusion. When building a model, multiple sources of information should be considered when determining what effects should be included. When using a method of moments estimation approach, using the Pseudo-Wald test, the score test, and the entropy-based test together would help the researcher make informed decisions.

The main focus of this paper was to compare the proposed measures with currently available measures. Goodness-of-fit measures will become available with the development of additional estimation techniques. However, recent developments in the Bayesian (Koskinen, 2004; Koskinen & Snijders, 2007) and Maximum Likelihood estimation (Snijders, Steglich, & Schweinberger, 2009) methods will lead to additional goodness-of-fit possibilities. An approximated likelihood function in the Maximum Likelihood estimation procedure will allow for an alternative way of estimating co-evolution models and will present additional measures of model fit.

Snijders (2001) used a method of moments approach for continuous time Markov models to estimate longitudinal network data models. The panel data available and prior work done on Markov models for longitudinal network analysis make continuous time Markov models a natural choice for a framework for actor-based co-evolution models. The method of moments approach gives an easy estimation technique that can lay the foundation for future development. Although the method of moments approach can be used for estimation, new approaches have advantages over this initially proposed technique. Bayesian (Koskinen, 2004; Koskinen & Snijders, 2007) and Maximum Likelihood estimation (Snijders, Steglich & Schweinberger, 2009) approaches offer unique and shared benefits over a method of moments approach. With actors that change connections and attributes over time, Bayesian inference seems a natural fit for co-evolution models. Bayesian methods have theoretical and applied benefits when compared to the alternative estimation methods. Bayesian methods allow for improved estimation with a small increase in computation time. The randomly generated networks needed for the estimation process adapted in this paper can be used as a Gibbs sample in a Bayesian approach. Gibbs sampling is a special case of the more general Metropolis-Hastings approach taken in this paper and in the estimation of Exponential Family of Random Graph Models (ERGMs).

Both the Bayesian and Maximum Likelihood approaches have asymptotic advantages, although the asymptotic behavior of the three estimation techniques is not well understood. On a practical note, using the method of moment estimation technique in the specification of a prior distribution in Bayesian estimation would provide the benefit of an educated guess for starting parameters.

The R^2 for Maximum Likelihood estimation outlined in this paper can be applied once the Maximum Likelihood estimation technique is incorporated into the RSiena package and becomes more widely used. For now, the fit measure is unavailable for use, but as the methodology becomes more widely adopted, its use seems straightforward and desirable. The adoption of the Maximum Likelihood estimation and the use of Bayesian estimation will be seen with increased frequency.

Further work could also look at the behavior of models for networks with between 25 and 50 actors. Many of the reported results showed that models with 25 actors behaved differently than models with 50 or more actors. A more detailed look could help us understand for understanding of how large a network must be to begin seeing consistent results. Simulating network and attribute data for networks varying between 25 and 50 would allow for conclusions about when distributions appear as expected, and when unexpected results such as non-normal distributions no longer appear in model results.

To ensure significant attribute parameter estimates, the attribute levels within an actor were rearranged to loosely reflect the actor's network activity, measured by outdegree. Without this crucial reordering, none of the parameters would have been significant significant when the model converged. For example, multiple actors with attribute levels $0, 1, 0$ or $1, 0, 1$ resulted in models that would not converge. For actors with relatively high outdegree over time, attribute levels across time were rearranged to be constant or increasing. For actors with relatively low outdegree over time, levels were rearranged to be constant or decreasing.

Given how the network and attributes were randomly created, there was no way to tell what parameters would show interesting results in a sensitivity analysis. Parameter estimates that are either very significant or never significant would not display interesting behavior. Future work should include a sensitivity analysis, taking a detailed look at when a parameter estimate alternates between inclusion and removal in the final model. A sensitivity analysis provides information on how varying the inputs into a model affect the outcomes of a model. The sensitivity of each goodness-of-fit measure could explored by comparing the number of instances a significant parameter is correctly included in the model. Measures that are sensitive to small changes in the standard error of the associated statistic may be too responsive to change. Measures that are not sensitive enough lack the ability to differentiate among models and ignore the preference for a parsimonious model.

The main goals of this dissertation were

(a) to extend Snijders' Pseudo t-test statistic to a Pseudo-Wald test statistic,

(b) to extend Schweinberger's score test to a co-evolution model framework,

(c) to propose an entropy-based goodness-of-fit measure for actor-based co-evolution models,

(d) to propose a generalized R^2 measure for use with Maximum Likelihood estimation, and

(e) to conduct a simulation study to determine the behaviors and performance of measures.

Each of these goals was addressed in previous chapters 5, 6, and 7. Results from the simulation study confirm the behavior of the measures for effect inclusion and goodness-of-fit discussed. Some results highlight the need for future research. For example, one area for future work should address the behavior of parameters when both structural parameters and parameters capturing co-evolution are jointly tested. The simulation here dealt with structural parameters in the structural model and co-evolution parameters (assuming structural effects were included) in the co-evolution model. The real advantage of the work presented in this paper is the ability to test parameters across both types of models concurrently. With an appropriate approach to building a model, this advancement will shorten the time it takes to build a model using a forward selection technique.

A RSiena Code and Output

A.1 RSiena Score Test Example Code

The following R code produces 20 co-evolution model runs with 25 actors, a bernoulli attribute, and reporting the score test statistic results.

```
library(RSiena)

n<-20

setwd('C:/Documents and Settings/Bethany/Desktop/sim/')

time1<-as.matrix(read.table("time1.txt"))

time2<-as.matrix(read.table("time2.txt"))

time3<-as.matrix(read.table("time3.txt"))

sim25time1<-time1[88:112,88:112]

sim25time2<-time2[88:112,88:112]

sim25time3<-time3[88:112,88:112]

att200<-as.matrix(read.table("att200u.txt"))

att25<-att200[88:112,]

at25<-sienaNet(att25,type='behavior')

sim25<-sienaNet(array(c(sim25time1,sim25time2,sim25time3),dim=c(25,25,3)))

projs <- paste('sim25', 1:20, sep='')

ans <- vector('list',20)

mydata<-sienaDataCreate(sim25,at25)

setwd('C:/Documents and Settings/Bethany/Desktop/sim/sim25cb/round1/')

myeff<-getEffects(mydata)

myeff[myeff$effectName=='outdegree(density)' & myeff$type=='eval',

'include']=TRUE

myeff[myeff$effectName=='reciprocity' & myeff$type=='eval',

'include']=TRUE
```

```
myeff[myeff$effectName=='transitive triplets' & myeff$type=='eval',
'include']=TRUE
myeff[myeff$effectName=='3-cycles' & myeff$type=='eval','include']
=TRUE
myeff[myeff$effectName=='transitive ties' & myeff$type=='eval',
'include']=TRUE
myeff[myeff$effectName=='outdegree - popularity (sqrt)' &
myeff$type=='eval','include']=TRUE
myeff[myeff$effectName=='outdegree - popularity (sqrt)' &
myeff$type=='eval','fix'] <- TRUE
myeff[myeff$effectName=='outdegree - popularity (sqrt)' &
myeff$type=='eval','test'] <- TRUE
myeff[myeff$effectName=='outdegree - popularity (sqrt)' &
myeff$type=='eval',
'initialValue'] <- 0
myeff[myeff$effectName=='at25 alter' & myeff$type=='eval',
'include']=TRUE
myeff[myeff$effectName=='at25 alter' & myeff$type=='eval',
'fix'] <- TRUE
myeff[myeff$effectName=='at25 alter' & myeff$type=='eval',
'test'] <- TRUE
myeff[myeff$effectName=='at25 alter' & myeff$type=='eval',
'initialValue'] <- 0
myeff[myeff$effectName=='at25 ego' & myeff$type=='eval',
'include']=TRUE
myeff[myeff$effectName=='at25 ego' & myeff$type=='eval',
'fix'] <- TRUE
myeff[myeff$effectName=='at25 ego' & myeff$type=='eval',
'test'] <- TRUE
myeff[myeff$effectName=='at25 ego' & myeff$type=='eval',
'initialValue'] <- 0
myeff[57,9]=TRUE
```

```
myeff[57,11]=TRUE
myeff[57,12]=TRUE
myeff[57,13]=0
myeff[myeff$effectName=='behavior at25 linear shape' &
myeff$type=='eval','include']=TRUE
#myeff[myeff$effectName=='behavior at25 quadratic shape' &
myeff$type=='eval','include']=TRUE
#myeff[myeff$effectName=='behavior at25 quadratic shape' &
myeff$type=='eval','fix'] <- TRUE
#myeff[myeff$effectName=='behavior at25 quadratic shape' &
myeff$type=='eval','test'] <- TRUE
#myeff[myeff$effectName=='behavior at25 quadratic shape' &
myeff$type=='eval',
'initialValue'] <- 0
myeff[myeff$effectName=='behavior at25 average similarity' &
myeff$type=='eval','include']=TRUE
myeff[myeff$effectName=='behavior at25 average similarity' &
myeff$type=='eval','fix'] <- TRUE
myeff[myeff$effectName=='behavior at25 average similarity' &
myeff$type=='eval','test'] <- TRUE
myeff[myeff$effectName=='behavior at25 average similarity' &
myeff$type=='eval',
'initialValue'] <- 0
for(i in 1:n){
mymodel25<-sienaModelCreate(useStdInits=TRUE,projname=projs[i])
print01Report(mydata,myeff,modelname = 'sim25')
ans[[i]]<-siena07(mymodel25,data=mydata,effects=myeff,
batch=FALSE,verbose=TRUE)}

answer1<-cbind(ans[[1]]$theta,diag(ans[[1]]$covtheta),ans[[2]]$theta,
diag(ans[[2]]$covtheta),ans[[3]]$theta,diag(ans[[3]]$covtheta),
ans[[4]]$theta,diag(ans[[4]]$covtheta),ans[[5]]$theta,
```

```
diag(ans[[5]]$covtheta),ans[[6]]$theta,diag(ans[[6]]$covtheta),
ans[[7]]$theta,diag(ans[[7]]$covtheta),ans[[8]]$theta,
diag(ans[[8]]$covtheta),ans[[9]]$theta,diag(ans[[9]]$covtheta),
ans[[10]]$theta,diag(ans[[10]]$covtheta),ans[[11]]$theta,
diag(ans[[11]]$covtheta),ans[[12]]$theta,diag(ans[[12]]$covtheta),
ans[[13]]$theta,diag(ans[[13]]$covtheta),ans[[14]]$theta,
diag(ans[[14]]$covtheta),ans[[15]]$theta,diag(ans[[15]]$covtheta),
ans[[16]]$theta,diag(ans[[16]]$covtheta),ans[[17]]$theta,
diag(ans[[17]]$covtheta),ans[[18]]$theta,diag(ans[[18]]$covtheta),
ans[[19]]$theta,diag(ans[[19]]$covtheta),ans[[20]]$theta,
diag(ans[[20]]$covtheta))

write.table(answer1, file ="answer1.csv", sep = ",", col.names = NA)
```

A.2 RSiena Output

The following is included as an example of what RSiena supplies as output following a model run. Again, this example was for a co-evolution model with three time points, 25 actors, a bernoulli attribute level, and reporting the score test statistic results. Following the output is a brief description of important parts.

```
-----------------------------------
New Analysis started.
Date and time: 18/03/2010 13:29:52
New results follow.
-----------------------------------


Siena version 1.0.9 (18 Jan 10) R-forge revision: 52


@1
Estimation by stochastic approximation algorithm.
```

```
=================================================


Random initialization of random number stream.

Current random number seed is 39458.

Model Type 1: Standard actor-oriented model

Estimation method: unconditional moment estimation.


Time duration for simulations in each period is 1.0.

Standard errors are estimated with the likelihood ratio method.

Initial value of gain parameter is  0.2000000.

Number of subphases in Phase 2 is 4.


Initial parameter values are

  1. rate:  constant sim25 rate (period 1)            4.5840

  2. rate:  constant sim25 rate (period 2)            2.6705

  3. eval:  outdegree (density)                      -0.2292

  4. eval:  reciprocity                               0.0000

  5. eval:  transitive triplets                       0.0000

  6. eval:  3-cycles                                  0.0000

  7. eval:  transitive ties                           0.0000

  8. eval:  outdegree - popularity (sqrt)             0.0000(fixed)

  9. eval:  at25 alter                                0.0000(fixed)

 10. eval:  at25 ego                                  0.0000(fixed)

 11. eval:  same at25                                 0.0000(fixed)

 12. rate:  rate at25 (period 1)                      0.3800

 13. rate:  rate at25 (period 2)                      0.6200

 14. eval:  behavior at25 linear shape                0.6105

 15. eval:  behavior at25 average similarity          0.0000(fixed)



Observed values of target statistics are

  1. Amount of network change in period 1             55.0000
```

```
  2. Amount of network change in period 2              32.0000
  3. Number of ties                                   252.0000
  4. Number of reciprocated ties                      216.0000
  5. Number of transitive triplets                    442.0000
  6. 3-cycles                                         149.0000
  7. Number of ties with transitive closure           208.0000
  8. Sum of indegrees x sqrt(outdegree)               636.2672
  9. Sum of indegrees x at25                          -40.5200
 10. Sum of outdegrees x at25                         -34.5200
 11. Same values on at25                              160.0000
 12. Amount of behavioral change in period 1 on at25    7.0000
 13. Amount of behavioral change in period 2 on at25   13.0000
 14. beh. at25 cent. sum                                3.6667
 15. beh. at25 average similarity                       1.3017

 15 parameters, 15 statistics

Estimation of derivatives by the LR method (type 1).

@2
End of stochastic approximation algorithm, phase 3.
---------------------------------------------------

Total of 3074 iterations.
Parameter estimates based on 2074 iterations,
convergence diagnostics, covariance and derivative
matrices based on 1000 iterations.

Information for convergence diagnosis.
Averages, standard deviations, and t-ratios for
deviations from targets:
  1.  -0.0990   6.9082  -0.0143
```

```
  2.  -0.3210   5.9138  -0.0543
  3.  -0.2640   9.8531  -0.0268
  4.  -0.4700  11.7573  -0.0400
  5.   4.7480  53.8898   0.0881
  6.  -1.5320  18.3439  -0.0835
  7.  -0.7090  14.4323  -0.0491
  8.  -8.0428  35.1712  -0.2287     (fixed parameter)
  9.   6.8216   3.7002   1.8436     (fixed parameter)
 10.   3.9766   3.9107   1.0169     (fixed parameter)
 11.  -9.8610   7.1906  -1.3714     (fixed parameter)
 12.  -0.0180   2.0823  -0.0086
 13.  -0.2620   2.4983  -0.1049
 14.  -0.1380   3.3042  -0.0418
 15.  -3.2063   2.1965  -1.4597     (fixed parameter)

Good convergence is indicated by the t-ratios
of non-fixed parameters being close to zero.



@2
Estimation Results.
-------------------

Regular end of estimation algorithm.
Total of 3074 iteration steps.

@3
Estimates and standard errors

Network Dynamics
 1. rate:  constant sim25 rate (period 1)    2.6765(   0.3933)
 2. rate:  constant sim25 rate (period 2)    2.8685(   0.7683)
```

```
 3. eval:  outdegree (density)              -2.9199(   0.4324)
 4. eval:  reciprocity                       4.6090(   0.5973)
 5. eval:  transitive triplets              -0.2129(   0.2558)
 6. eval:  3-cycles                          0.6265(   0.5061)
 7. eval:  transitive ties                   0.2055(   0.3295)
 8. eval:  outdegree - popularity (sqrt)     0.0000(  fixed  )
 9. eval:  at25 alter                        0.0000(  fixed  )
10. eval:  at25 ego                          0.0000(  fixed  )
11. eval:  same at25                         0.0000(  fixed  )
Behavior Dynamics

12. rate:  rate at25 (period 1)              0.7489(   0.4667)
13. rate:  rate at25 (period 2)              4.1803(   9.1345)
14. eval:  behavior at25 linear shape        0.2753(   0.5091)
15. eval:  behavior at25 average similarity  0.0000(  fixed  )


@3
Covariance matrices

(Values of the covariance matrix of estimates
  are meaningless for the fixed parameters.)

Covariance matrix of estimates (correlations below diagonal):
0.155      0.020     -0.043      0.038     -0.008      0.026
    -0.013     12.980    12.980     12.980     12.980      0.005
    -0.212      0.004     12.980
0.067      0.590     -0.087      0.070     -0.005      0.003
    -0.022     25.353    25.353     25.353     25.353     -0.002
    -1.980     0.065     25.353
-0.253     -0.261      0.187     -0.135      0.012     -0.051
    -0.024     14.269    14.269     14.269     14.269      0.010
     0.441     -0.015    14.269
```

```
0.163      0.152     -0.524      0.357     -0.050      0.121
    -0.023     19.712    19.712     19.712     19.712      0.005
     1.174     -0.047    19.712
-0.079     -0.028      0.109     -0.330      0.065     -0.119
    -0.019      8.443    8.443      8.443      8.443      0.000
    -0.276      0.010    8.443
0.131      0.007     -0.234      0.399     -0.922      0.256
    -0.003     16.702    16.702    16.702     16.702      0.008
     0.883     -0.036    16.702
-0.102     -0.088     -0.169     -0.116     -0.221     -0.019
     0.109     10.874    10.874     10.874     10.874     -0.006
     0.298     -0.004    10.874
1.044      0.688      2.415      0.687      2.065      2.063
     1.246    999.000   134.864    134.864    134.864     33.000
     12.980    16.702   134.864
2.039      0.448      1.127      1.343      1.345      0.963
     2.434      0.130    999.000   129.502    129.502     15.400
     25.353     10.874    129.502
1.148      1.359     22.057      0.756      4.081     18.844
     1.370      0.125    0.125     999.000    124.653    301.438
     14.269    33.000   124.653
1.586      1.359      1.229      1.044      4.081      1.050
      1.893     0.190    0.190       0.190    999.000     16.801
      19.712   33.000   189.571
0.029     -0.007      0.050      0.020     -0.003      0.035
     -0.040      1.044    1.044      1.044      1.044      0.218
      0.895     -0.088    15.400
-0.059     -0.282      0.112      0.215     -0.118      0.191
      0.099      1.044    1.044      1.044      1.044      0.210
      83.439     -3.197    301.438
0.019      0.167     -0.067     -0.154      0.080     -0.141
     -0.024      1.044    1.044      1.044      1.044     -0.371
```

```
     -0.688      0.259     16.801
0.679      1.359      2.415      0.447      4.081      2.063
      0.811      0.190    0.190      0.190      0.190      2.237
      0.029      2.051    999.000


Derivative matrix of expected statistics X by parameters and
covariance/correlation matrix of X can be found using
summary(ans) within R, or by using the 'verbose' option
in Siena07.


@2
Generalised score test <c>
--------------------------


Testing the goodness-of-fit of the model restricted by
 (1)   eval:  outdegree - popularity (sqrt)            =   0.0000
 (2)   eval:  at25 alter                               =   0.0000
 (3)   eval:  at25 ego                                 =   0.0000
 (4)   eval:  same at25                                =   0.0000
 (5)   eval:  behavior at25 average similarity         =   0.0000
__________________________________________________


Joint test:
-----------
   c =   9.9686   d.f. = 5   p-value =   0.0761


(1) tested separately:
-----------------------
 - two-sided:
  c =   1.3610   d.f. = 1  p-value =   0.2434
 - one-sided (normal variate):   1.1666
```

```
(2) tested separately:
----------------------
 - two-sided:
  c =   3.6375   d.f. = 1  p-value =   0.0565
 - one-sided (normal variate):  -1.9072

(3) tested separately:
----------------------
 - two-sided:
  c =   0.8482   d.f. = 1  p-value =   0.3570
 - one-sided (normal variate):  -0.9210

(4) tested separately:
----------------------
 - two-sided:
  c =   3.3503   d.f. = 1  p-value =   0.0672
 - one-sided (normal variate):   1.8304

(5) tested separately:
----------------------
 - two-sided:
  c =   2.1721   d.f. = 1  p-value =   0.1405
 - one-sided (normal variate):   1.4738
-------------------------------------------------

One-step estimates:

rate:  constant sim25 rate (period 1)              2.7622
rate:  constant sim25 rate (period 2)              3.1488
eval:  outdegree (density)                        -4.8520
eval:  reciprocity                                 4.7641
eval:  transitive triplets                        -0.5671
```

```
eval:  3-cycles                                        1.3316
eval:  transitive ties                                 0.2029
eval:  outdegree - popularity (sqrt)                   0.3342
eval:  at25 alter                                     -1.0687
eval:  at25 ego                                       -0.6768
eval:  same at25                                       2.2516
rate:  rate at25 (period 1)                            0.8171
rate:  rate at25 (period 2)                           -0.4792
eval:  behavior at25 linear shape                      0.2854
eval:  behavior at25 average similarity                1.7511


Total computation time 27.85 seconds.
```

There are four important sections of interest included in the output above. First, the third column in the section titled "Information for convergence diagnosis" contains t-ratios (average divided by standard deviation) for the deviations between simulated values of the statistics and the observed values. As a guideline, convergence less than 0.1 in absolute value is excellent, and less than 0.2 in absolute value is good.

The second important section, titled "Estimates and Standard Errors," contains the parameter estimates and standard errors. Rate parameters reflect the average number of unobserved changes made during that time period by an actor. The other parameters estimates are weights in the evaluation function. Standard errors are useful in testing if the parameter is significantly different than zero. The convergence and the covariance matrix values for fixed parameters are meaningless and expected. Fixing parameters that are significantly different than zero to zero should cause those parameters to have poor fit.

The third important section is the covariance matrix, used to check for collinearity among estimated parameters. Parameters that are highly collinear may not contribute unique information to the model. This collinearity check should not be used as the sole determination of effect inclusion in a model. The collinearity is a good place to look when the model starts to produce unexpected outcomes or fails to converge. As noted before, the need to remove the quadratic shape effect from the bernoulli co-evolution model but not the normal co-evolution model was discovered in the covariance matrix of the bernoulli co-evolution model.

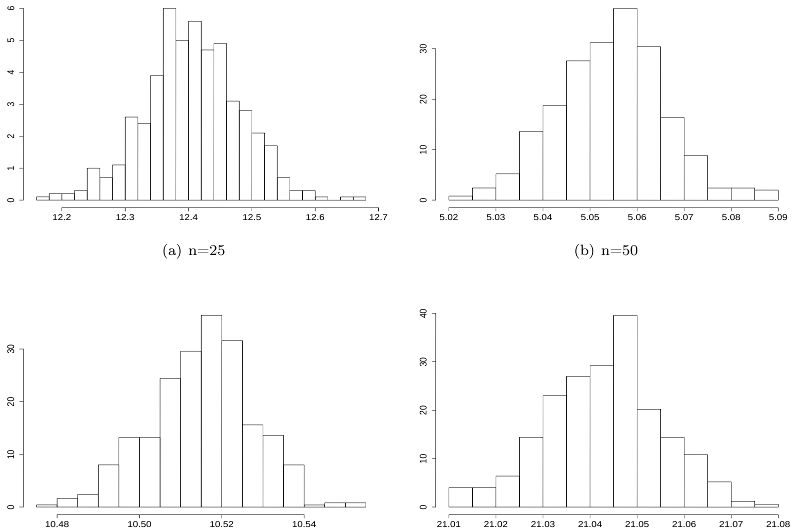
Last, the score tests are reported in the section titled "Generalised score test". An overall, joint score test provides information about the importance of including all tested parameters. Score tests for individual parameters contribute information to how much added value of each parameter. When score test values are large, the restricted model shows a large amount of misfit, implying that the parameter of interest should be included in the final model.

For the two-sided test, as the number of observations increases the distribution of the test approximates the chi-square distribution, with degrees of freedom equal to the number of restricted parameters. The one-sided test can be approximated as standard normal. A negative value for the one-sided score test implies that the parameter estimate should be negative also. One-step estimates provide approximations of what the estimates would be if the model were estimated again, but without restrictions.

B Distributions of Parameter Estimates - Certain Parameters Restricted to Equal 0

B.1 Structural Model

Three parameters were included in each model as baseline measures: rate parameter time 1, rate parameter time 2, and density.



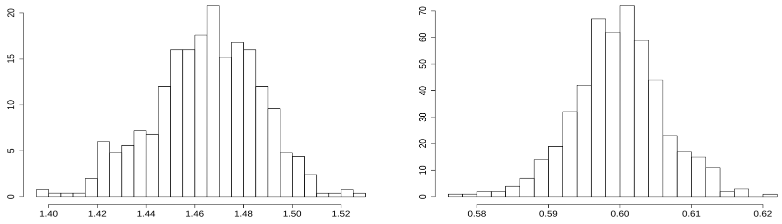
(a) n=25

(b) n=50

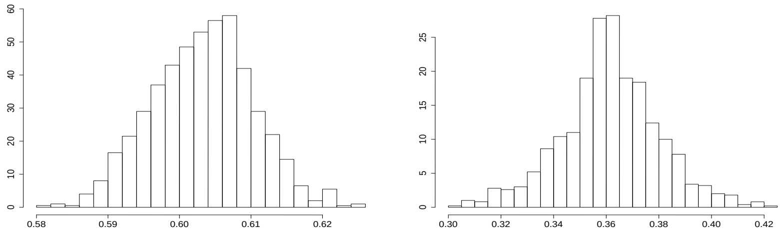
(c) n=100

(d) n=200

Figure B.1: Structural Model Score - Network Rate Time 1

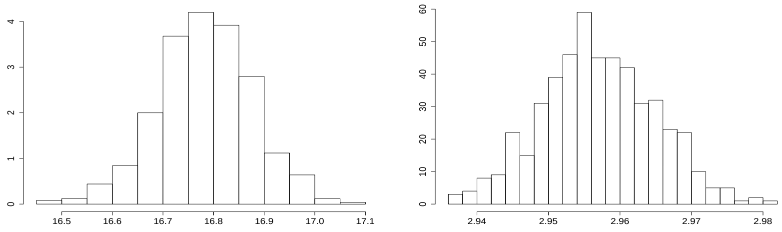


(a) n=25 (b) n=50

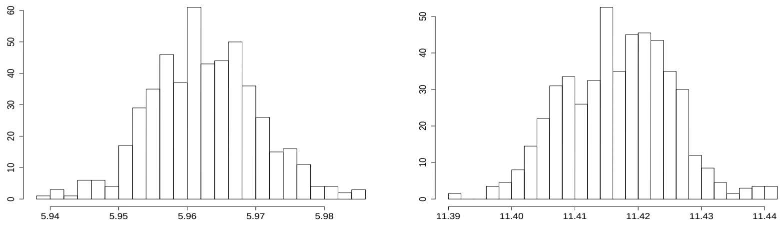


(c) n=100 (d) n=200

Figure B.2: Structural Model Score - Network Rate Time 1 SE

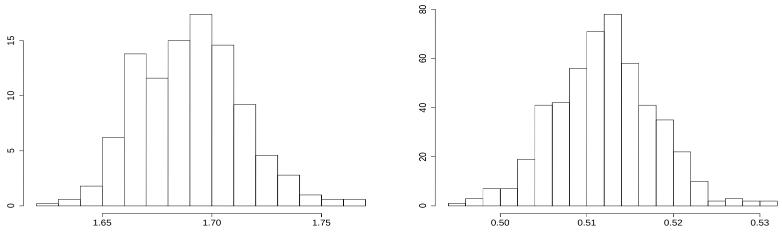


(a) n=25 (b) n=50



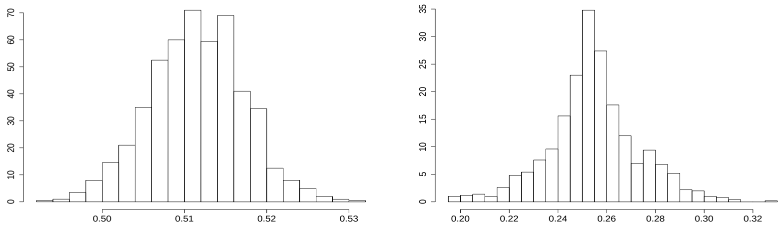
(c) n=100 (d) n=200

Figure B.3: Structural Model Score - Network Rate Time 2



(a) n=25

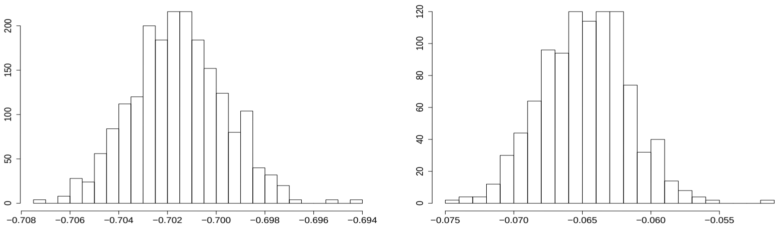
(b) n=50



(c) n=100

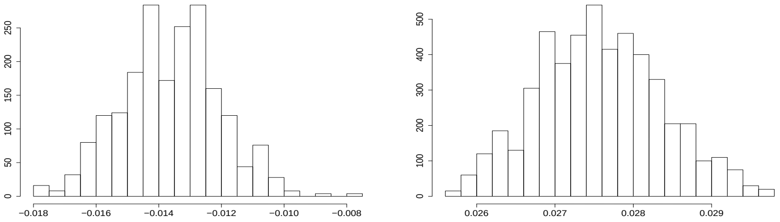
(d) n=200

Figure B.4: Structural Model Score - Network Rate Time 2 SE



(a) n=25

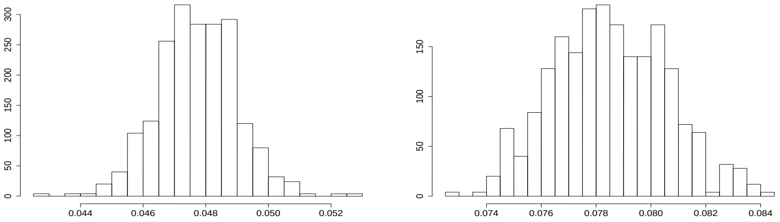
(b) n=50



(c) n=100

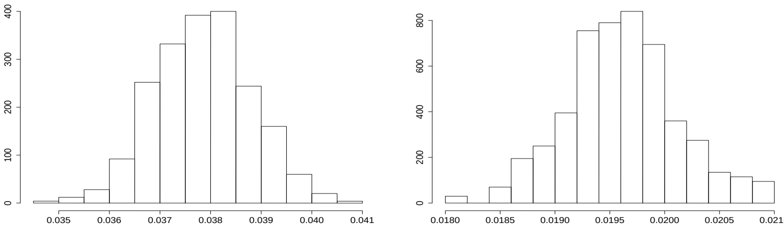
(d) n=200

Figure B.5: Structural Model Score - Density



(a) n=25

(b) n=50

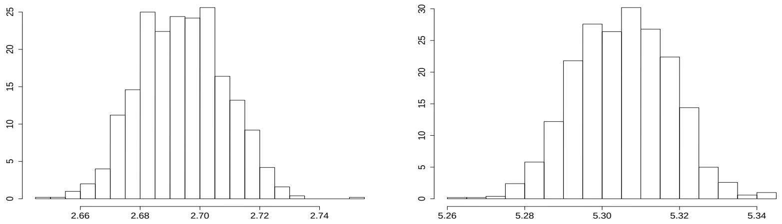


(c) n=100

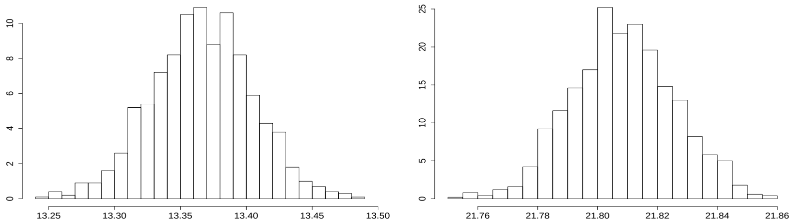
(d) n=200

Figure B.6: Structural Model Score - Density SE

B.2 Co-evolution Model - Bernoulli Attribute

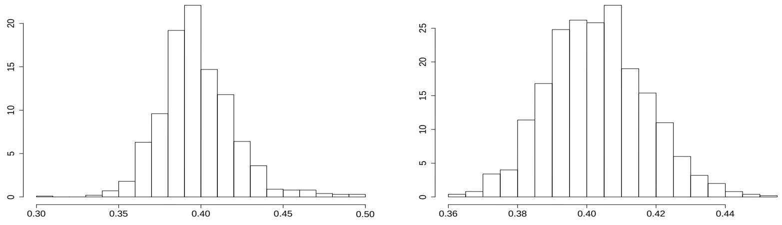


(a) n=25 (b) n=50



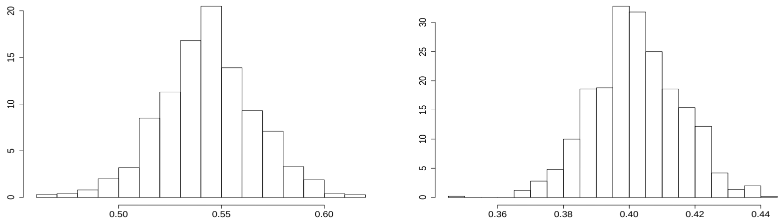
(c) n=100 (d) n=200

Figure B.7: Co-evolution Model With Bernoulli Attribute Score - Network Rate Time 1



(a) n=25

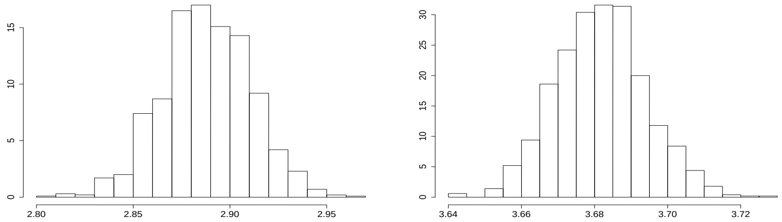
(b) n=50



(c) n=100

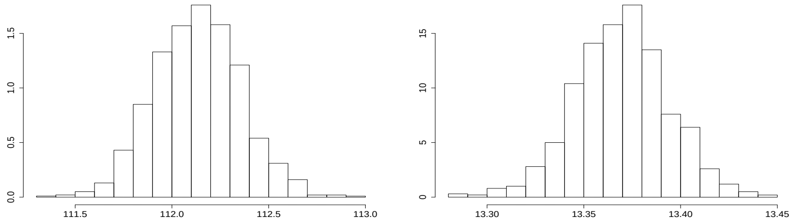
(d) n=200

Figure B.8: Co-evolution Model With Bernoulli Attribute Score - Network Rate Time 1 SE



(a) n=25

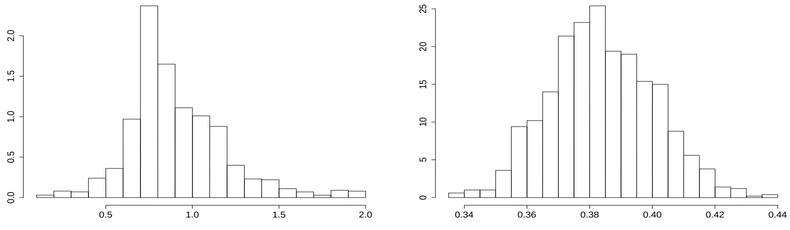
(b) n=50



(c) n=100

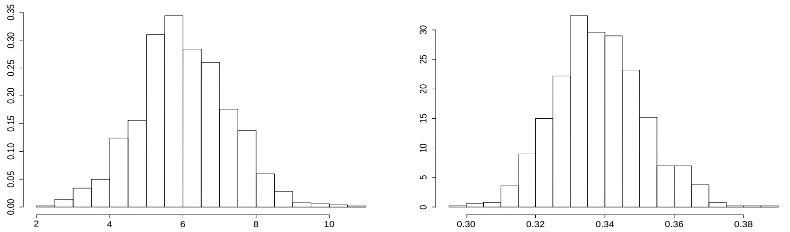
(d) n=200

Figure B.9: Co-evolution Model With Bernoulli Attribute Score - Network Rate Time 2



(a) n=25

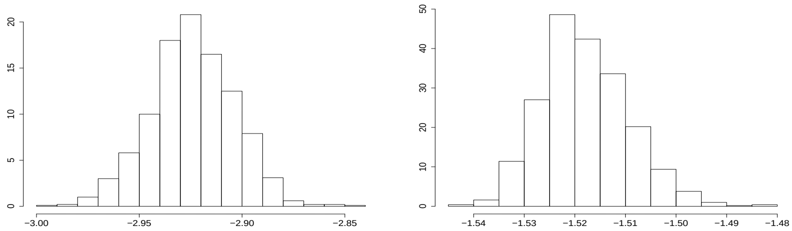
(b) n=50



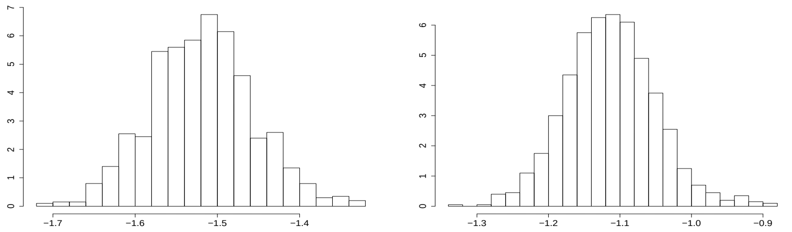
(c) n=100

(d) n=200

Figure B.10: Co-evolution Model With Bernoulli Attribute Score - Network Rate Time 2 SE

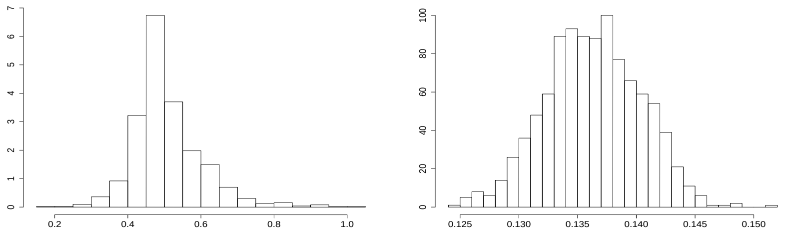


(a) n=25 (b) n=50

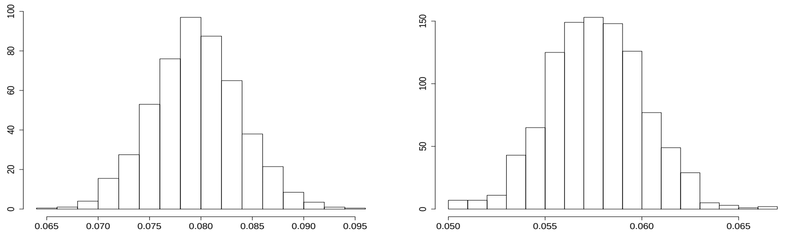


(c) n=100 (d) n=200

Figure B.11: Co-evolution Model With Bernoulli Attribute Score - Density

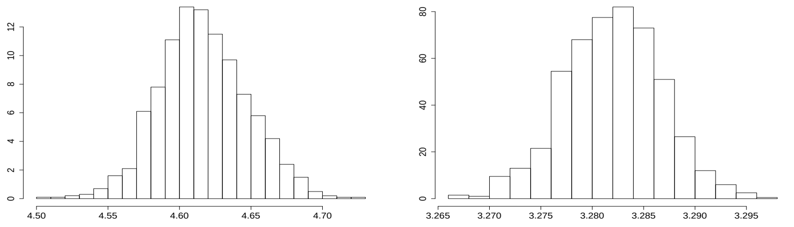


(a) n=25 (b) n=50



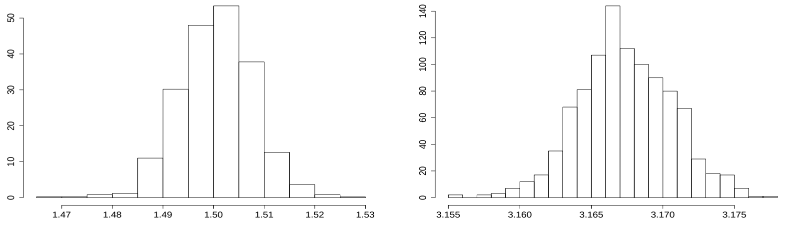
(c) n=100 (d) n=200

Figure B.12: Co-evolution Model With Bernoulli Attribute Score - Density SE



(a) n=25

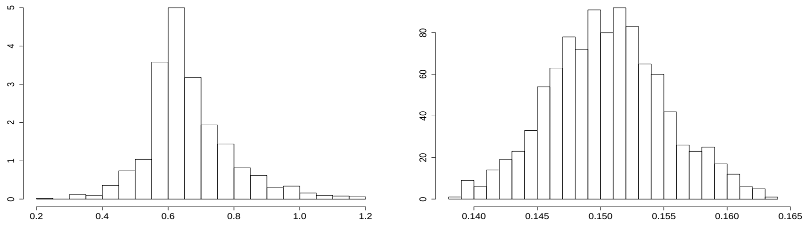
(b) n=50



(c) n=100

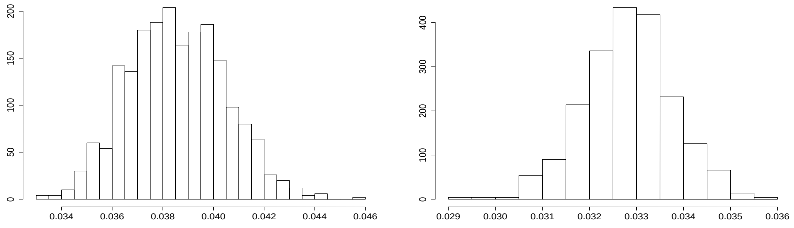
(d) n=200

Figure B.13: Co-evolution Model With Bernoulli Attribute Score - Reciprocity



(a) n=25

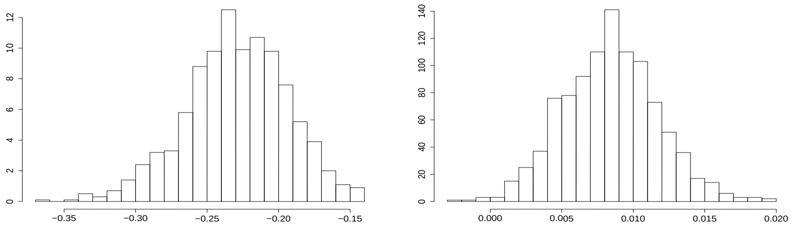
(b) n=50



(c) n=100

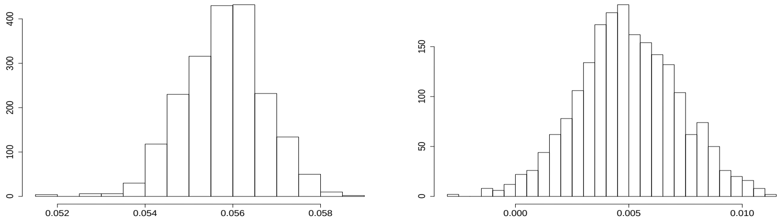
(d) n=200

Figure B.14: Co-evolution Model With Bernoulli Attribute Score - Reciprocity SE



(a) n=25

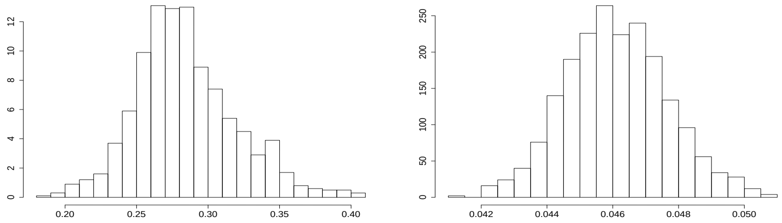
(b) n=50



(c) n=100

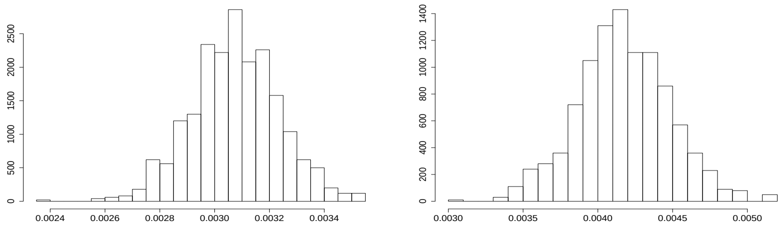
(d) n=200

Figure B.15: Co-evolution Model With Bernoulli Attribute Score - Transitive Triplet



(a) n=25

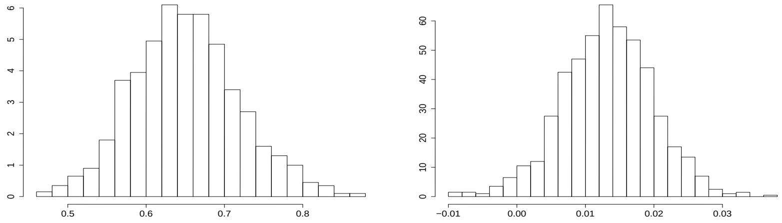
(b) n=50



(c) n=100

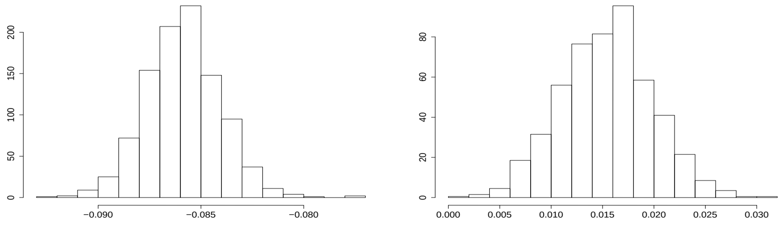
(d) n=200

Figure B.16: Co-evolution Model With Bernoulli Attribute Score - Transitive Triplet SE



(a) n=25

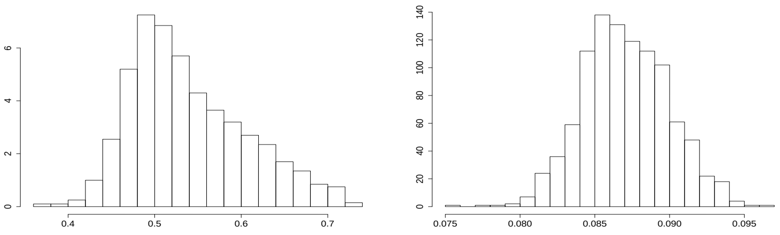
(b) n=50



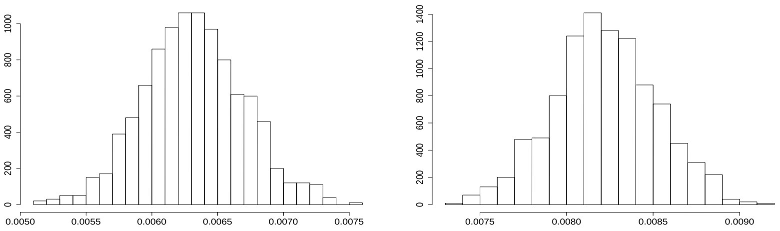
(c) n=100

(d) n=200

Figure B.17: Co-evolution Model With Bernoulli Attribute Score - 3-cycles

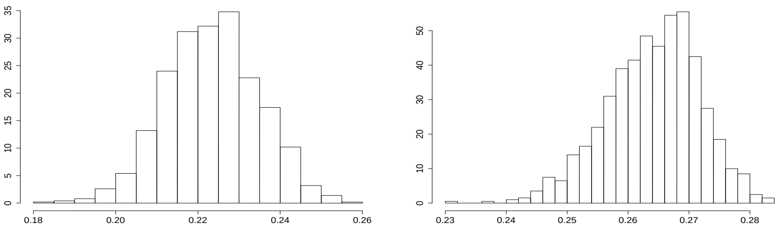


(a) n=25 (b) n=50

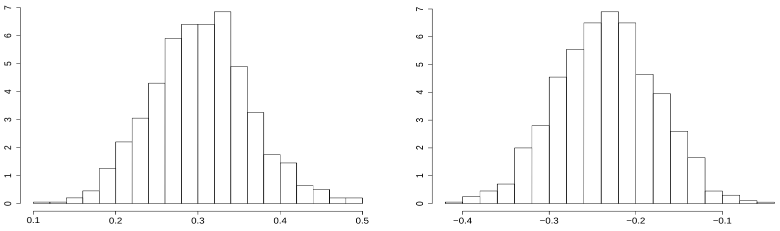


(c) n=100 (d) n=200

Figure B.18: Co-evolution Model With Bernoulli Attribute Score - 3-cycles SE

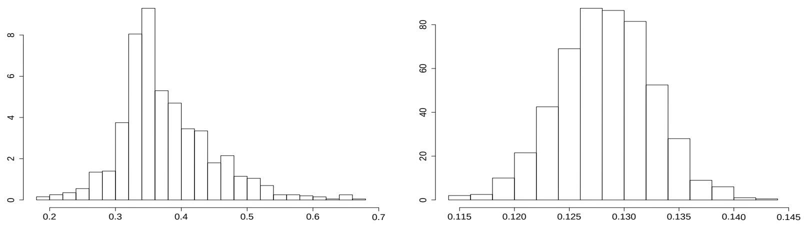


(a) n=25 (b) n=50

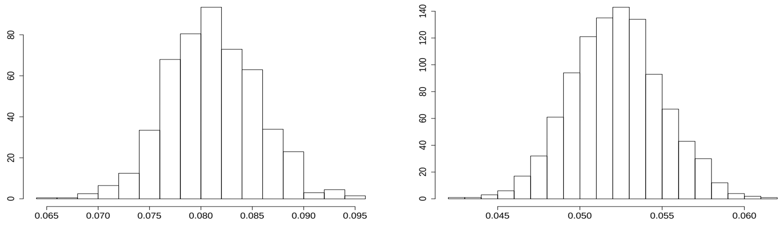


(c) n=100 (d) n=200

Figure B.19: Co-evolution Model With Bernoulli Attribute Score - Transitive Ties

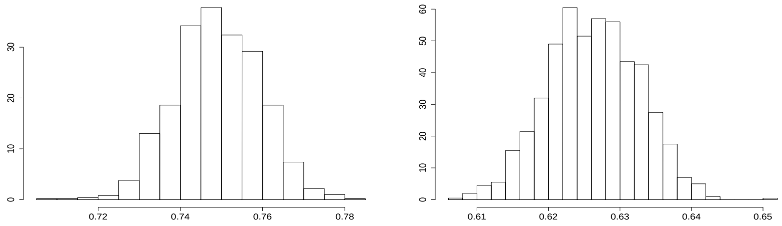


(a) n=25 (b) n=50

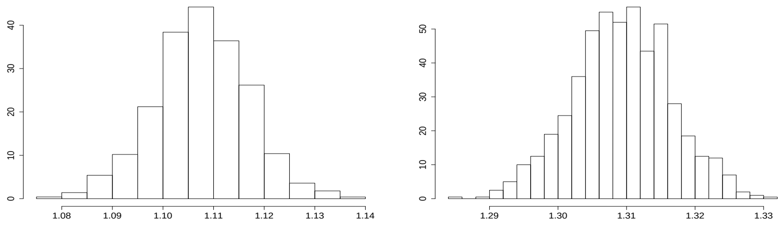


(c) n=100 (d) n=200

Figure B.20: Co-evolution Model With Bernoulli Attribute Score - Transitive Ties SE

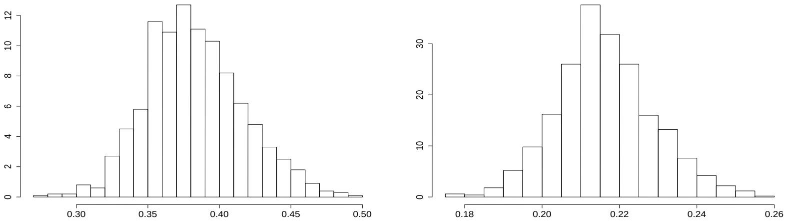


(a) n=25 (b) n=50



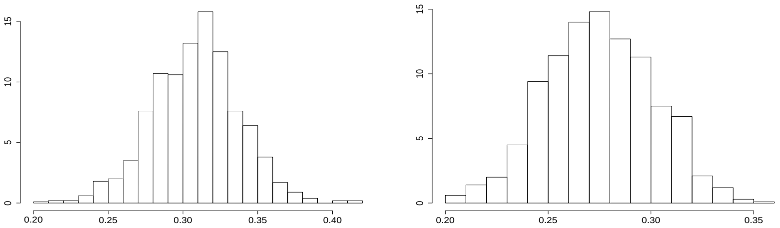
(c) n=100 (d) n=200

Figure B.21: Co-evolution Model With Bernoulli Attribute Score - Attribute Rate Time 1



(a) n=25

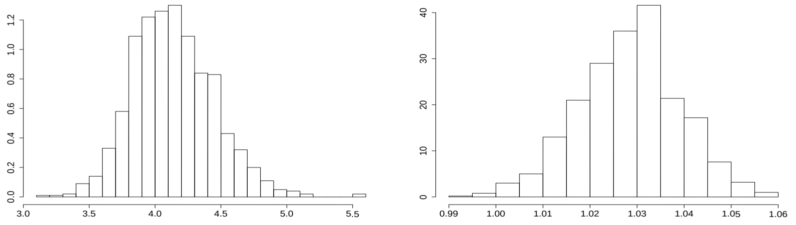
(b) n=50



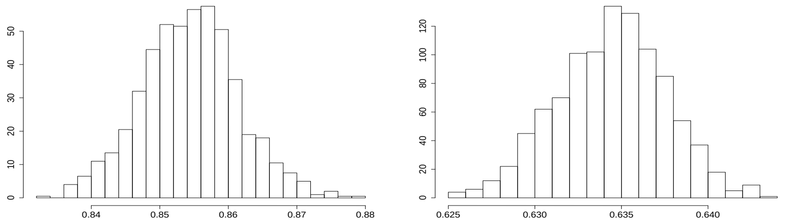
(c) n=100

(d) n=200

Figure B.22: Co-evolution Model With Bernoulli Attribute Score - Attribute Rate Time 1 SE

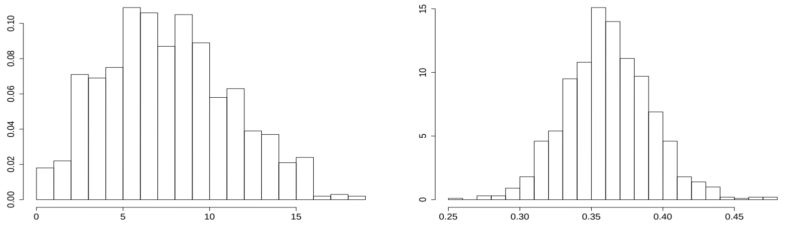


(a) n=25 (b) n=50

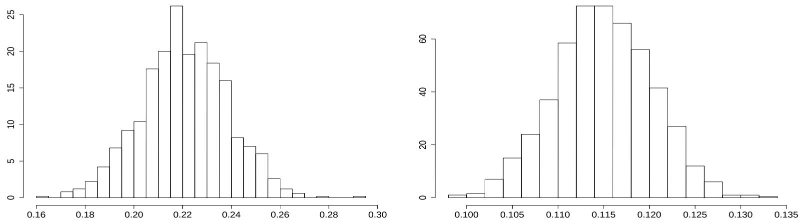


(c) n=100 (d) n=200

Figure B.23: Co-evolution Model With Bernoulli Attribute Score - Attribute Rate Time 2

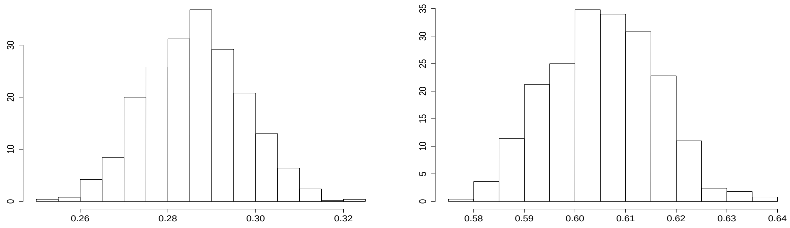


(a) n=25 (b) n=50

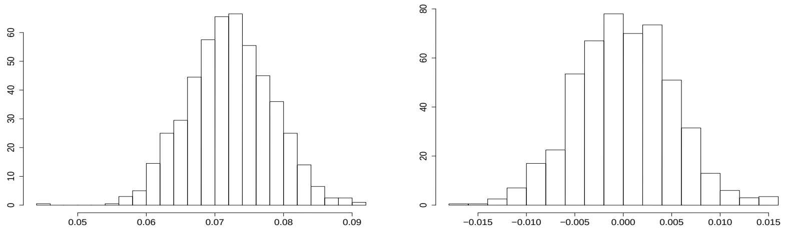


(c) n=100 (d) n=200

Figure B.24: Co-evolution Model With Bernoulli Attribute Score - Attribute Rate Time 2 SE

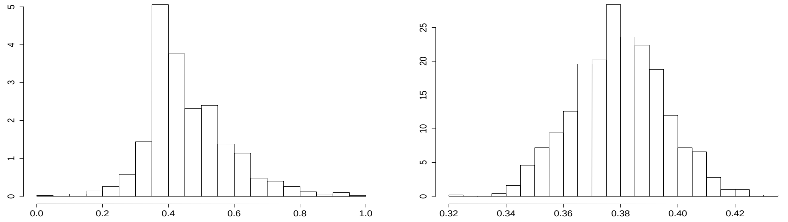


(a) n=25 (b) n=50

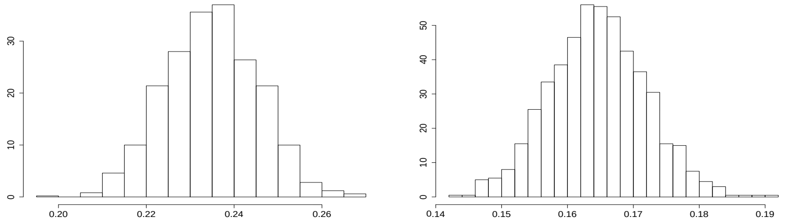


(c) n=100 (d) n=200

Figure B.25: Co-evolution Model With Bernoulli Attribute Score - Linear Shape

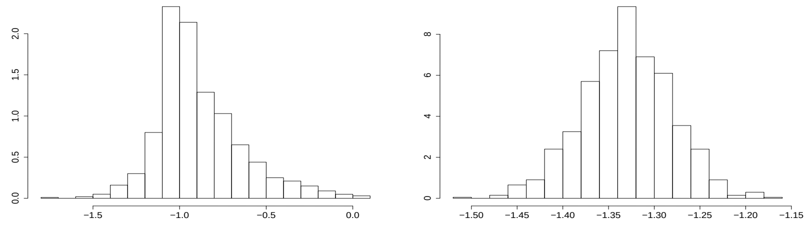


(a) n=25 (b) n=50

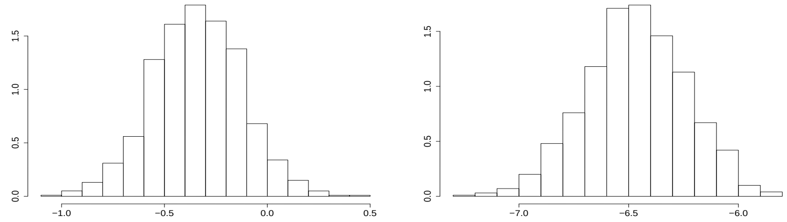


(c) n=100 (d) n=200

Figure B.26: Co-evolution Model With Bernoulli Attribute Score - Linear Shape SE

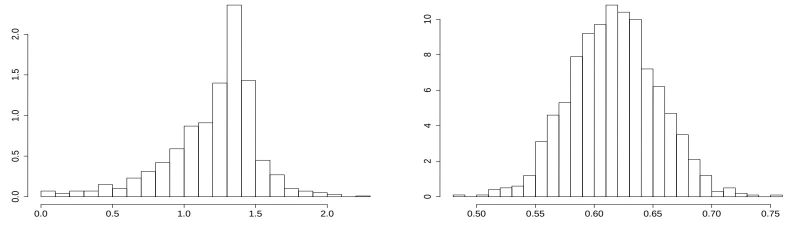


(a) n=25 (b) n=50

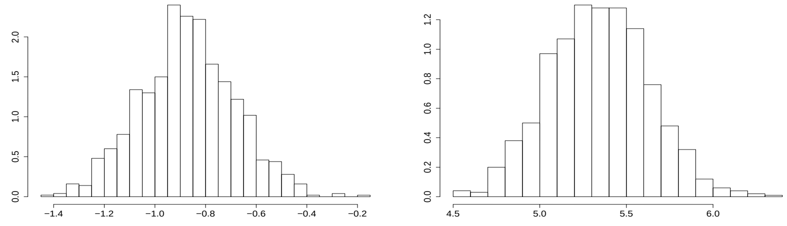


(c) n=100 (d) n=200

Figure B.27: Co-evolution Model With Bernoulli Attribute - Attribute Ego Score Test - one sided

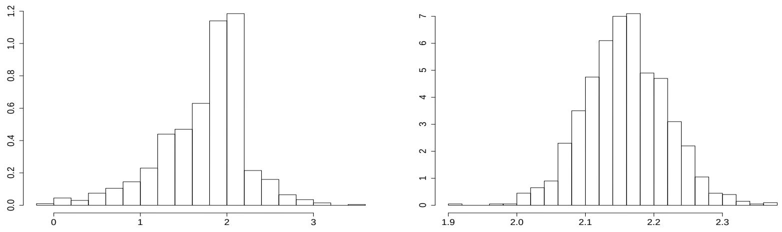


(a) n=25 (b) n=50

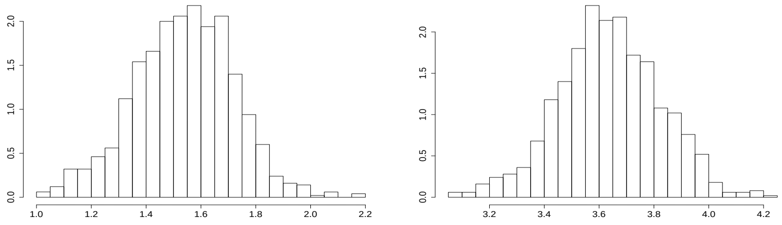


(c) n=100 (d) n=200

Figure B.28: Co-evolution Model With Bernoulli Attribute - Outdegree-Popularity (Square Root) Score Test - one sided



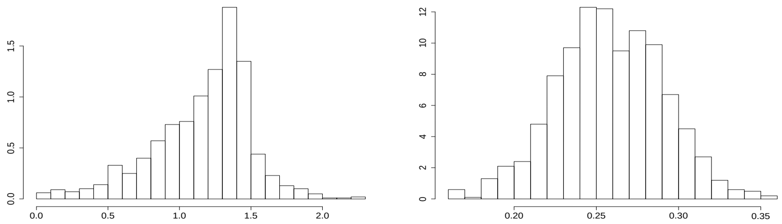
(a) n=25 (b) n=50



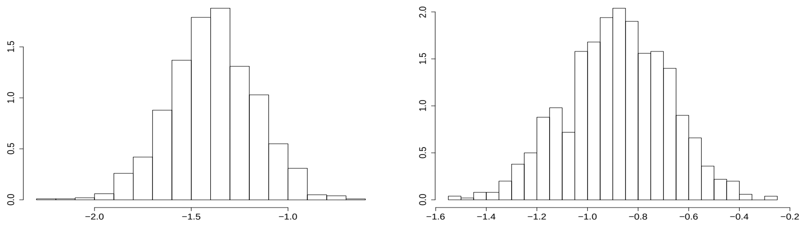
(c) n=100 (d) n=200

Figure B.29: Co-evolution Model With Bernoulli Attribute - Same Attribute Score Test - one sided

B.3 Co-evolution Model With Normal $(\mu = 3, \sigma = 1)$ Attribute

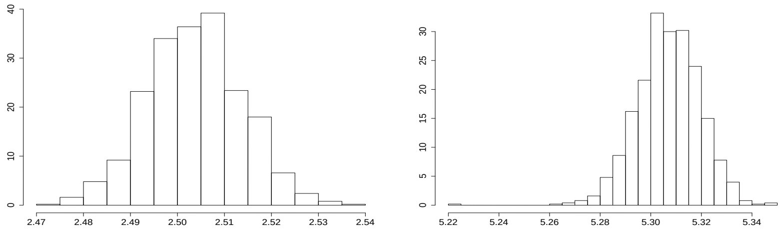


(a) n=25 (b) n=50

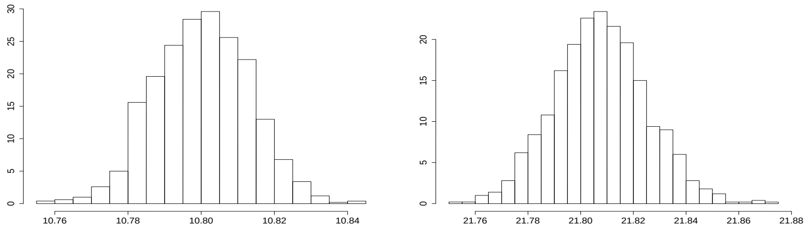


(c) n=100 (d) n=200

Figure B.30: Co-evolution Model With Bernoulli Attribute - Average Similarity Score Test - one sided

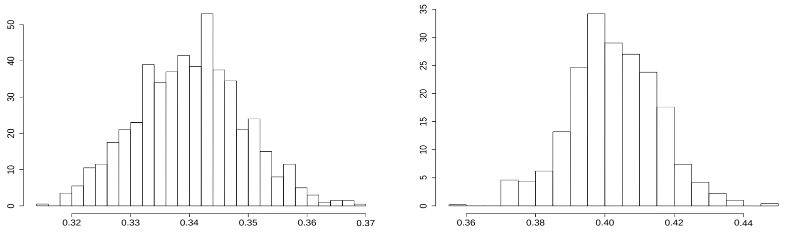


(a) n=25 (b) n=50



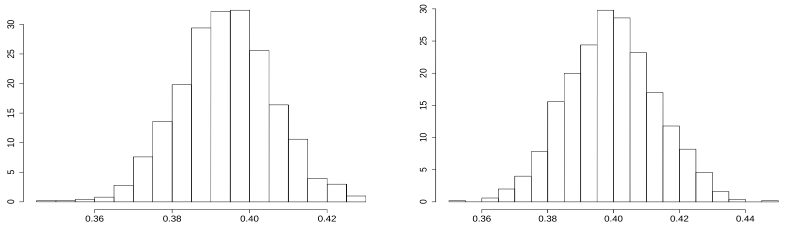
(c) n=100 (d) n=200

Figure B.31: Co-evolution Model With Normal Attribute Score - Network Rate Time 1



(a) n=25

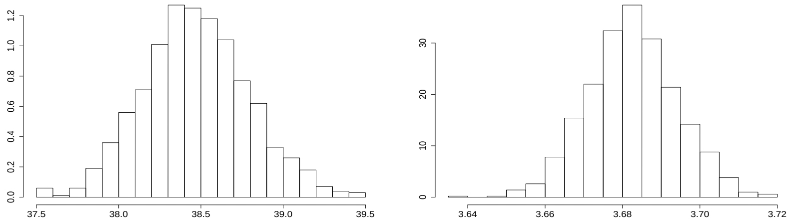
(b) n=50



(c) n=100

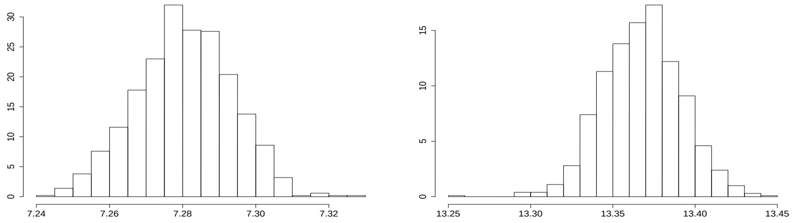
(d) n=200

Figure B.32: Co-evolution Model With Normal Attribute Score - Network Rate Time 1 SE



(a) n=25

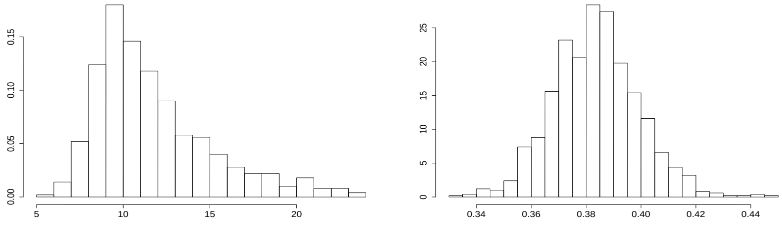
(b) n=50



(c) n=100

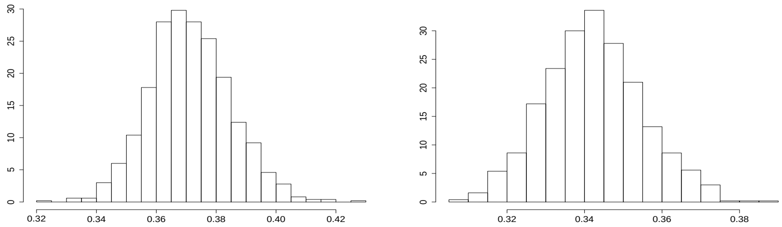
(d) n=200

Figure B.33: Co-evolution Model With Normal Attribute Score - Network Rate Time 2



(a) n=25

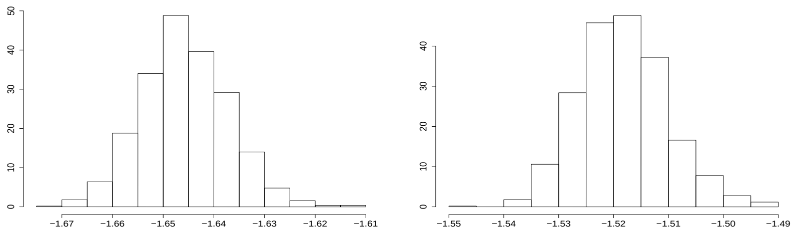
(b) n=50



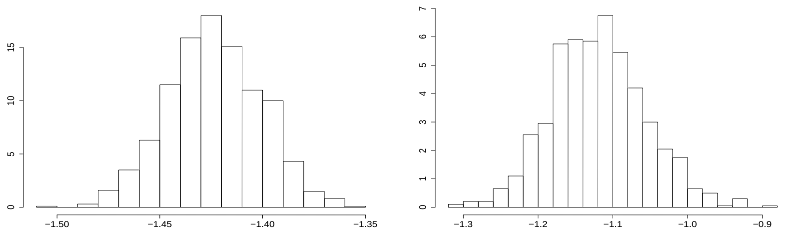
(c) n=100

(d) n=200

Figure B.34: Co-evolution Model With Normal Attribute Score - Network Rate Time 2 SE

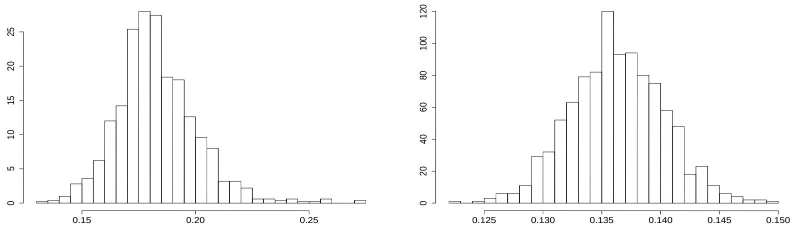


(a) n=25 (b) n=50

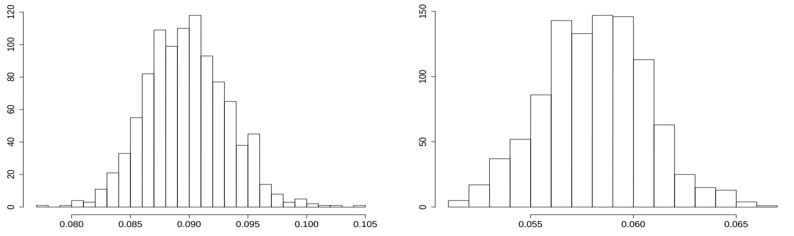


(c) n=100 (d) n=200

Figure B.35: Co-evolution Model With Normal Attribute Score - Density

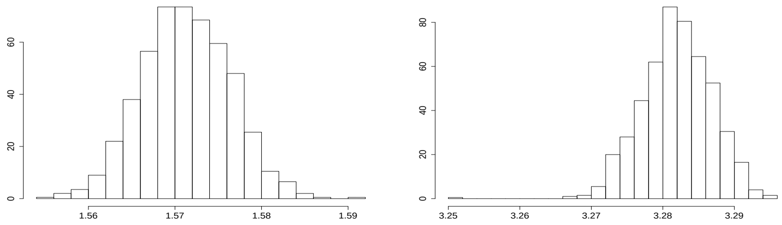


(a) n=25 (b) n=50

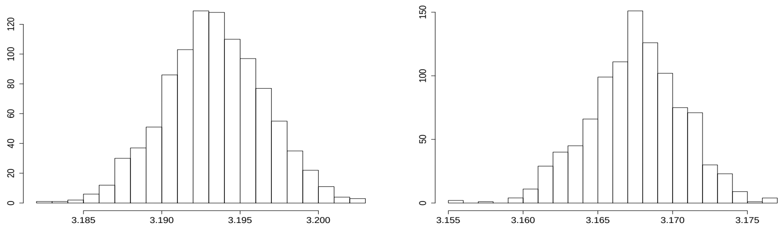


(c) n=100 (d) n=200

Figure B.36: Co-evolution Model With Normal Attribute Score - Density SE

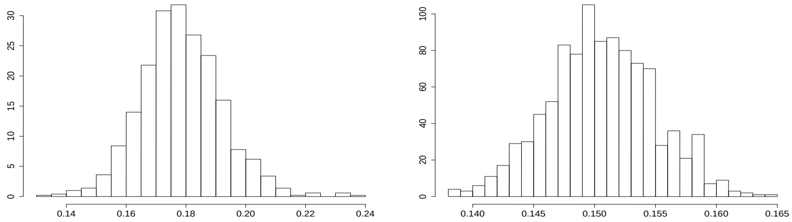


(a) n=25 (b) n=50

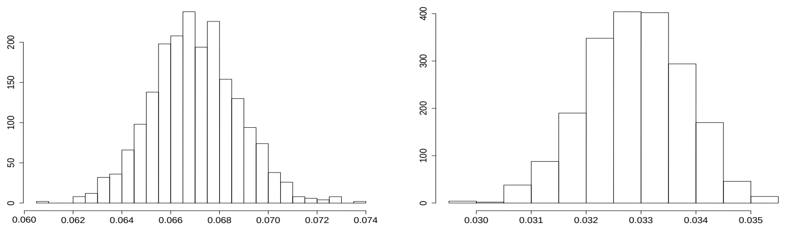


(c) n=100 (d) n=200

Figure B.37: Co-evolution Model With Normal Attribute Score - Reciprocity

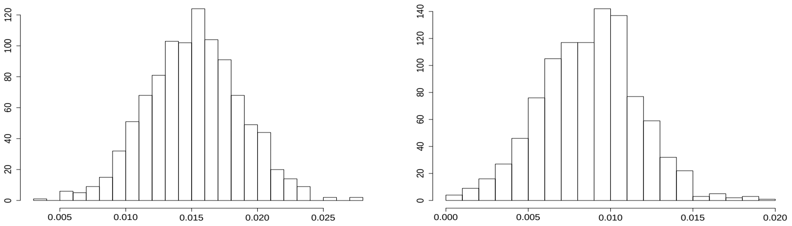


(a) n=25 (b) n=50



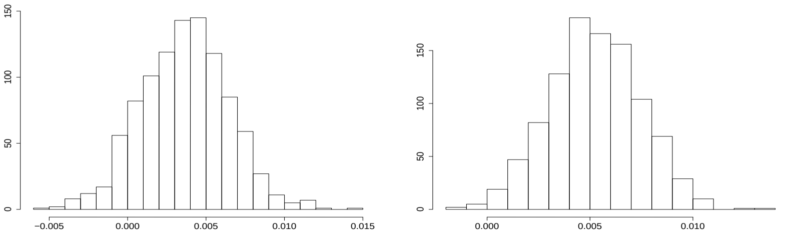
(c) n=100 (d) n=200

Figure B.38: Co-evolution Model With Normal Attribute Score - Reciprocity SE



(a) n=25

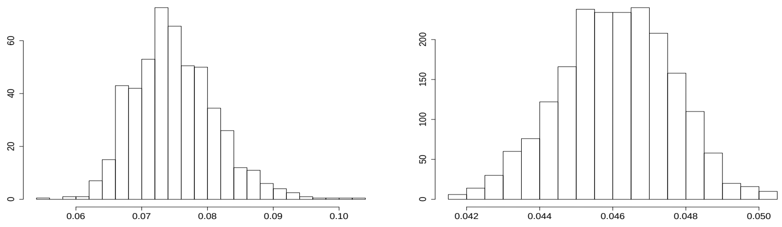
(b) n=50



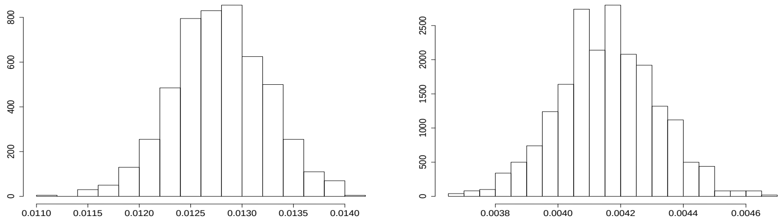
(c) n=100

(d) n=200

Figure B.39: Co-evolution Model With Normal Attribute Score - Transitive Triplet

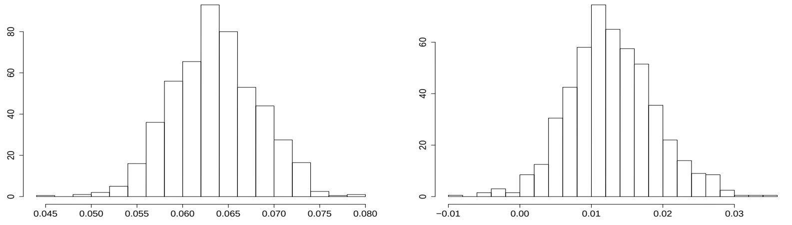


(a) n=25 (b) n=50

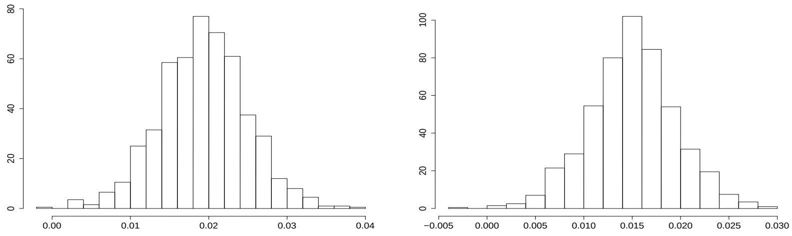


(c) n=100 (d) n=200

Figure B.40: Co-evolution Model With Normal Attribute Score - Transitive Triplet SE

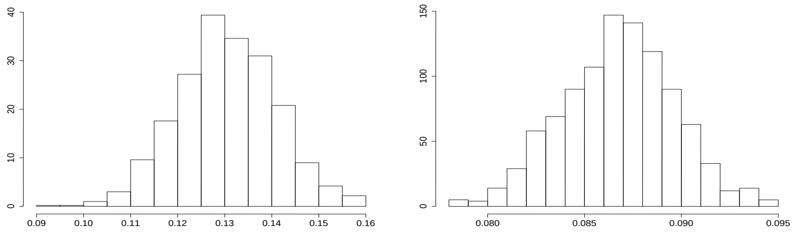


(a) n=25 (b) n=50

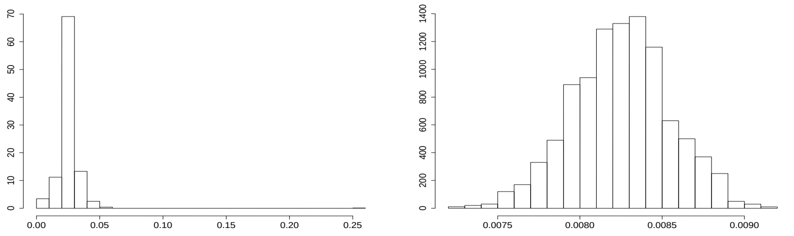


(c) n=100 (d) n=200

Figure B.41: Co-evolution Model With Normal Attribute Score - 3-cycles

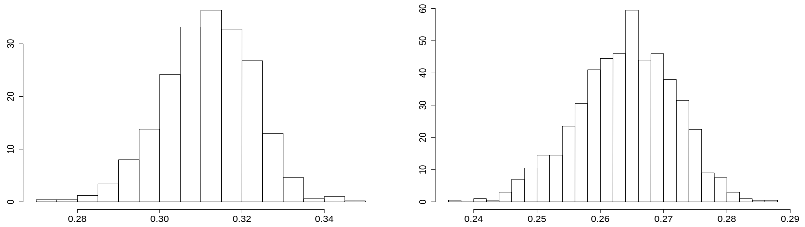


(a) n=25 (b) n=50

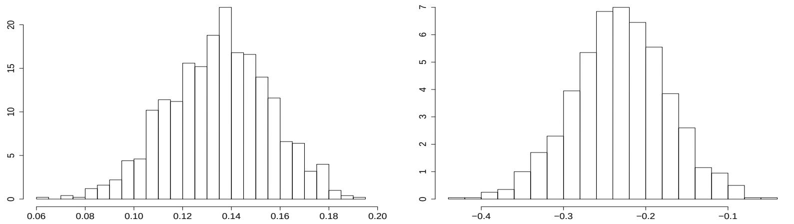


(c) n=100 (d) n=200

Figure B.42: Co-evolution Model With Normal Attribute Score - 3-cycles SE

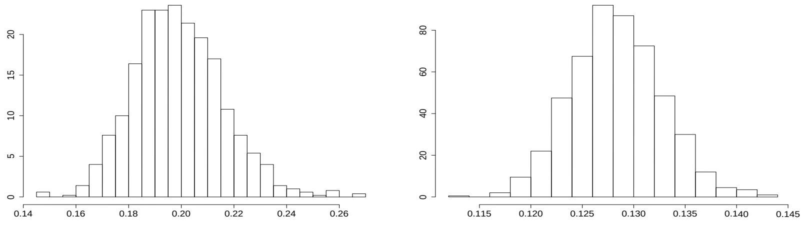


(a) n=25 (b) n=50



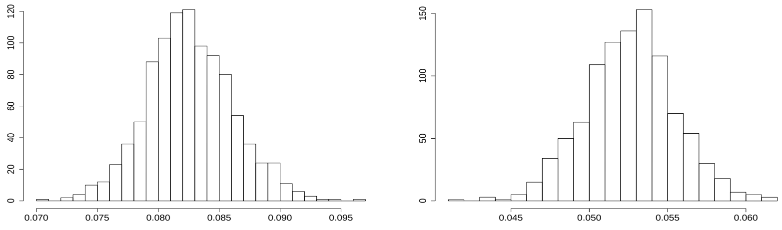
(c) n=100 (d) n=200

Figure B.43: Co-evolution Model With Normal Attribute Score - Transitive Ties



(a) n=25

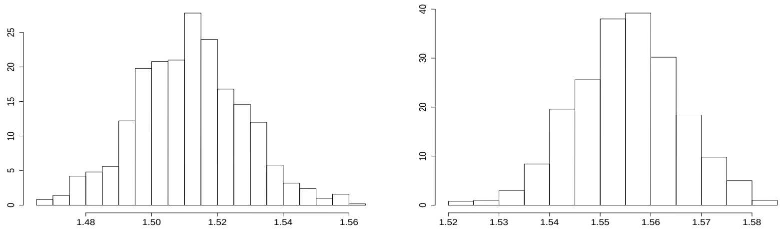
(b) n=50



(c) n=100

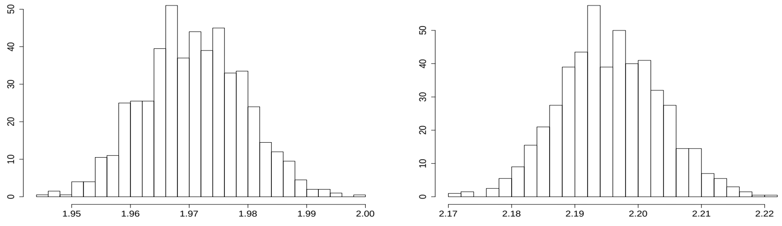
(d) n=200

Figure B.44: Co-evolution Model With Normal Attribute Score - Transitive Ties SE



(a) n=25

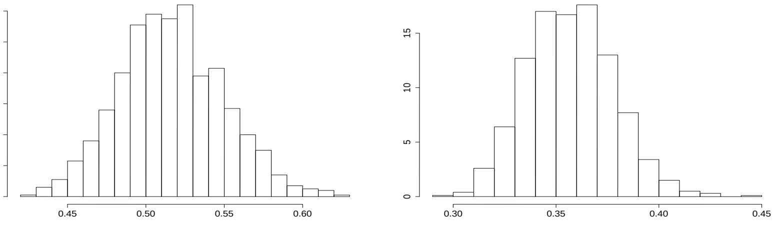
(b) n=50



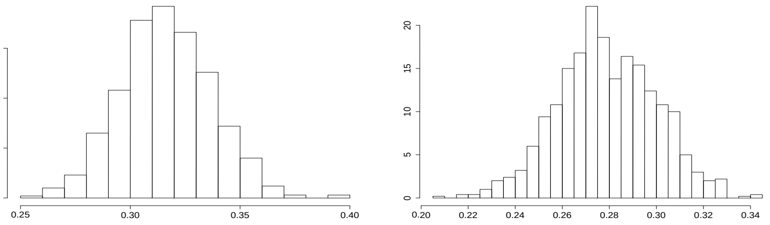
(c) n=100

(d) n=200

Figure B.45: Co-evolution Model With Normal Attribute Score - Attribute Rate Time 1

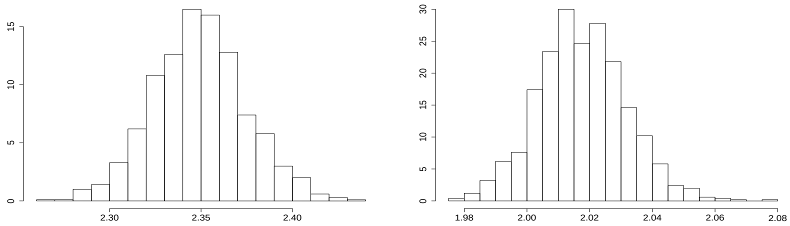


(a) n=25 (b) n=50

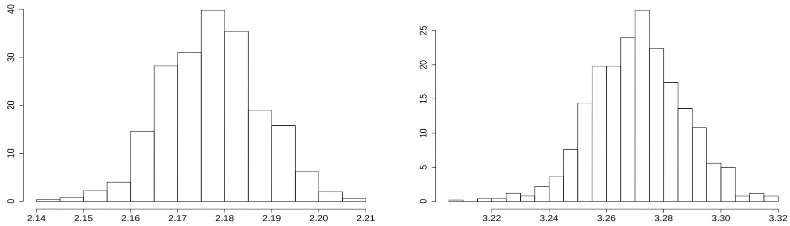


(c) n=100 (d) n=200

Figure B.46: Co-evolution Model With Normal Attribute Score - Attribute Rate Time 1 SE

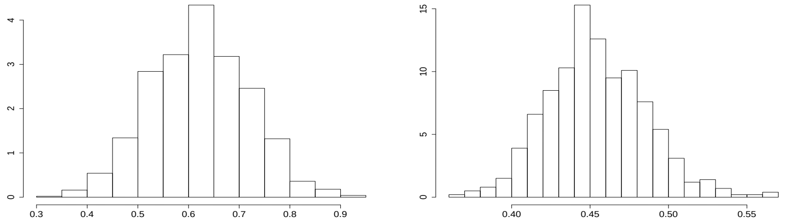


(a) n=25 (b) n=50

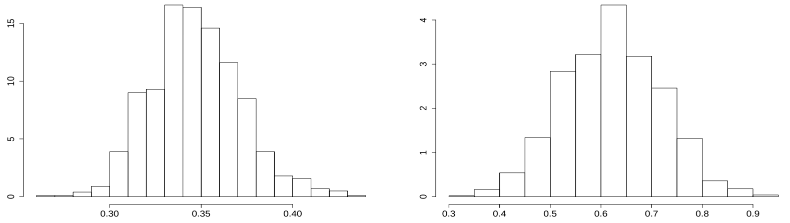


(c) n=100 (d) n=200

Figure B.47: Co-evolution Model With Normal Attribute Score - Attribute Rate Time 2

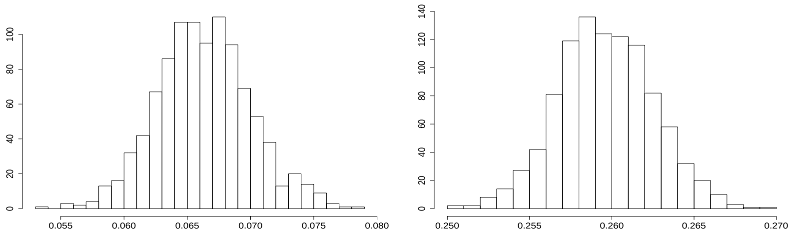


(a) n=25 (b) n=50



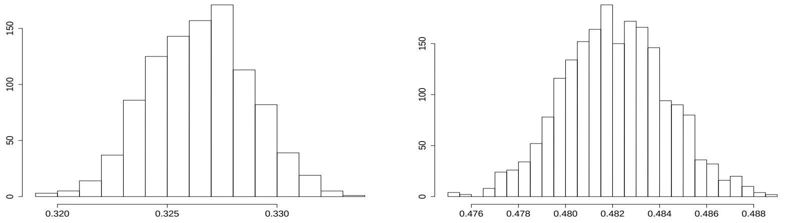
(c) n=100 (d) n=200

Figure B.48: Co-evolution Model With Normal Attribute Score - Attribute Rate Time 2 SE



(a) n=25

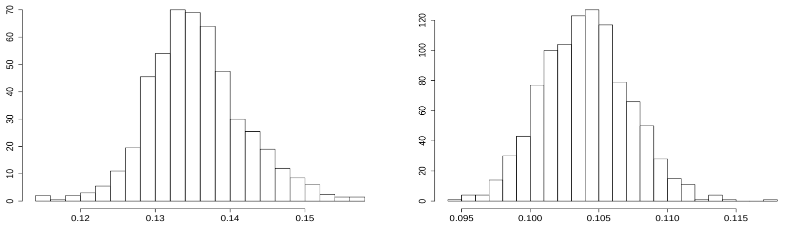
(b) n=50



(c) n=100

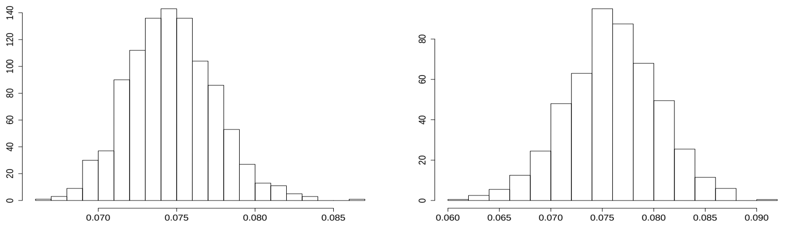
(d) n=200

Figure B.49: Co-evolution Model With Normal Attribute Score - Linear Shape



(a) n=25

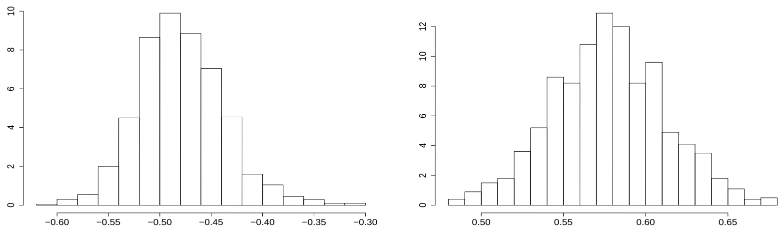
(b) n=50



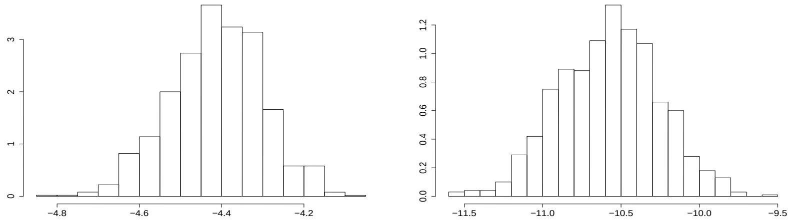
(c) n=100

(d) n=200

Figure B.50: Co-evolution Model With Normal Attribute Score - Linear Shape SE

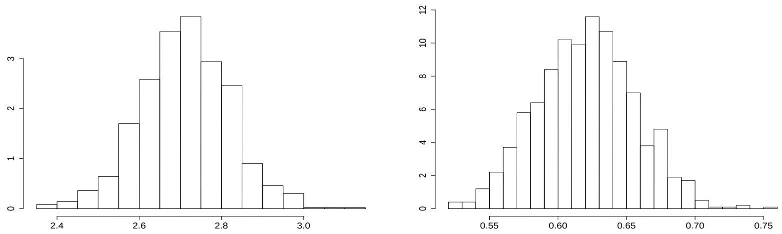


(a) n=25 (b) n=50

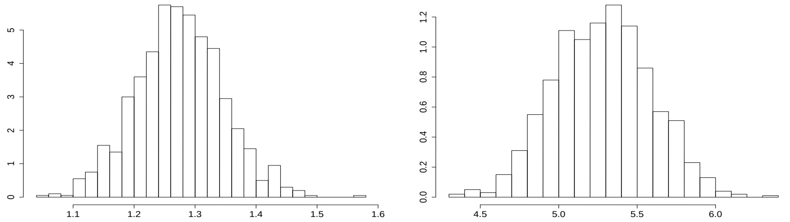


(c) n=100 (d) n=200

Figure B.51: Co-evolution Model With Normal Attribute - Attribute Ego Score Test - one sided

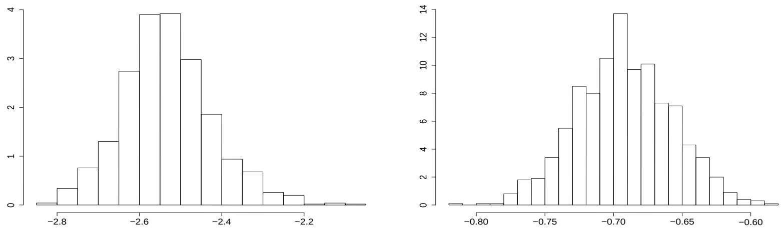


(a) n=25 (b) n=50

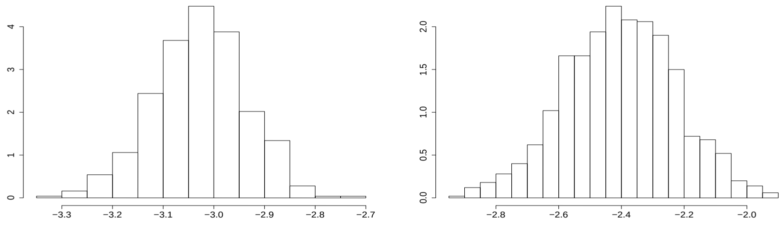


(c) n=100 (d) n=200

Figure B.52: Co-evolution Model With Normal Attribute - Outdegree-Popularity (Square Root) Score Test - one sided

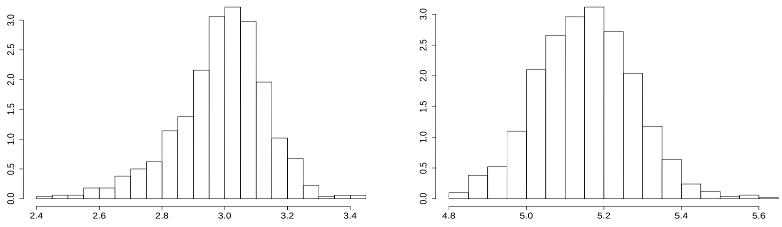


(a) n=25 (b) n=50

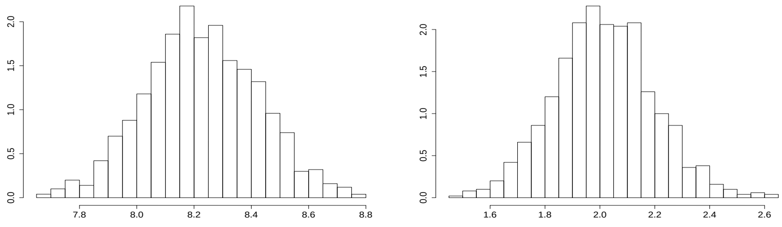


(c) n=100 (d) n=200

Figure B.53: Co-evolution Model With Normal Attribute - Same Attribute Score Test - one sided



(a) n=25 (b) n=50

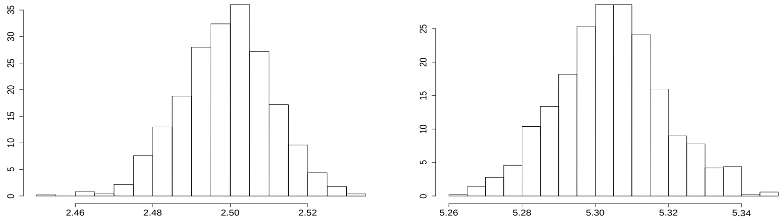


(c) n=100 (d) n=200

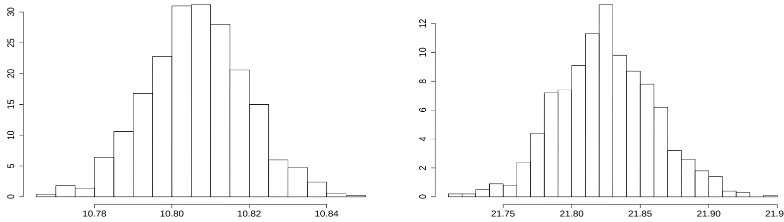
Figure B.54: Co-evolution Model With Normal Attribute - Average Similarity Score Test - one sided

C Distributions of Parameter Estimates For Full Model - All Parameters Allowed To Vary - Pseudo-Wald and Entropy Tests

C.1 Structural Model

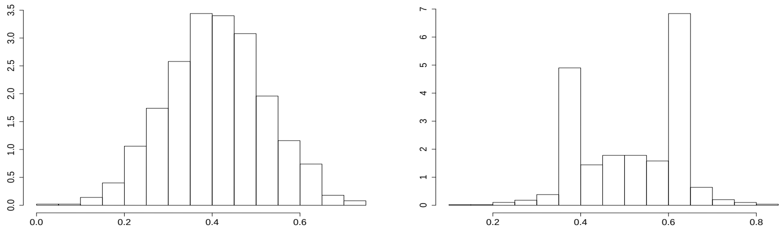


(a) n=25 (b) n=50

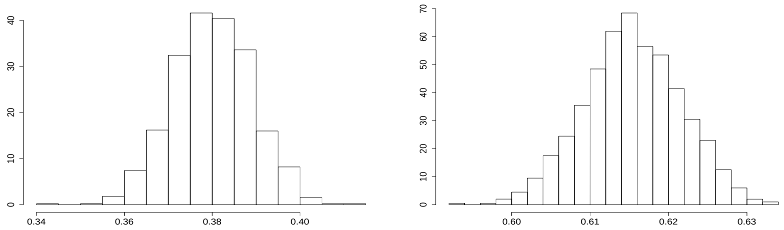


(c) n=100 (d) n=200

Figure C.1: Structural Model Pseudo-Wald and Entropy Tests - Network Rate Time 1

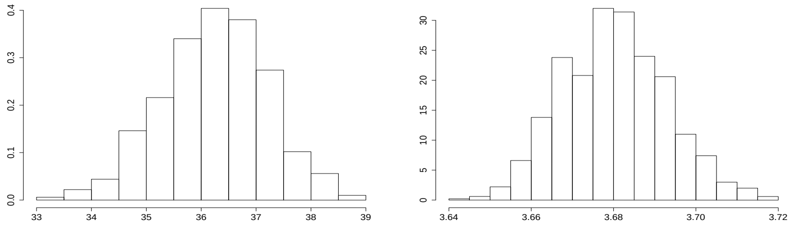


(a) n=25 (b) n=50



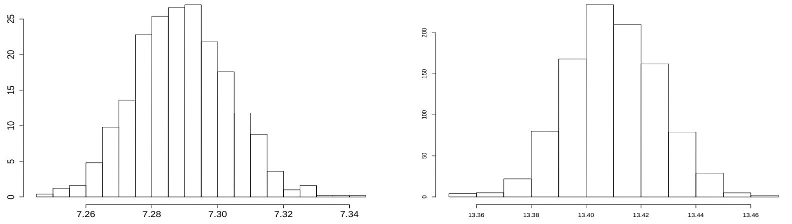
(c) n=100 (d) n=200

Figure C.2: Structural Model Pseudo-Wald and Entropy Tests - Network Rate Time 1 SE



(a) n=25

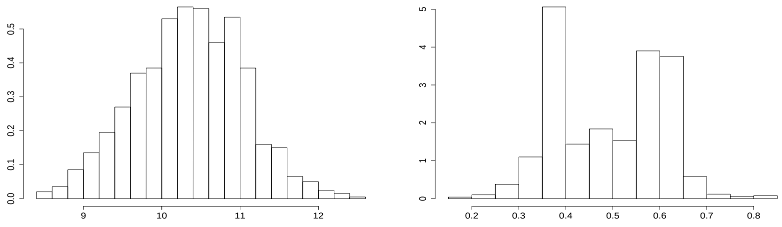
(b) n=50



(c) n=100

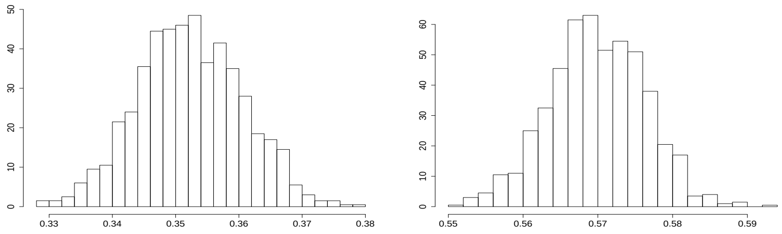
(d) n=200

Figure C.3: Structural Model Pseudo-Wald and Entropy Tests - Network Rate Time 2



(a) n=25

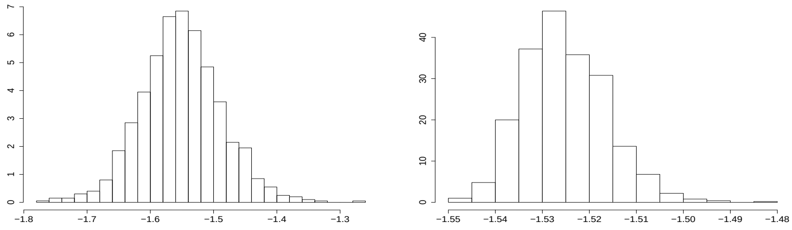
(b) n=50



(c) n=100

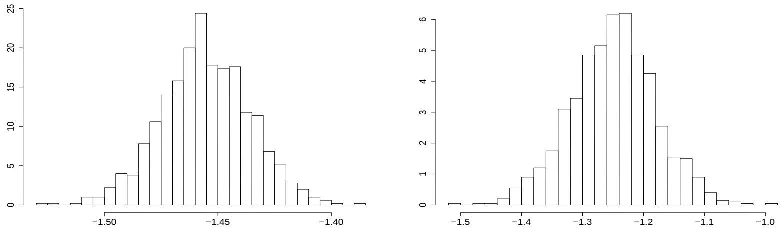
(d) n=200

Figure C.4: Structural Model Pseudo-Wald and Entropy Tests - Network Rate Time 2 SE



(a) n=25

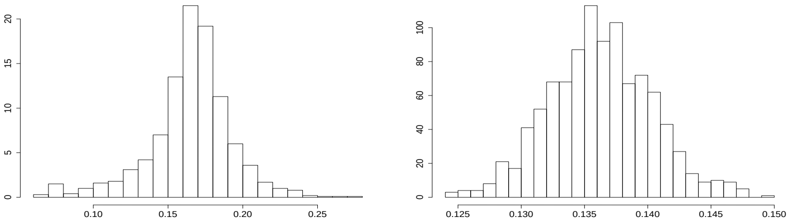
(b) n=50



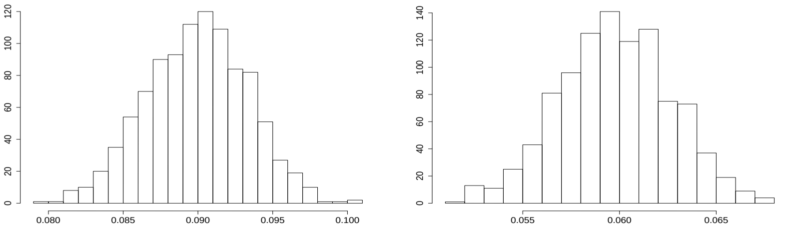
(c) n=100

(d) n=200

Figure C.5: Structural Model Pseudo-Wald and Entropy Tests - Density

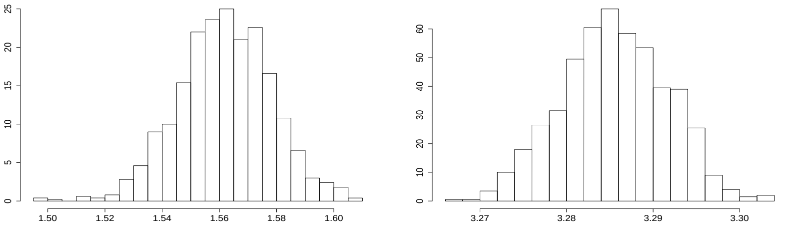


(a) n=25 (b) n=50

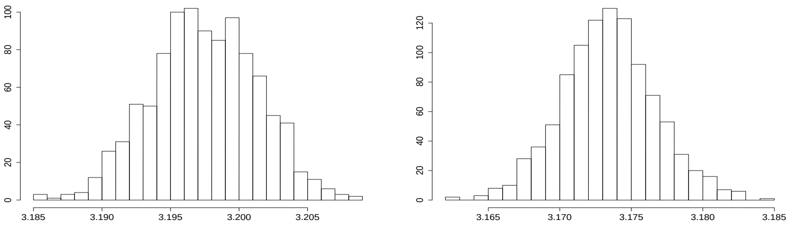


(c) n=100 (d) n=200

Figure C.6: Structural Model Pseudo-Wald and Entropy Tests - Density SE

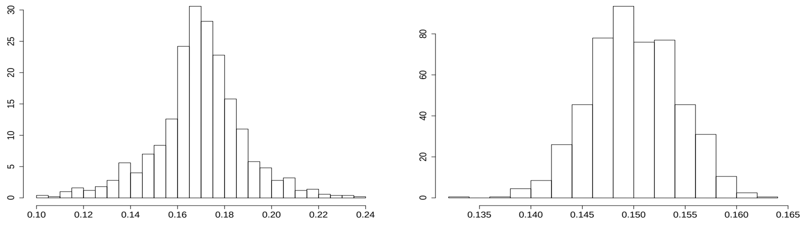


(a) n=25 (b) n=50



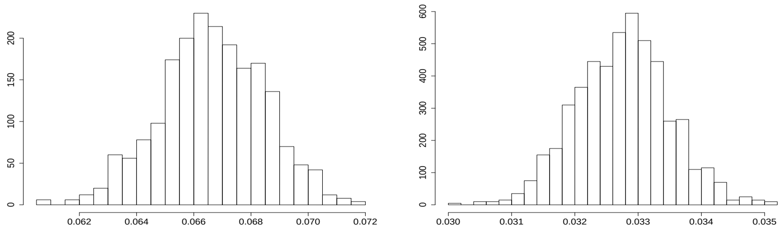
(c) n=100 (d) n=200

Figure C.7: Structural Model Pseudo-Wald and Entropy Tests - Reciprocity



(a) n=25

(b) n=50



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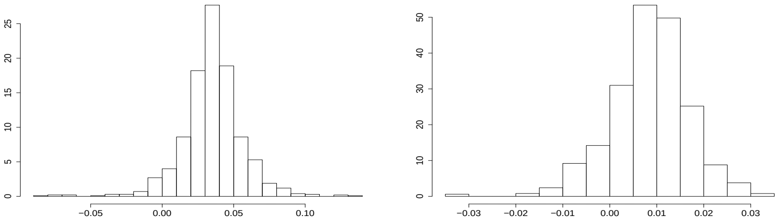
(d) n=200

Figure C.8: Structural Model Pseudo-Wald and Entropy Tests - Reciprocity SE



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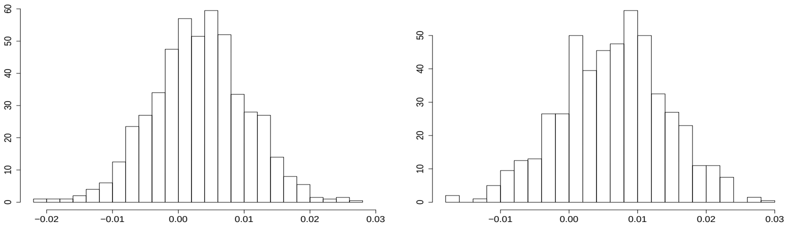

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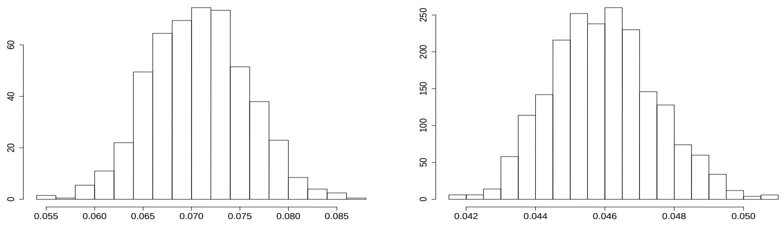
Figure C.9: Structural Model Pseudo-Wald and Entropy Tests - Transitive Triplets

C.2 Co-evolution Model With Bernoulli Attribute



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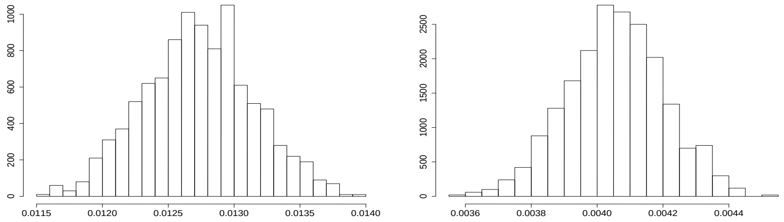
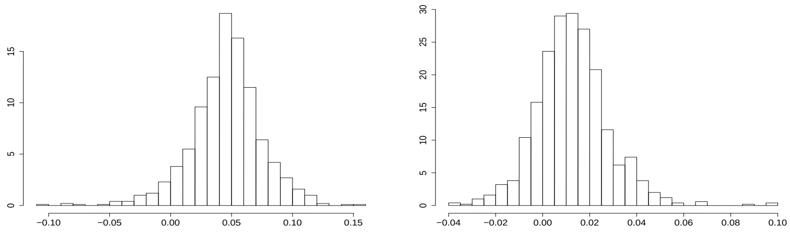


(c) n=100 (d) n=200

Figure C.10: Structural Model Pseudo-Wald and Entropy Tests - Transitive Triplets SE



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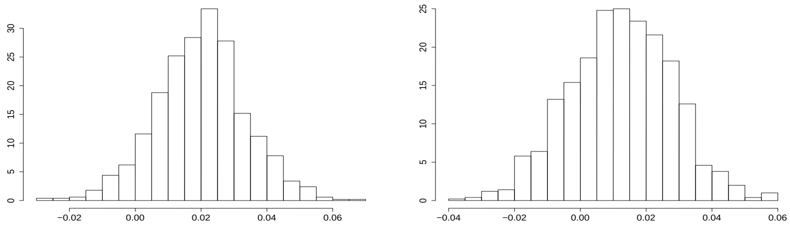

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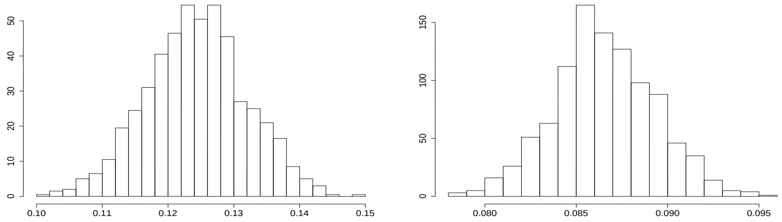
Figure C.11: Structural Model Pseudo-Wald and Entropy Tests - 3 Cycles



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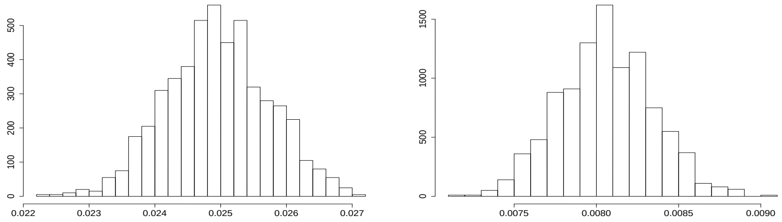

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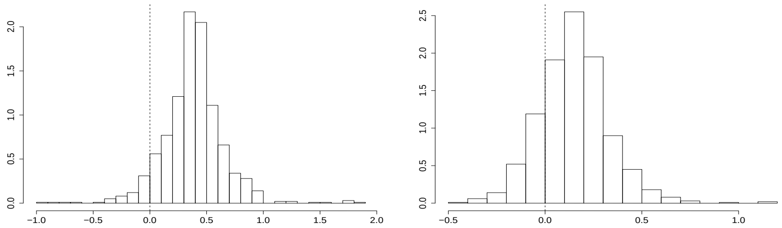
Figure C.12: Structural Model Pseudo-Wald and Entropy Tests - 3 Cycles SE



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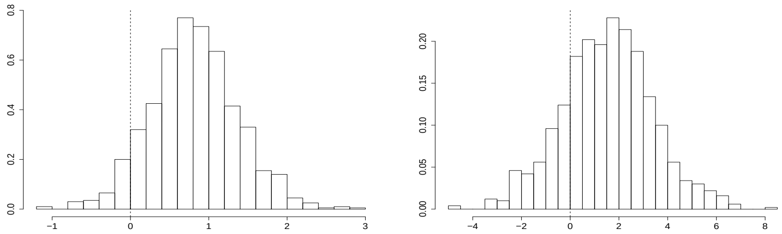

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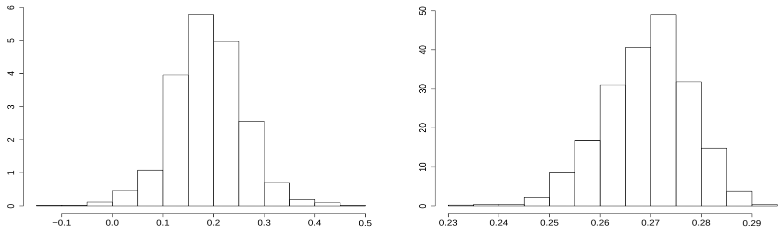
(d) n=200

Figure C.13: Structural Model Pseudo-Wald - 3 Cycles t-Test



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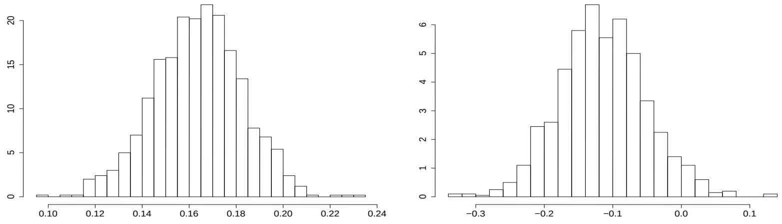

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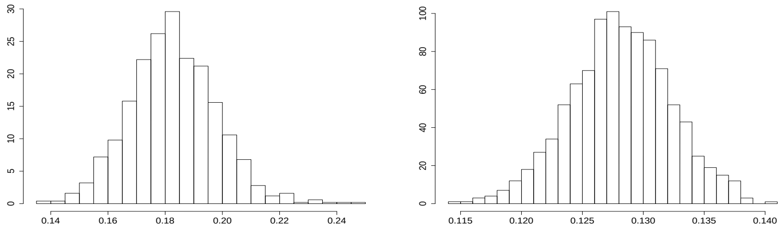
Figure C.14: Structural Model Pseudo-Wald and Entropy Tests - Transitive Ties



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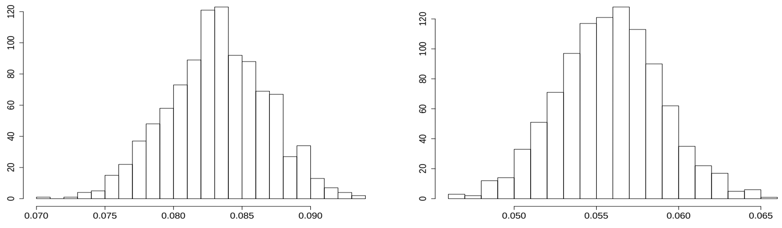
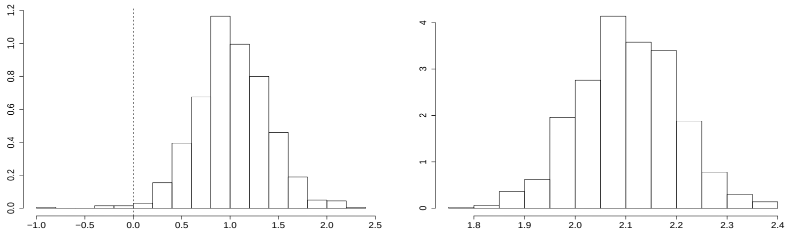


(c) n=100 (d) n=200

Figure C.15: Structural Model Pseudo-Wald and Entropy Tests - Transitive Ties SE



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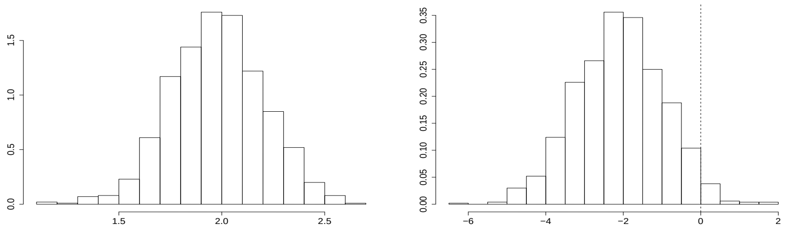
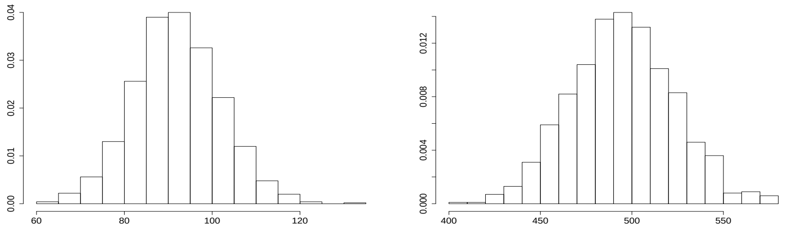


(c) n=100

(d) n=200

Figure C.16: Structural Model Pseudo-Wald - Transitive Ties t-Test



(a) n=25

(b) n=50

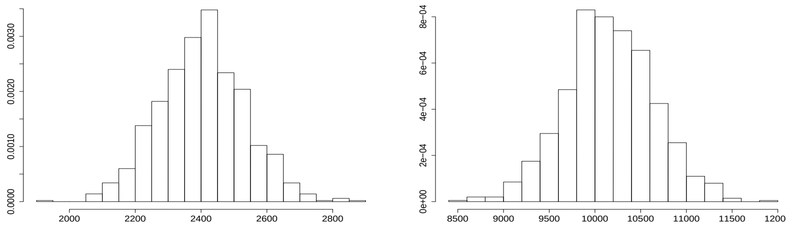


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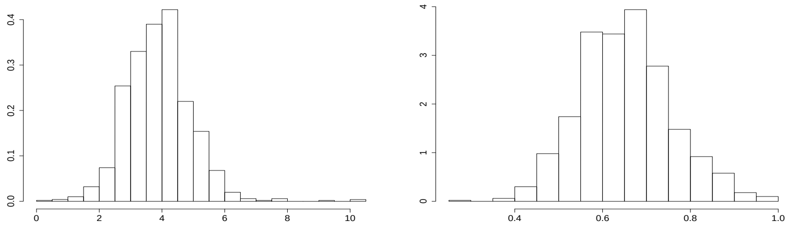
Figure C.17: Structural Model Pseudo-Wald - Reciprocity, Transitive Triplets and 3-Cycles



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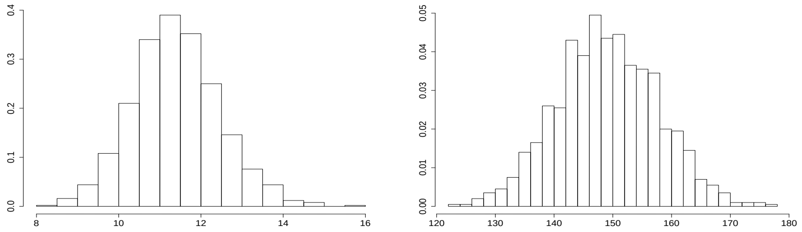

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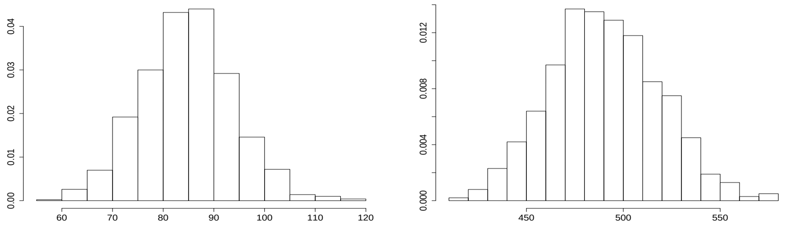
(d) n=200

Figure C.18: Structural Model Pseudo-Wald - Transitive Triplets and 3-Cycles



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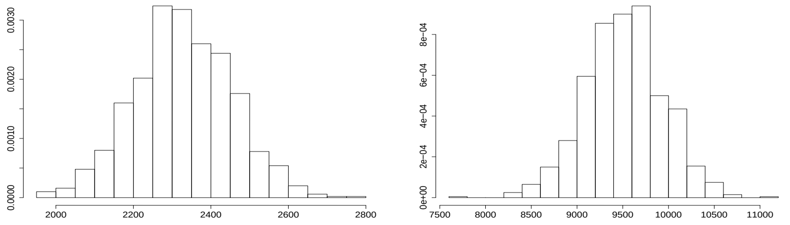

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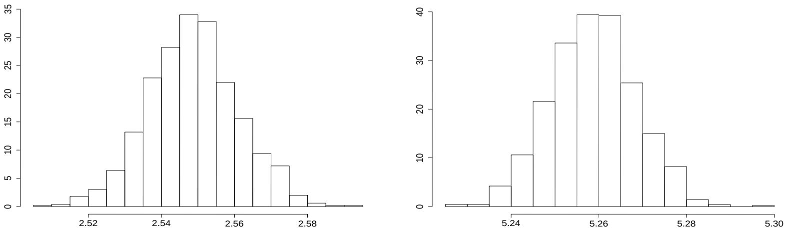
Figure C.19: Structural Model Pseudo-Wald - Reciprocity and Transitive Triplets



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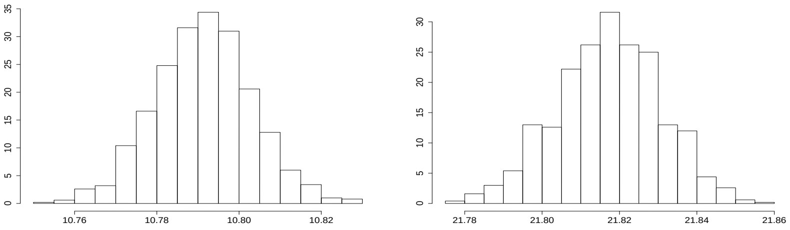

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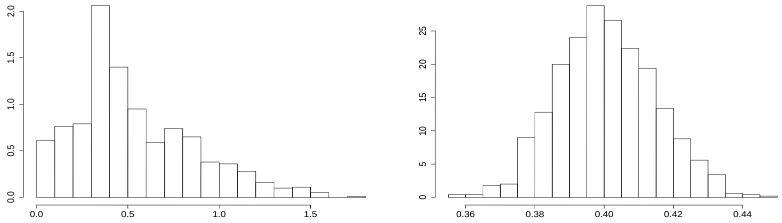
(d) n=100

Figure C.20: Co-evolution Model With Bernoulli Attribute Pseudo-Wald and Entropy Tests - Network Rate Time 1



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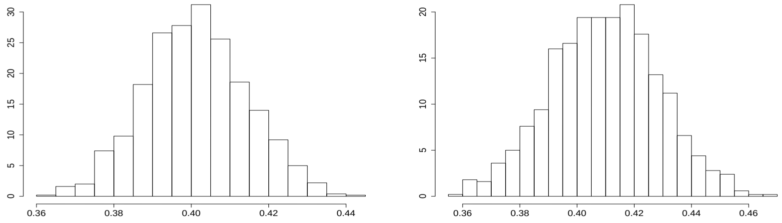
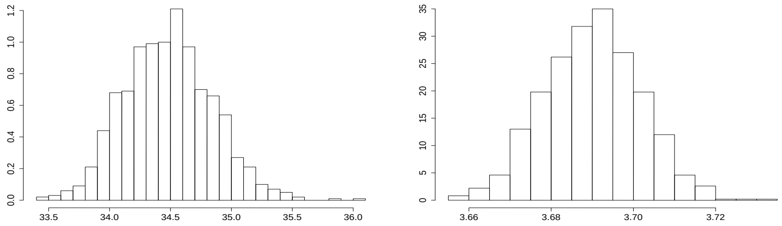
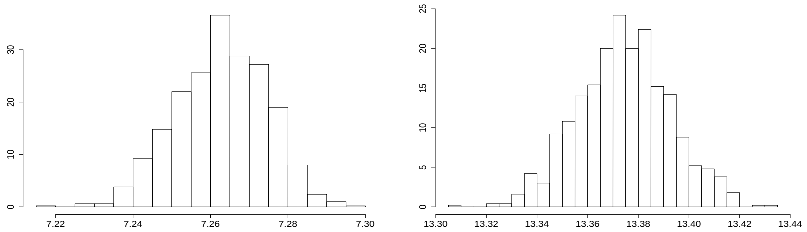


(c) n=100 (d) n=100

Figure C.21: Co-evolution Model With Bernoulli Attribute Pseudo-Wald and Entropy Tests - Network Rate Time 1 SE

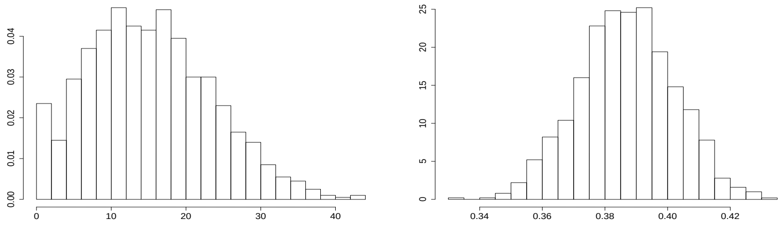


(a) n=25 (b) n=50

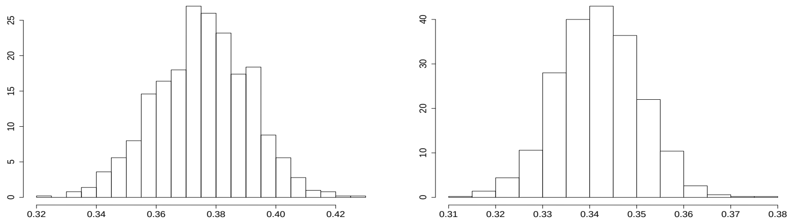


(c) n=100 (d) n=100

Figure C.22: Co-evolution Model With Bernoulli Attribute Pseudo-Wald and Entropy Tests - Network Rate Time 2

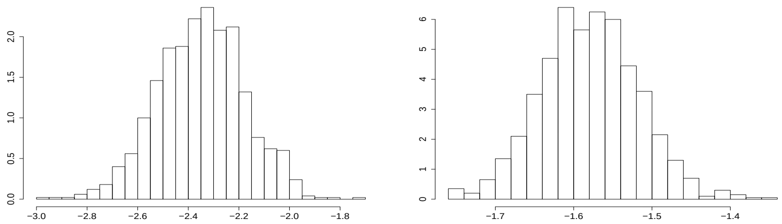


(a) n=25 (b) n=50

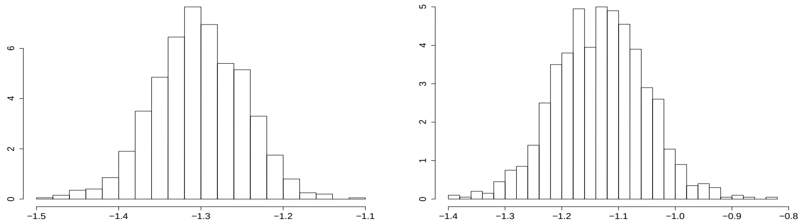


(c) n=100 (d) n=100

Figure C.23: Co-evolution Model With Bernoulli Attribute Pseudo-Wald and Entropy Tests - Network Rate Time 2 SE

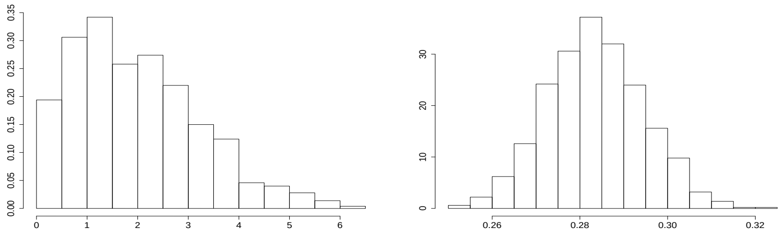


(a) n=25 (b) n=50



(c) n=100 (d) n=100

Figure C.24: Co-evolution Model With Bernoulli Attribute Pseudo-Wald and Entropy Tests - Density



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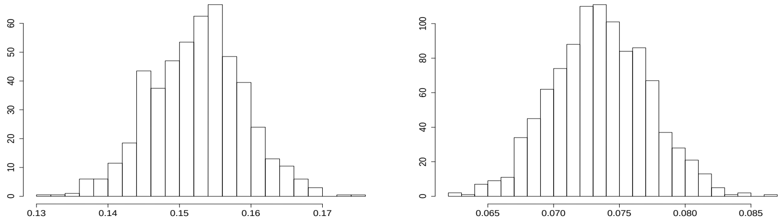
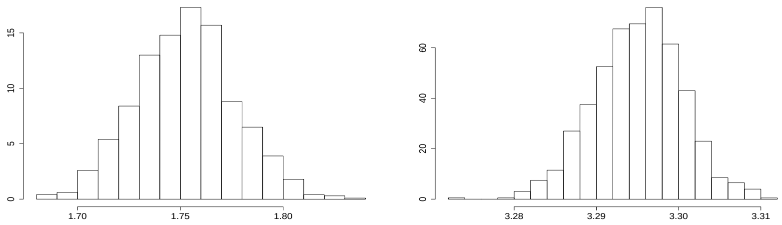


(c) n=100 (d) n=100

Figure C.25: Co-evolution Model With Bernoulli Attribute Pseudo-Wald and Entropy Tests - Density SE



(a) n=25 (b) n=50

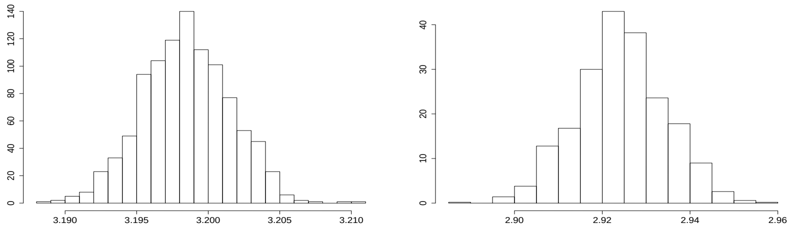


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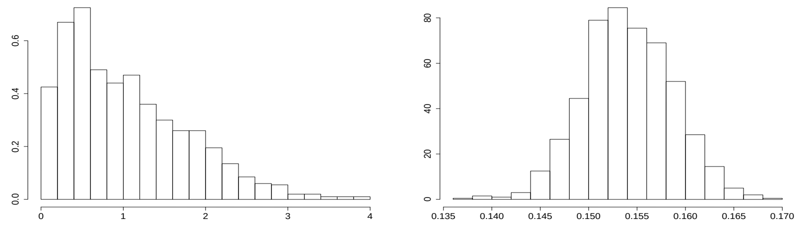
Figure C.26: Co-evolution Model With Bernoulli Attribute Pseudo-Wald and Entropy Tests - Reciprocity



(a) n=25

(b) n=50

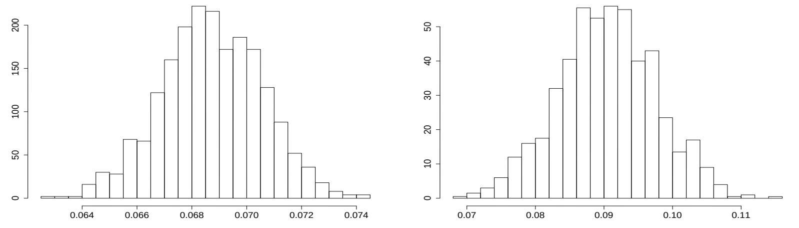


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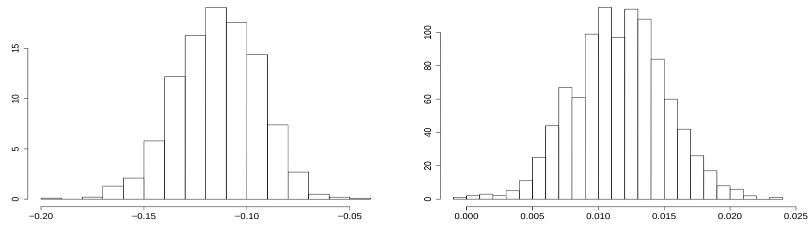
Figure C.27: Co-evolution Model With Bernoulli Attribute Pseudo-Wald and Entropy Tests - Reciprocity SE



(a) n=25

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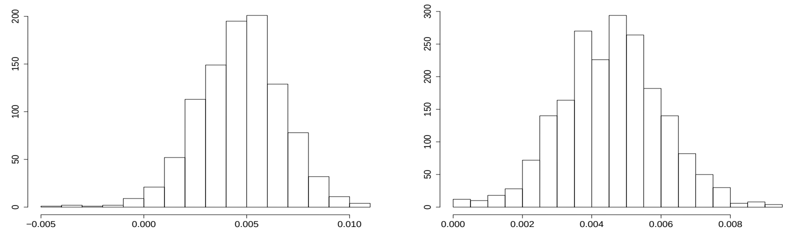
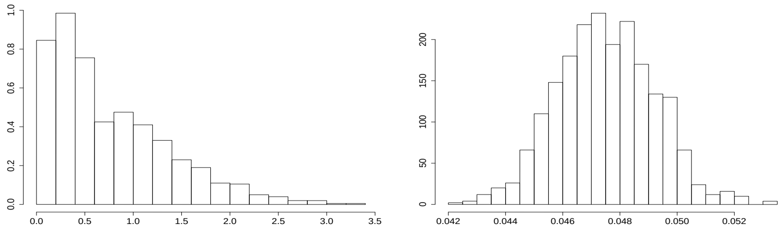


(c) n=100

(d) n=100

Figure C.28: Co-evolution Model With Bernoulli Attribute Pseudo-Wald and Entropy Tests - Transitive Triplets



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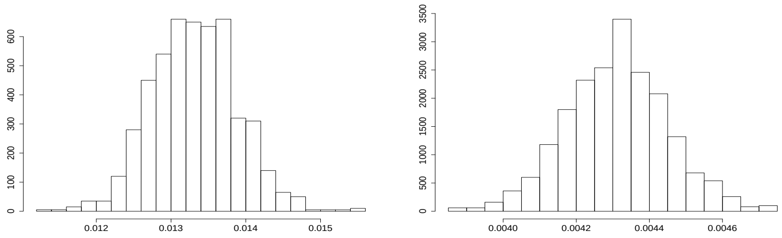
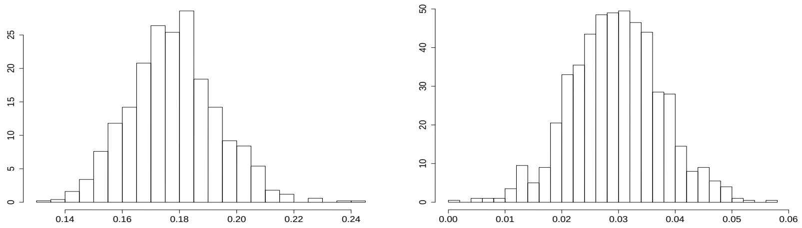


(c) n=100

(d) n=100

Figure C.29: Co-evolution Model With Bernoulli Attribute Pseudo-Wald and Entropy Tests - Transitive Triplets SE



(a) n=25

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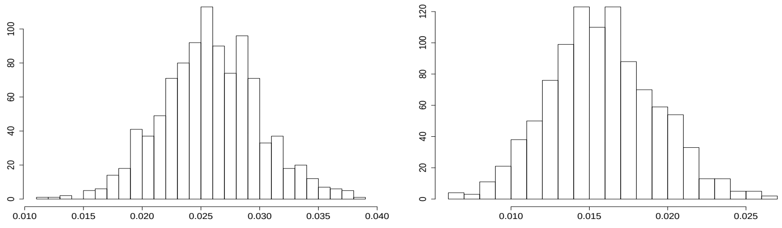

(c) n=100

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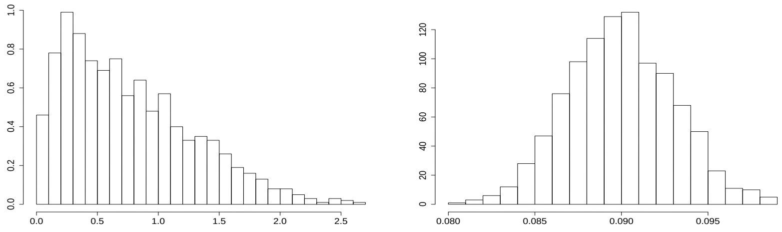
Figure C.30: Co-evolution Model With Bernoulli Attribute Pseudo-Wald and Entropy Tests - 3 Cycles



(a) n=25

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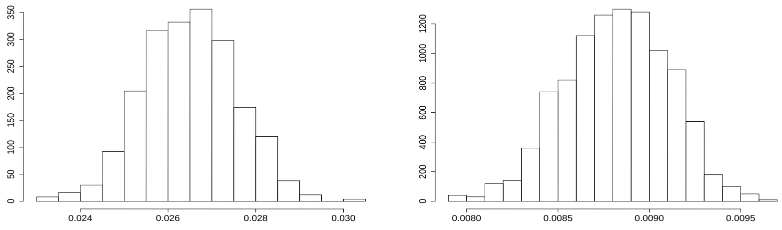
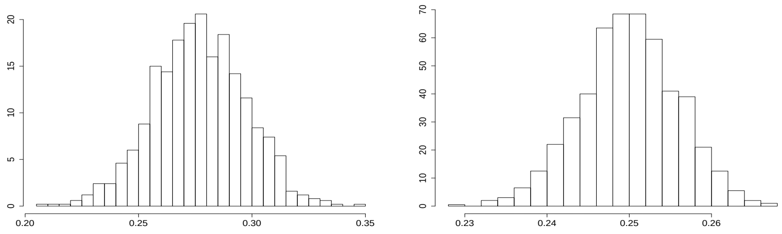


(c) n=100

(d) n=100

Figure C.31: Co-evolution Model With Bernoulli Attribute Pseudo-Wald and Entropy Tests - 3 Cycles SE



(a) n=25

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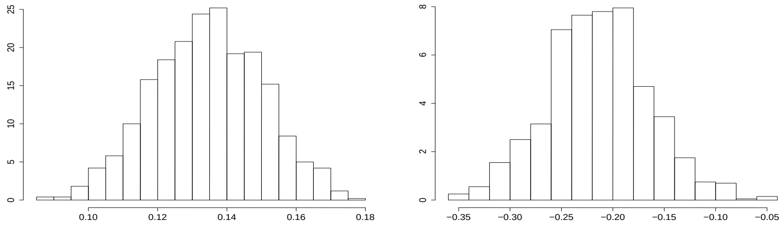
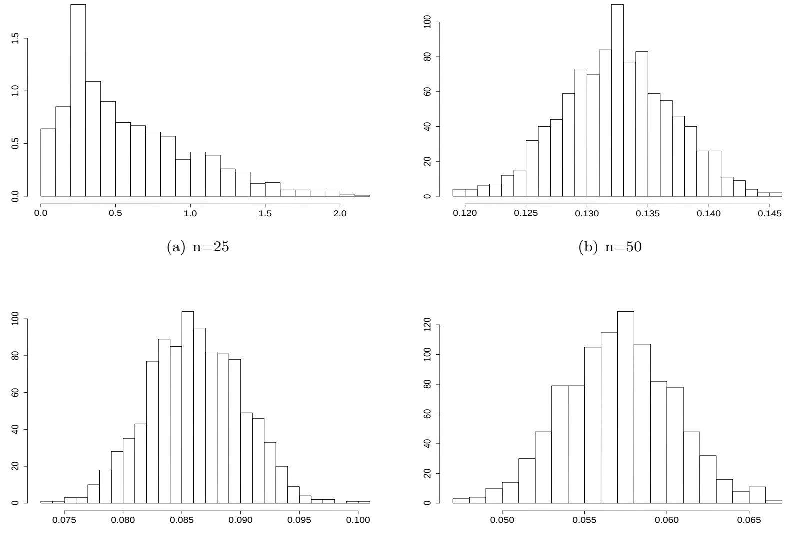


(c) n=100

(d) n=100

Figure C.32: Co-evolution Model With Bernoulli Attribute Pseudo-Wald and Entropy Tests - Transitive Ties



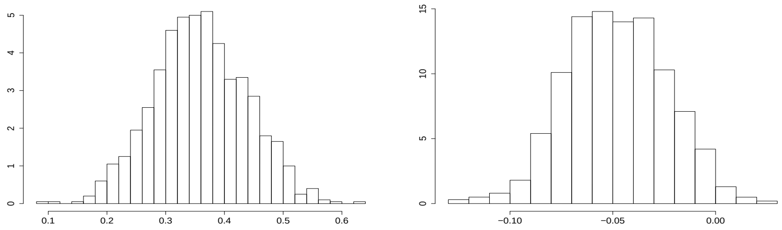
(a) n=25

(b) n=50

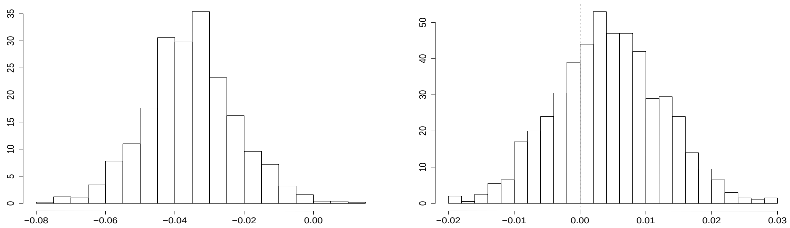
(c) n=100

(d) n=100

Figure C.33: Co-evolution Model With Bernoulli Attribute Pseudo-Wald and Entropy Tests - Transitive Ties SE

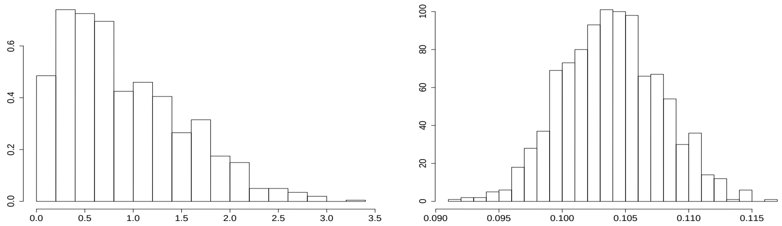


(a) n=25 (b) n=50

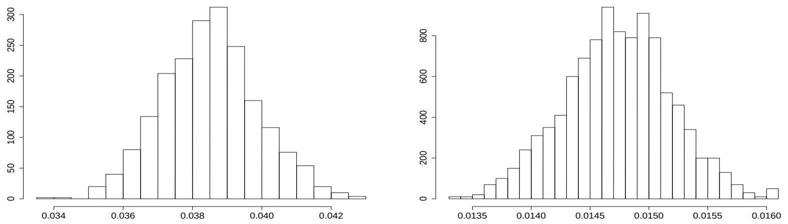


(c) n=100 (d) n=100

Figure C.34: Co-evolution Model With Bernoulli Attribute Pseudo-Wald and Entropy Tests - Outdegree-Popularity (Square Root)

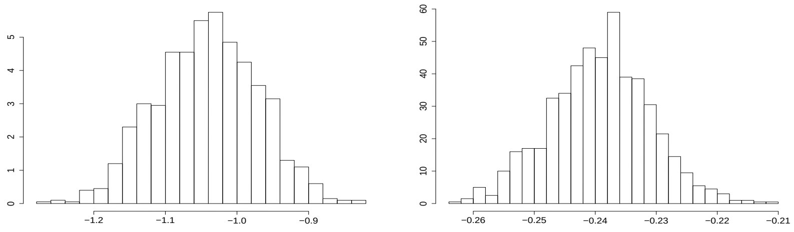


(a) n=25 (b) n=50

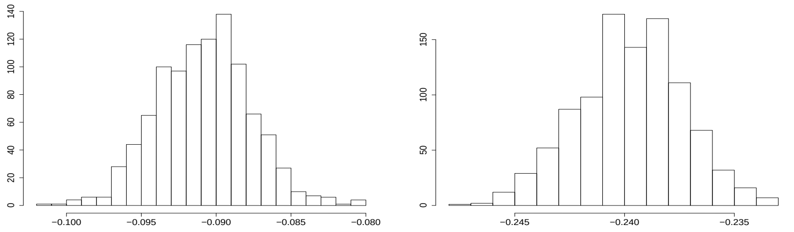


(c) n=100 (d) n=100

Figure C.35: Co-evolution Model With Bernoulli Attribute Pseudo-Wald and Entropy Tests - Outdegree-Popularity (Square Root) SE

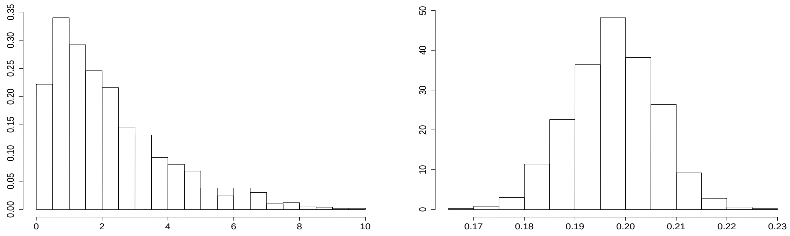


(a) n=25 (b) n=50

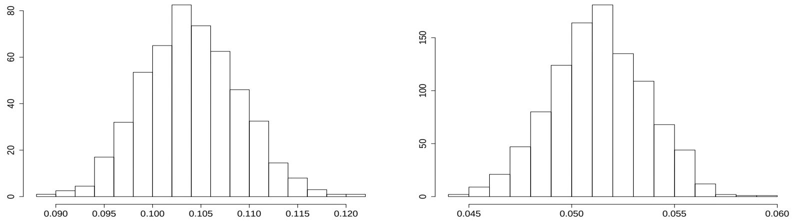


(c) n=100 (d) n=100

Figure C.36: Co-evolution Model With Bernoulli Attribute Pseudo-Wald and Entropy Tests - Attribute Alter

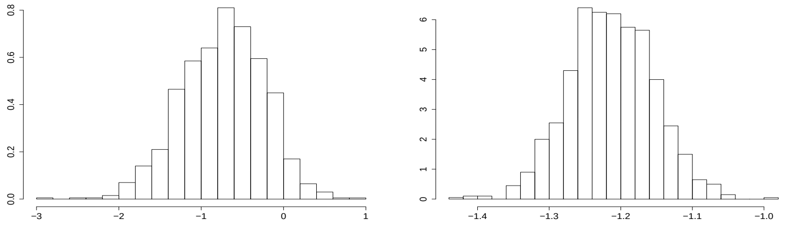


(a) n=25 (b) n=50

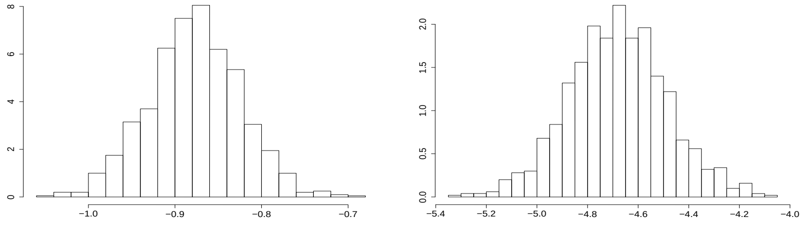


(c) n=100 (d) n=100

Figure C.37: Co-evolution Model With Bernoulli Attribute Pseudo-Wald and Entropy Tests - Attribute Alter SE

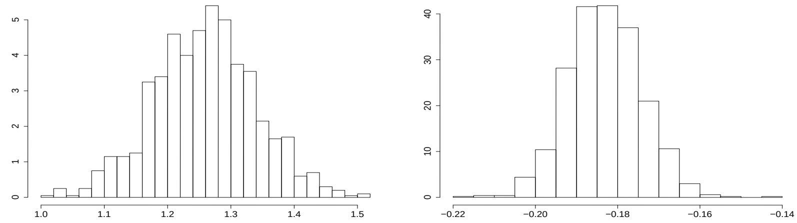


(a) n=25 (b) n=50



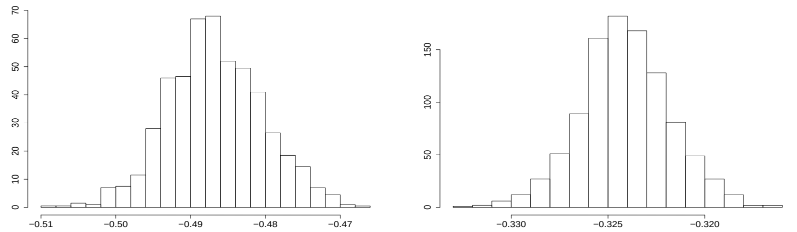
(c) n=100 (d) n=200

Figure C.38: Co-evolution Model With Bernoulli Attribute Pseudo-Wald - Attribute Alter t-Test



(a) n=25

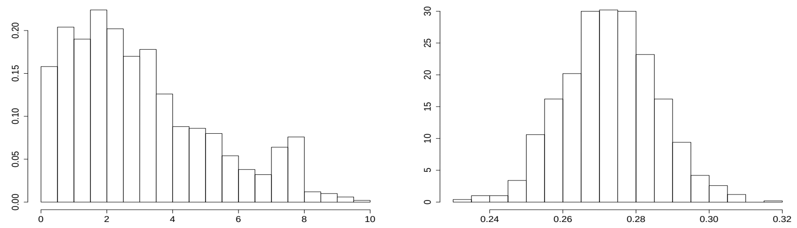
(b) n=50



(c) n=100

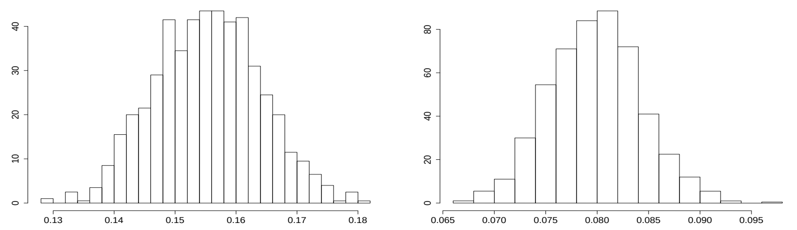
(d) n=100

Figure C.39: Co-evolution Model With Bernoulli Attribute Pseudo-Wald and Entropy Tests - Attribute Ego



(a) n=25

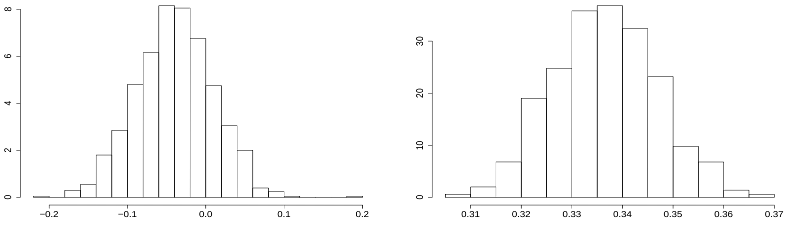
(b) n=50



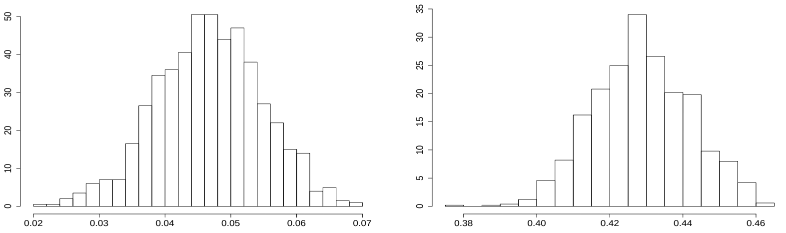
(c) n=100

(d) n=100

Figure C.40: Co-evolution Model With Bernoulli Attribute Pseudo-Wald and Entropy Tests - Attribute Ego SE

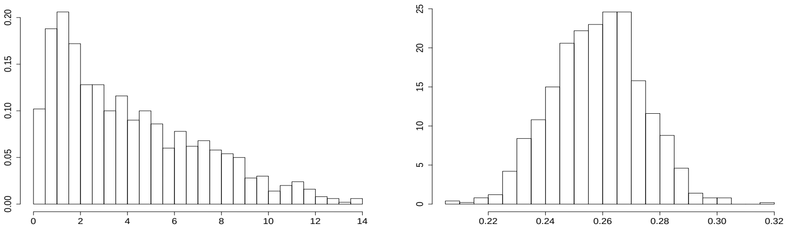


(a) n=25 (b) n=50

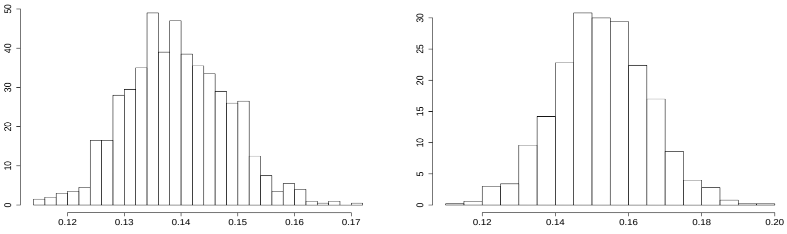


(c) n=100 (d) n=100

Figure C.41: Co-evolution Model With Bernoulli Attribute Pseudo-Wald and Entropy Tests - Attribute Same

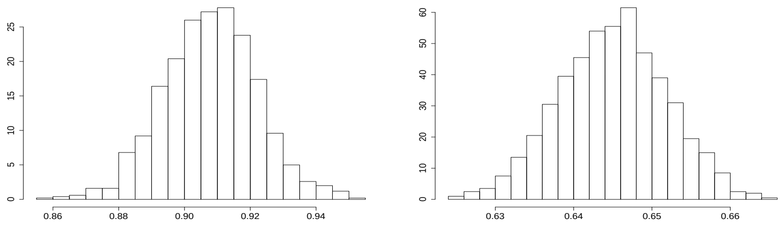


(a) n=25 (b) n=50



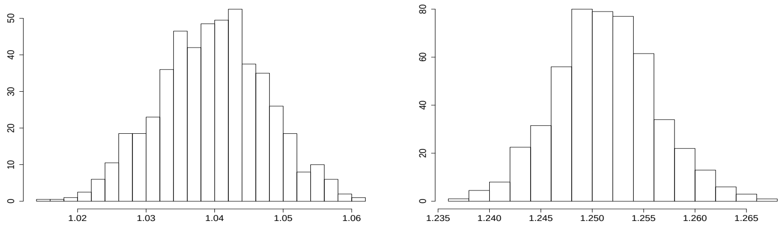
(c) n=100 (d) n=100

Figure C.42: Co-evolution Model With Bernoulli Attribute Pseudo-Wald and Entropy Tests - Attribute Same SE



(a) n=25

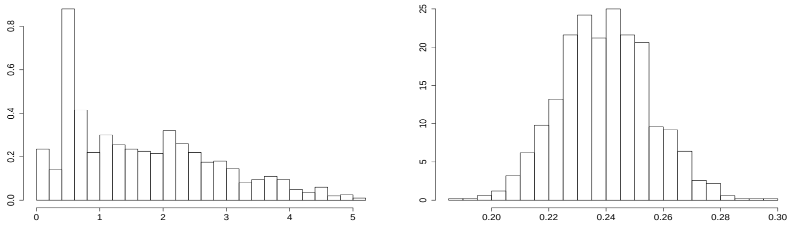
(b) n=50



(c) n=100

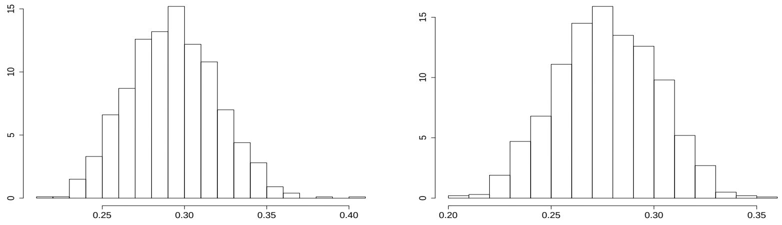
(d) n=100

Figure C.43: Co-evolution Model With Bernoulli Attribute Pseudo-Wald and Entropy Tests - Attribute Rate Time 1



(a) n=25

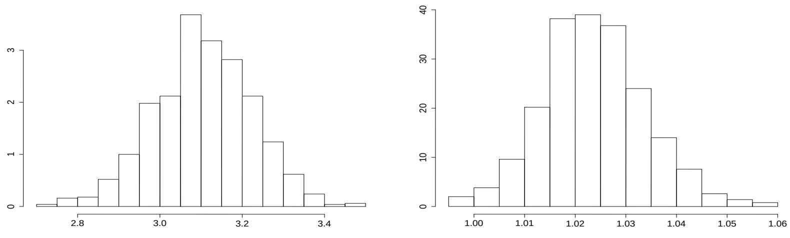
(b) n=50



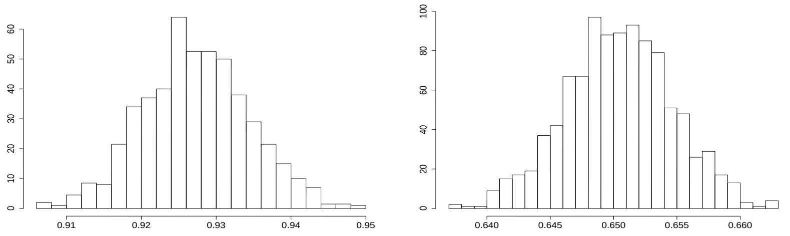
(c) n=100

(d) n=100

Figure C.44: Co-evolution Model With Bernoulli Attribute Pseudo-Wald and Entropy Tests - Attribute Rate Time 1 SE

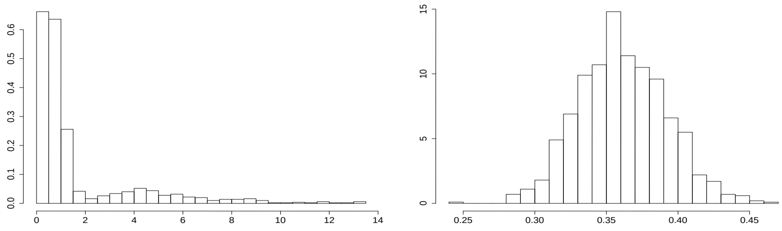


(a) n=25 (b) n=50

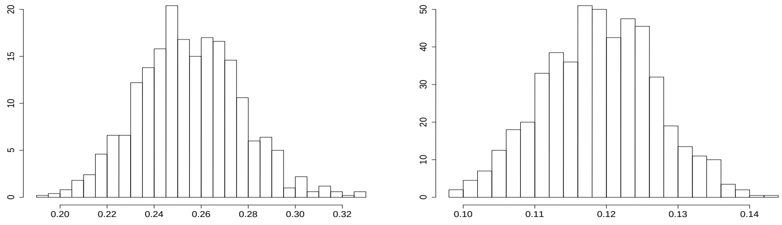


(c) n=100 (d) n=100

Figure C.45: Co-evolution Model With Bernoulli Attribute Pseudo-Wald and Entropy Tests - Attribute Rate Time 2

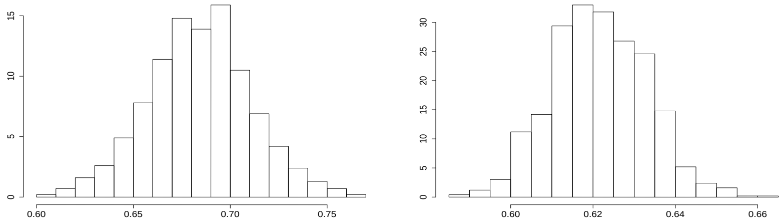


(a) n=25 (b) n=50

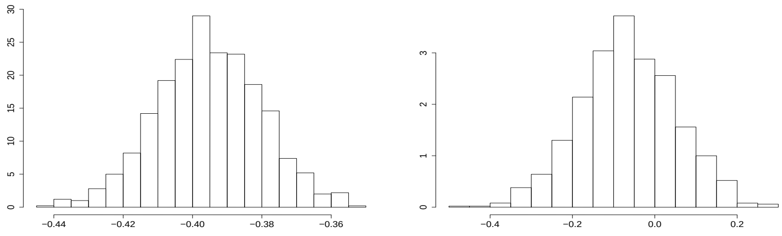


(c) n=100 (d) n=100

Figure C.46: Co-evolution Model With Bernoulli Attribute Pseudo-Wald and Entropy Tests - Attribute Rate Time 2 SE

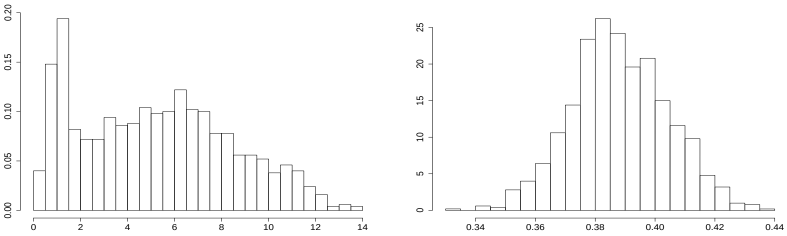


(a) n=25 (b) n=50

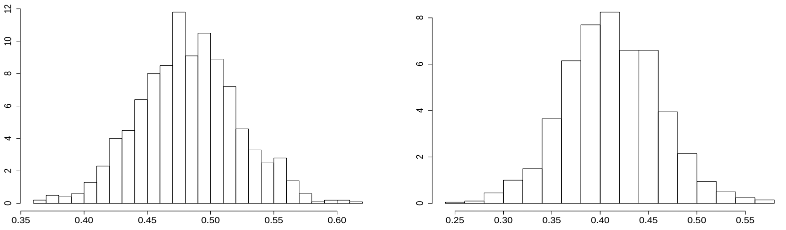


(c) n=100 (d) n=100

Figure C.47: Co-evolution Model With Bernoulli Attribute Pseudo-Wald and Entropy Tests - Linear Shape

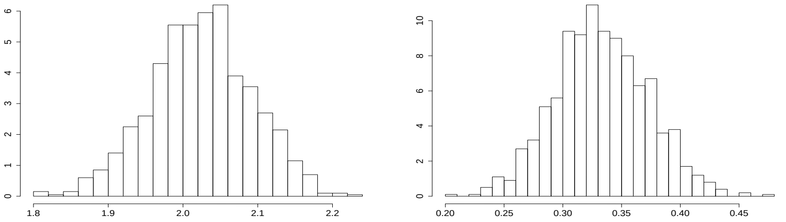


(a) n=25 (b) n=50

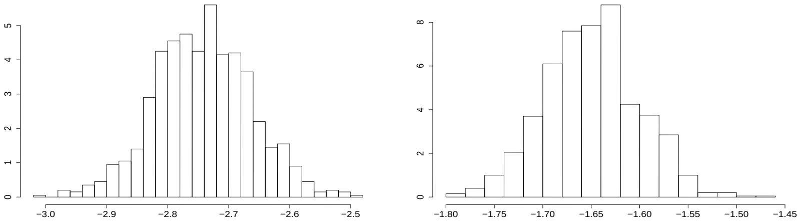


(c) n=100 (d) n=100

Figure C.48: Co-evolution Model With Bernoulli Attribute Pseudo-Wald and Entropy Tests - Linear Shape SE

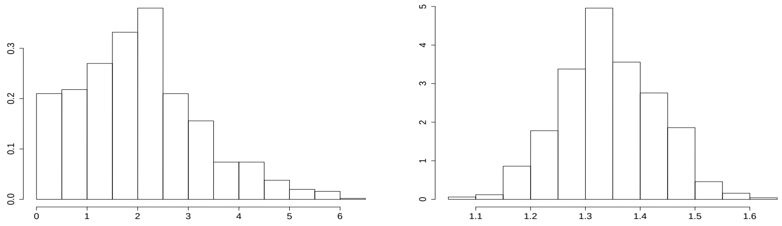


(a) n=25 (b) n=50

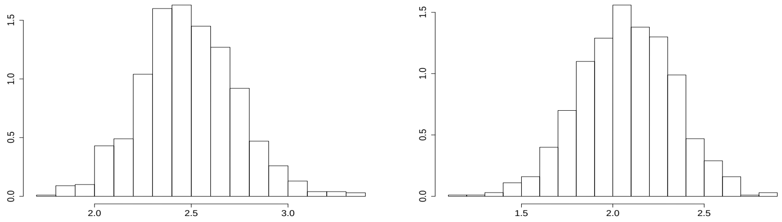


(c) n=100 (d) n=100

Figure C.49: Co-evolution Model With Bernoulli Attribute Pseudo-Wald and Entropy Tests - Average Similarity



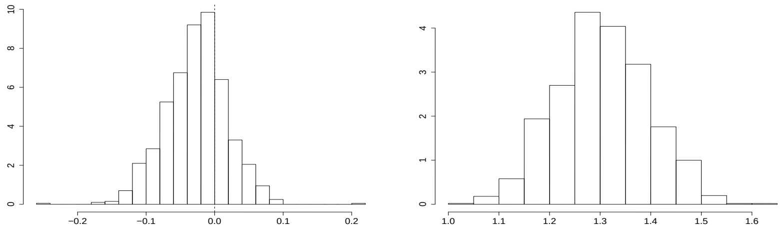
(a) n=25 (b) n=50



(c) n=100 (d) n=100

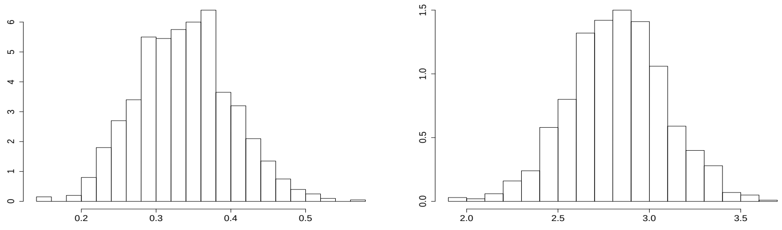
Figure C.50: Co-evolution Model With Bernoulli Attribute Pseudo-Wald and Entropy Tests - Average Similarity SE

C.3 Co-evolution Model With Normal $(\mu = 3, \sigma = 1)$ Attribute



(a) n=25

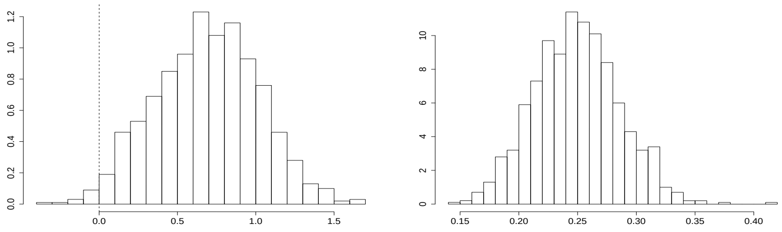
(b) n=50



(c) n=100

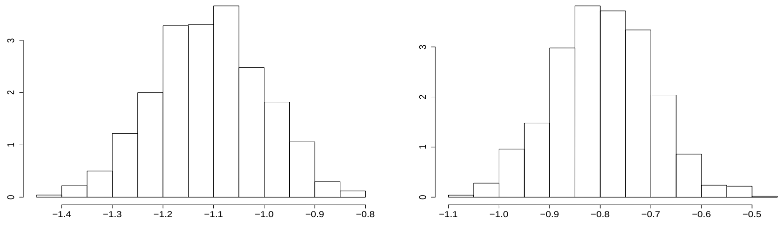
(d) n=200

Figure C.51: Co-evolution Model With Bernoulli Attribute Pseudo-Wald and Entropy Tests - Same Attribute t-Test



(a) n=25

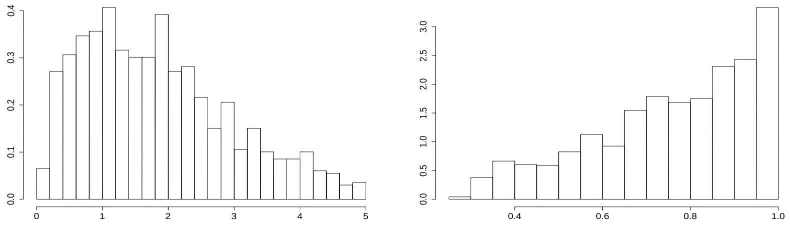
(b) n=50



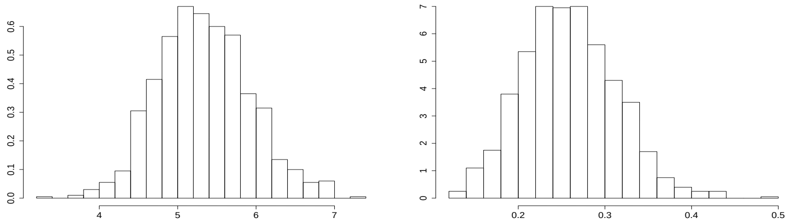
(c) n=100

(d) n=200

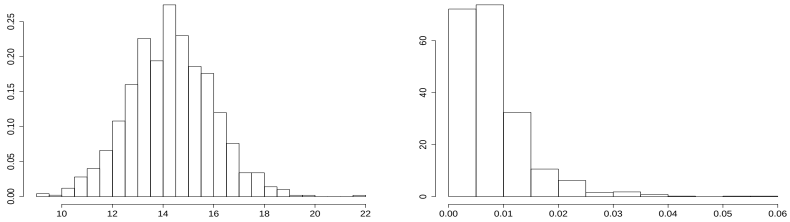
Figure C.52: Co-evolution Model With Bernoulli Attribute Pseudo-Wald and Entropy Tests - Average Similarity Attribute t-Test



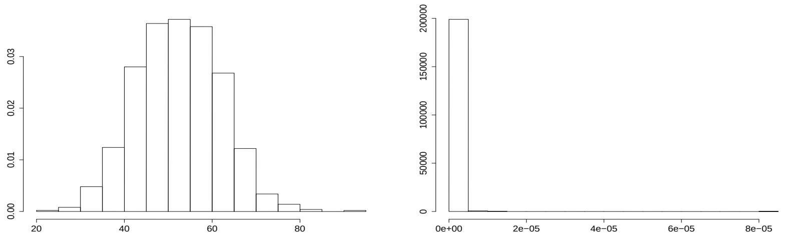
(a) Pseudo-Wald Test Statistic n=25 (b) Pseudo-Wald P-value n=25



(c) Pseudo-Wald Test Statistic n=50 (d) Pseudo-Wald P-value n=50

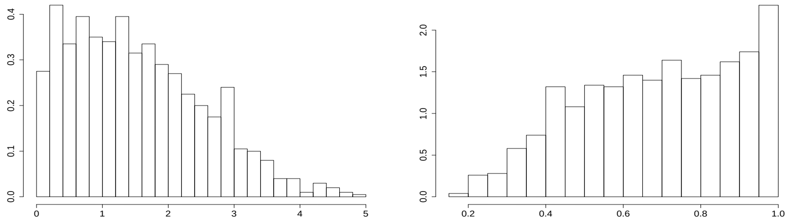


(e) Pseudo-Wald Test Statistic n=100 (f) Pseudo-Wald P-value n=100

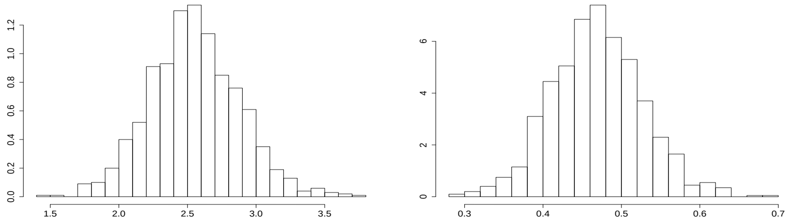


(g) Pseudo-Wald Test Statistic n=200 (h) Pseudo-Wald P-value n=200

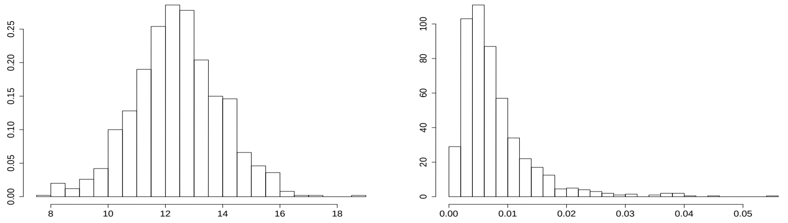
Figure C.53: Co-evolution Model With Bernoulli Attribute - Pseudo-Wald for Outdegree-Popularity (Square Root), Attribute Alter, Attribute Ego, and Attribute Same



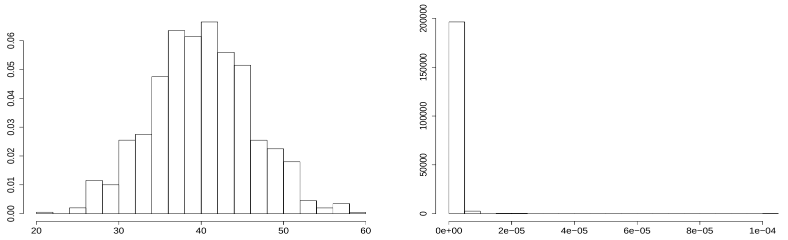
(a) Pseudo-Wald Test Statistic n=25 (b) Pseudo-Wald P-value n=25



(c) Pseudo-Wald Test Statistic n=50 (d) Pseudo-Wald P-value n=50

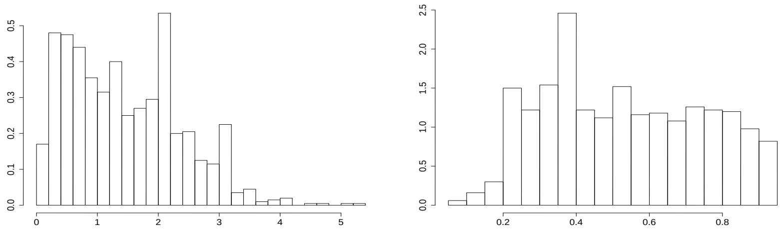


(e) Pseudo-Wald Test Statistic n=100 (f) Pseudo-Wald P-value n=100



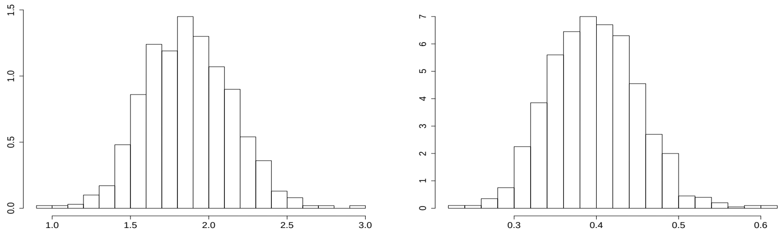
(g) Pseudo-Wald Test Statistic n=200 (h) Pseudo-Wald P-value n=200

Figure C.54: Co-evolution Model With Bernoulli Attribute - Pseudo-Wald for Outdegree-Popularity (Square Root), Attribute Alter, and Attribute Ego



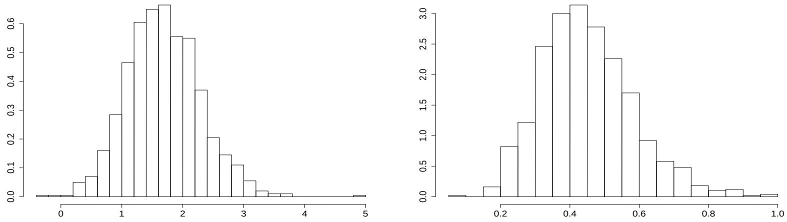
(a) Pseudo-Wald Test Statistic n=25

(b) Pseudo-Wald P-value n=25



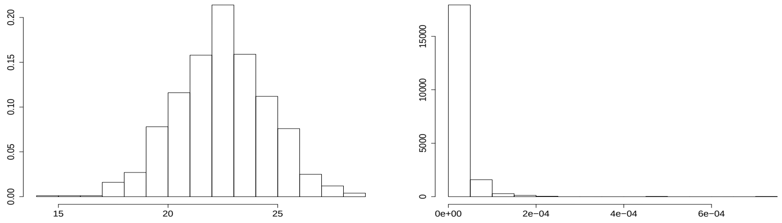
(c) Pseudo-Wald Test Statistic n=50

(d) Pseudo-Wald P-value n=50



(e) Pseudo-Wald Test Statistic n=100

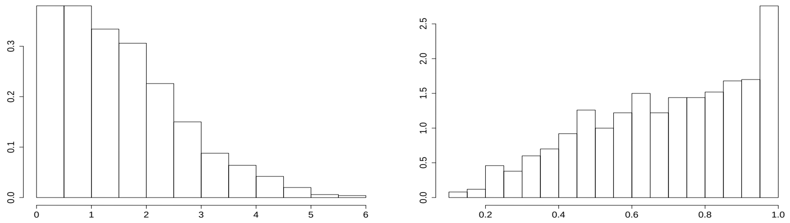
(f) Pseudo-Wald P-value n=100



(g) Pseudo-Wald Test Statistic n=200

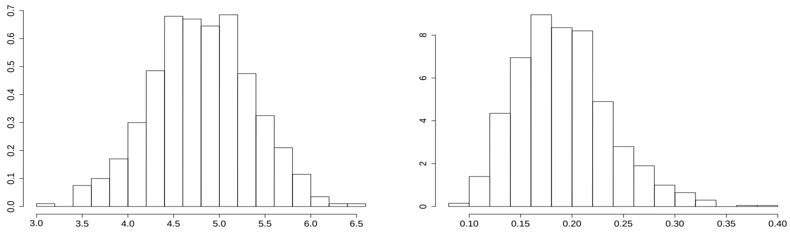
(h) Pseudo-Wald P-value n=200

Figure C.55: Co-evolution Model With Bernoulli Attribute - Pseudo-Wald for Outdegree-Popularity (Square Root) and Attribute Alter



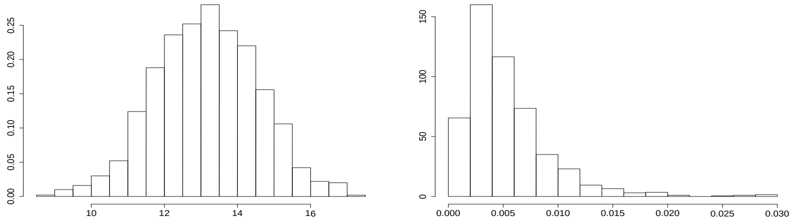
(a) Pseudo-Wald Test Statistic n=25

(b) Pseudo-Wald P-value n=25



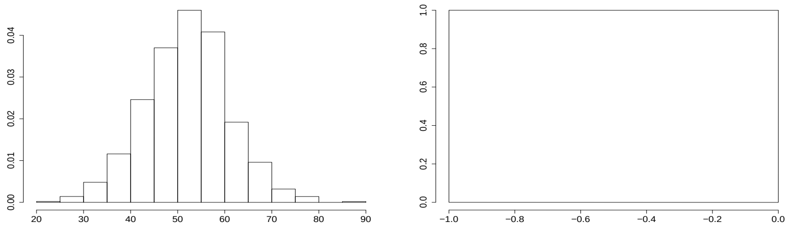
(c) Pseudo-Wald Test Statistic n=50

(d) Pseudo-Wald P-value n=50



(e) Pseudo-Wald Test Statistic n=100

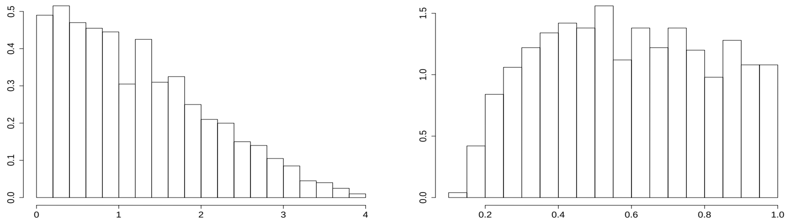
(f) Pseudo-Wald P-value n=100



(g) Pseudo-Wald Test Statistic n=200

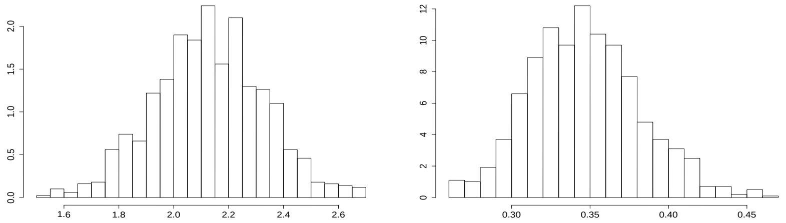
(h) Pseudo-Wald P-value n=200

Figure C.56: Co-evolution Model With Bernoulli Attribute - Pseudo-Wald for Attribute Alter, Attribute Ego and Attribute Same



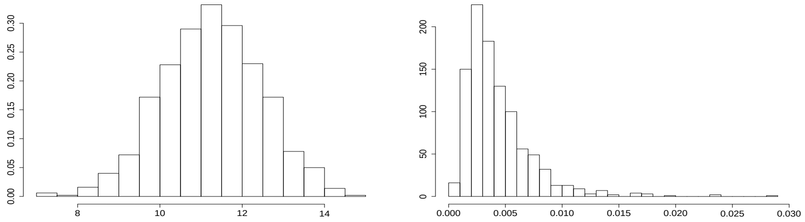
(a) Pseudo-Wald Test Statistic n=25

(b) Pseudo-Wald P-value n=25



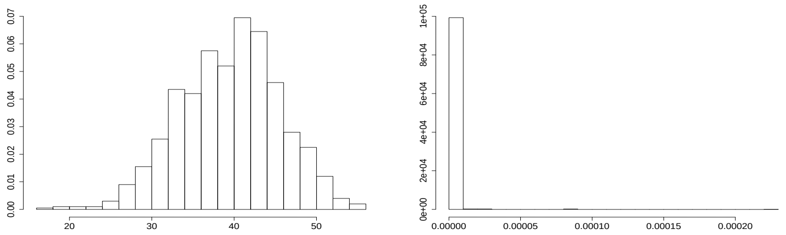
(c) Pseudo-Wald Test Statistic n=50

(d) Pseudo-Wald P-value n=50



(e) Pseudo-Wald Test Statistic n=100

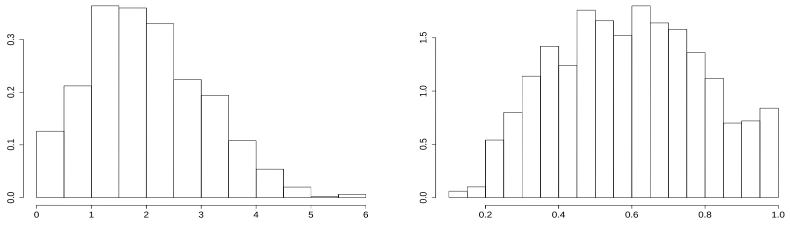
(f) Pseudo-Wald P-value n=100



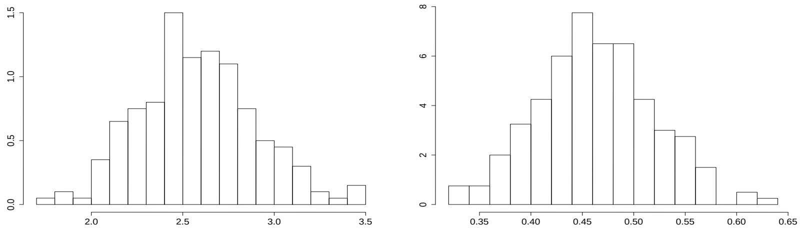
(g) Pseudo-Wald Test Statistic n=200

(h) Pseudo-Wald P-value n=200

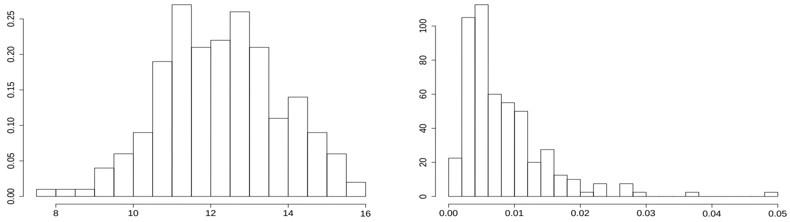
Figure C.57: Co-evolution Model With Bernoulli Attribute - Pseudo-Wald for Attribute Alter and Attribute Ego



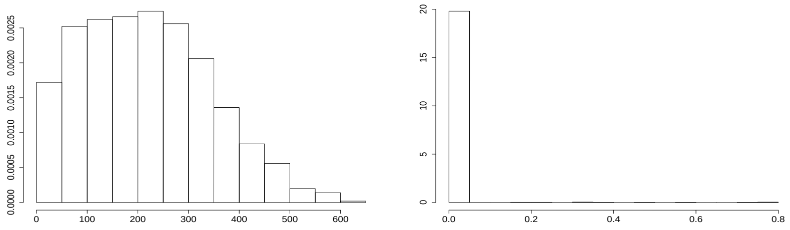
(a) Pseudo-Wald Test Statistic n=25 (b) Pseudo-Wald P-value n=25



(c) Pseudo-Wald Test Statistic n=50 (d) Pseudo-Wald P-value n=50

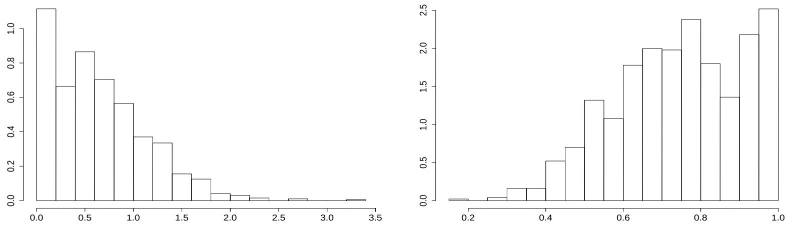


(e) Pseudo-Wald Test Statistic n=100 (f) Pseudo-Wald P-value n=100

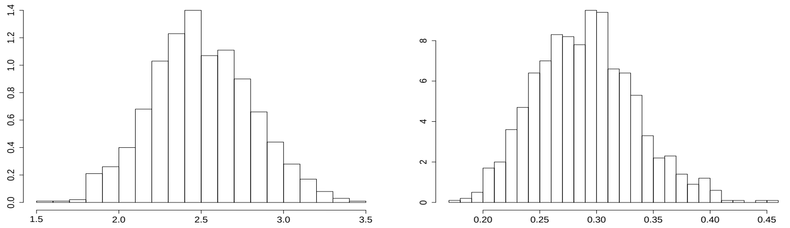


(g) Pseudo-Wald Test Statistic n=200 (h) Pseudo-Wald P-value n=200

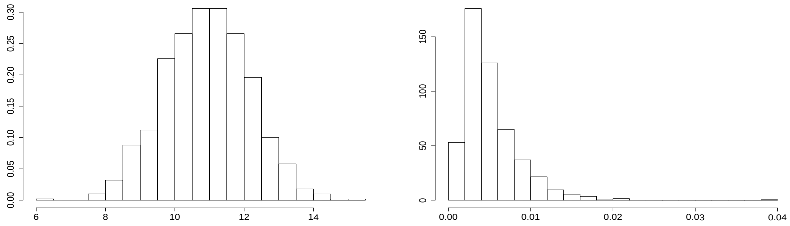
Figure C.58: Co-evolution Model With Bernoulli Attribute - Pseudo-Wald for Attribute Ego, Attribute Same, and Average Similarity



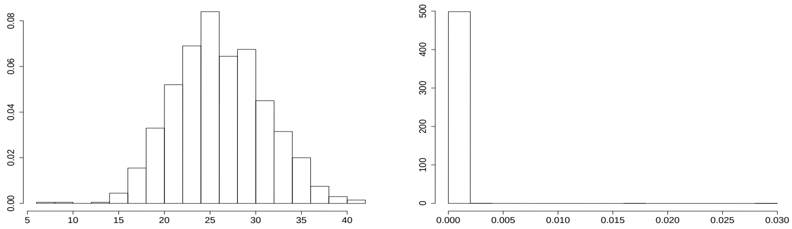
(a) Pseudo-Wald Test Statistic n=25 (b) Pseudo-Wald P-value n=25



(c) Pseudo-Wald Test Statistic n=50 (d) Pseudo-Wald P-value n=50

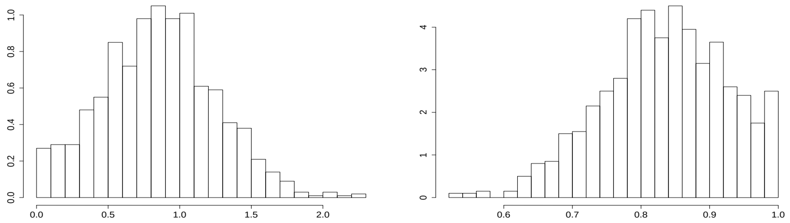


(e) Pseudo-Wald Test Statistic n=100 (f) Pseudo-Wald P-value n=100



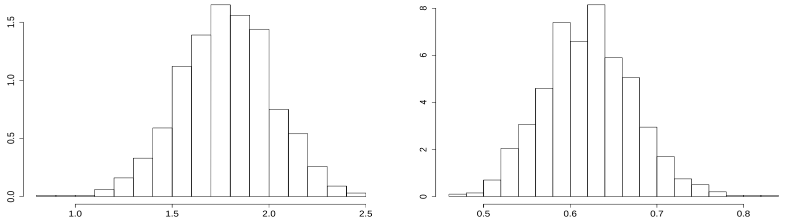
(g) Pseudo-Wald Test Statistic n=200 (h) Pseudo-Wald P-value n=200

Figure C.59: Co-evolution Model With Bernoulli Attribute - Pseudo-Wald for Attribute Ego and Attribute Same



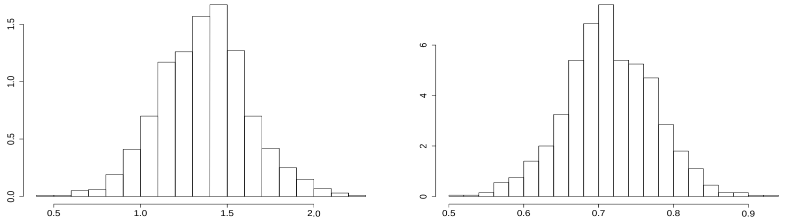
(a) Pseudo-Wald Test Statistic n=25

(b) Pseudo-Wald P-value n=25



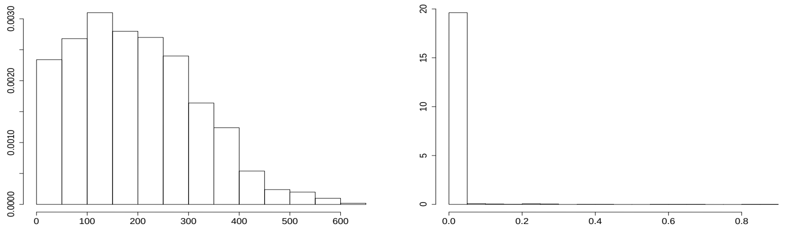
(c) Pseudo-Wald Test Statistic n=50

(d) Pseudo-Wald P-value n=50



(e) Pseudo-Wald Test Statistic n=100

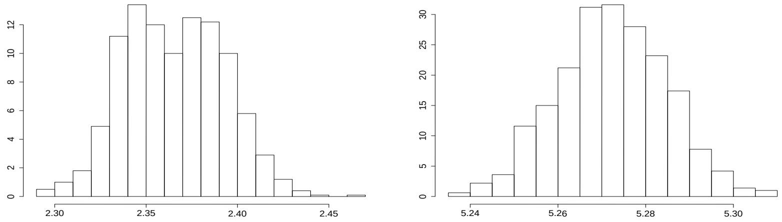
(f) Pseudo-Wald P-value n=100



(g) Pseudo-Wald Test Statistic n=200

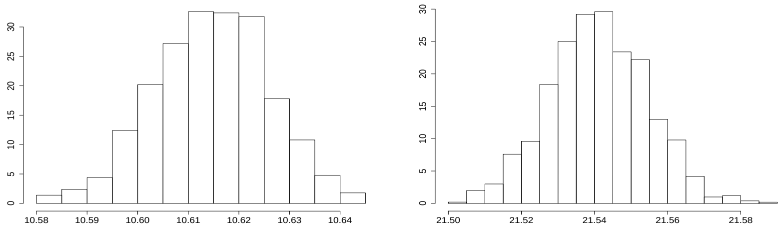
(h) Pseudo-Wald P-value n=200

Figure C.60: Co-evolution Model With Bernoulli Attribute - Pseudo-Wald for Attribute Same and Average Similarity



(a) n=25

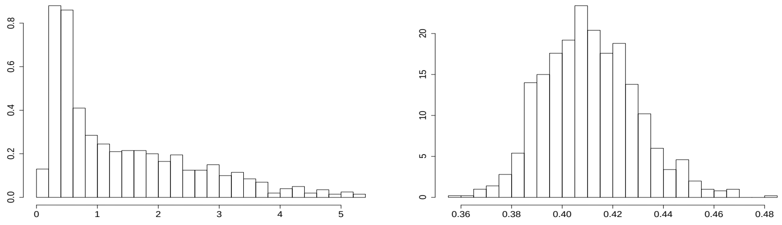
(b) n=50



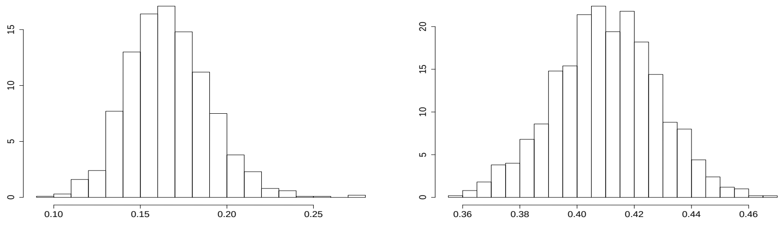
(c) n=100

(d) n=200

Figure C.61: Co-evolution Model With Normal Attribute Pseudo-Wald and Entropy Tests - Network Rate Time 1

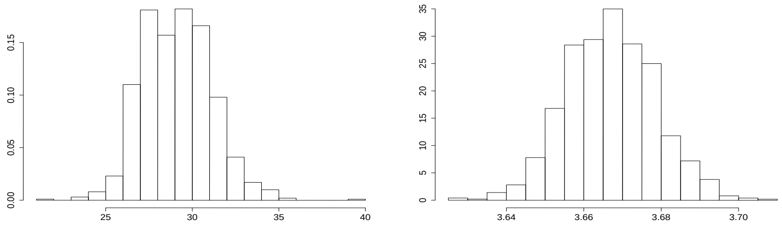


(a) n=25 (b) n=50

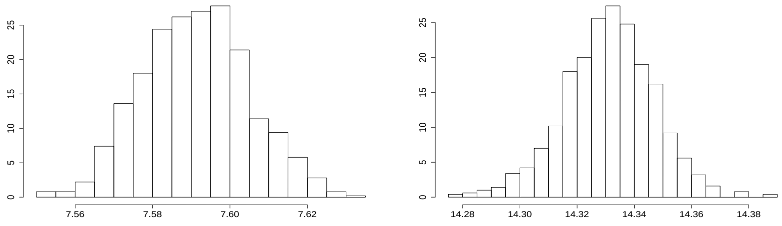


(c) n=100 (d) n=200

Figure C.62: Co-evolution Model With Normal Attribute Pseudo-Wald and Entropy Tests - Network Rate Time 1 SE

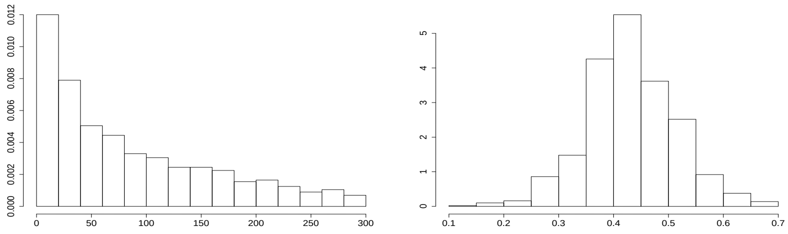


(a) n=25 (b) n=50

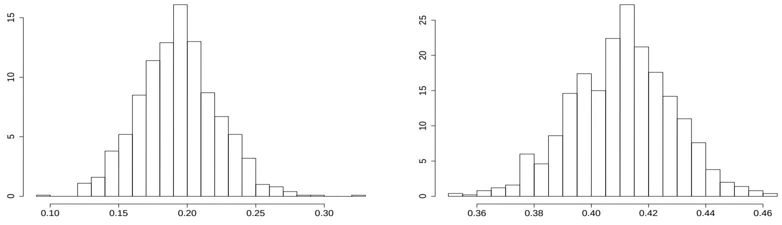


(c) n=100 (d) n=200

Figure C.63: Co-evolution Model With Normal Attribute Pseudo-Wald and Entropy Tests - Network Rate Time 2

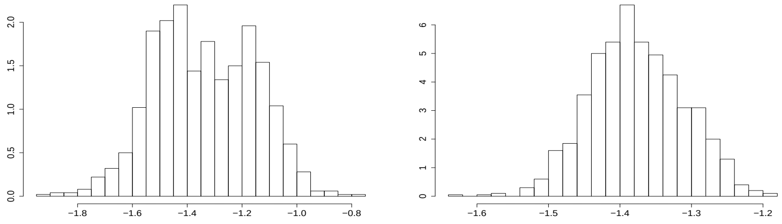


(a) n=25 (b) n=50

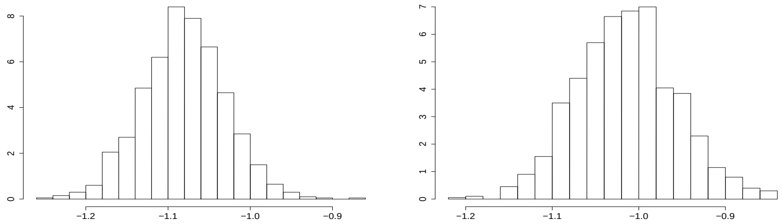


(c) n=100 (d) n=200

Figure C.64: Co-evolution Model With Normal Attribute Pseudo-Wald and Entropy Tests - Network Rate Time 2 SE

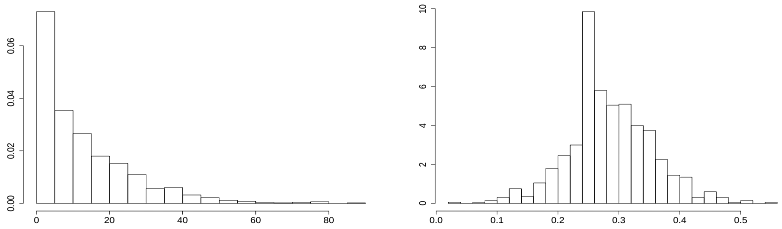


(a) n=25 (b) n=50

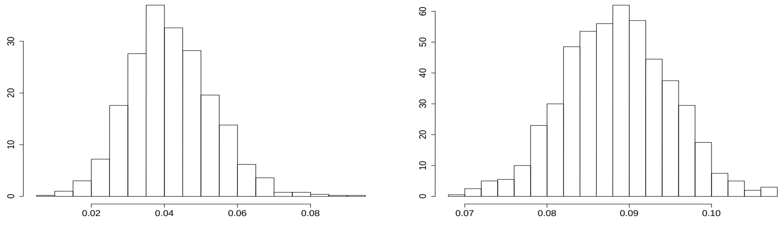


(c) n=100 (d) n=200

Figure C.65: Co-evolution Model With Normal Attribute Pseudo-Wald and Entropy Tests - Density

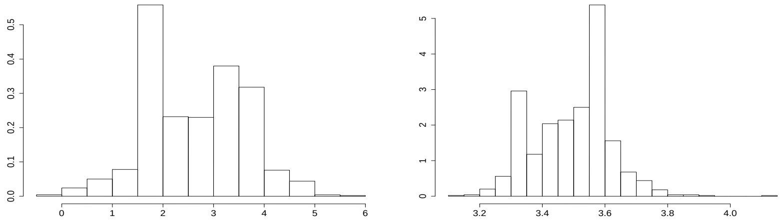


(a) n=25 (b) n=50

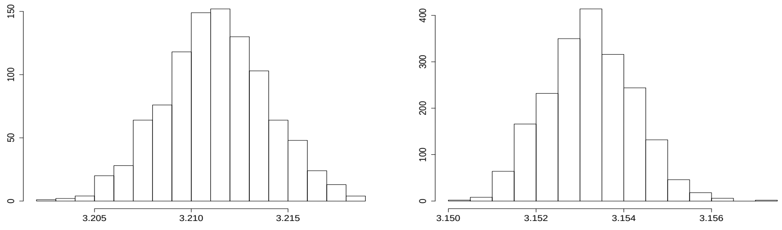


(c) n=100 (d) n=200

Figure C.66: Co-evolution Model With Normal Attribute Pseudo-Wald and Entropy Tests - Density SE



(a) n=25 (b) n=50



(c) n=100 (d) n=200

Figure C.67: Co-evolution Model With Normal Attribute Pseudo-Wald and Entropy Tests - Reciprocity

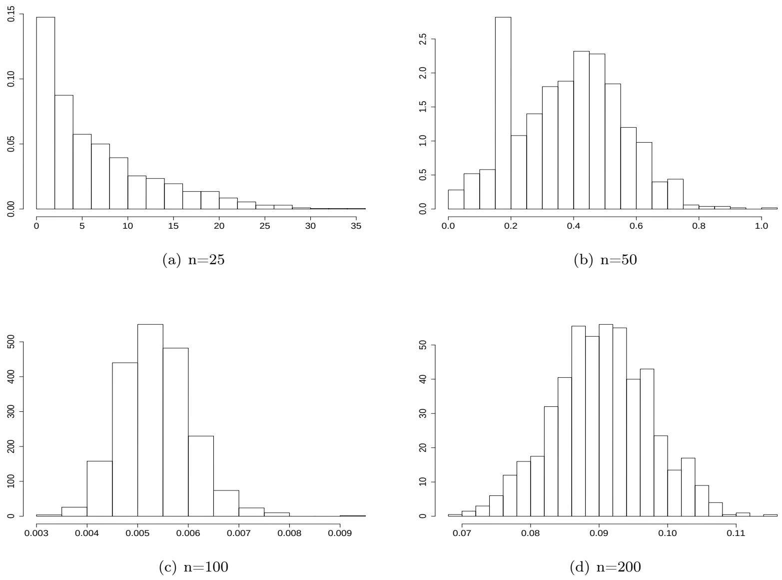


Figure C.68: Co-evolution Model With Normal Attribute Pseudo-Wald and Entropy Tests - Reciprocity SE

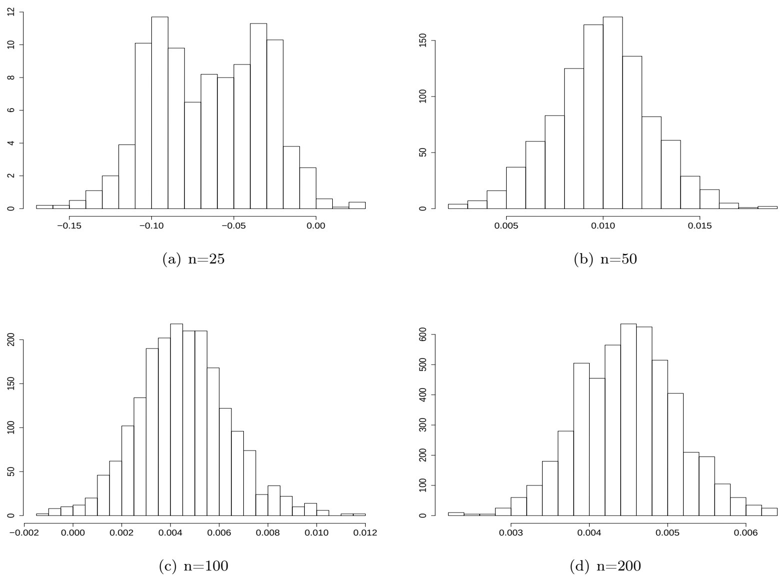
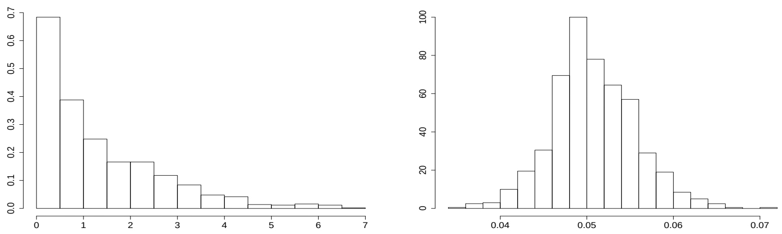
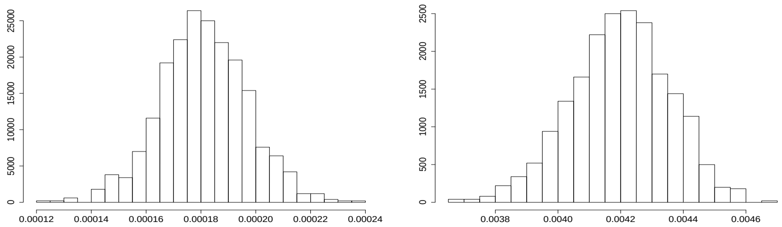


Figure C.69: Co-evolution Model With Normal Attribute Pseudo-Wald and Entropy Tests - Transitive Triplets

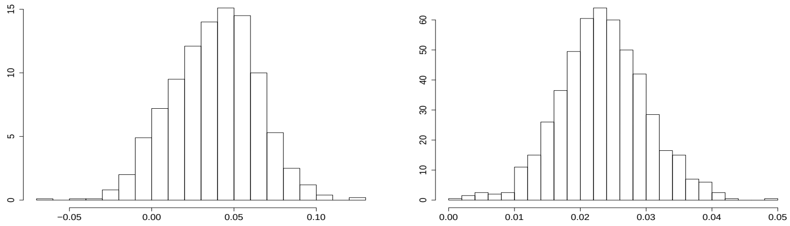


(a) n=25 (b) n=50

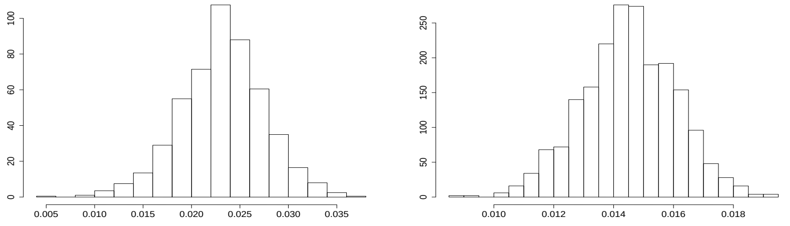


(c) n=100 (d) n=200

Figure C.70: Co-evolution Model With Normal Attribute Pseudo-Wald and Entropy Tests - Transitive Triplets SE

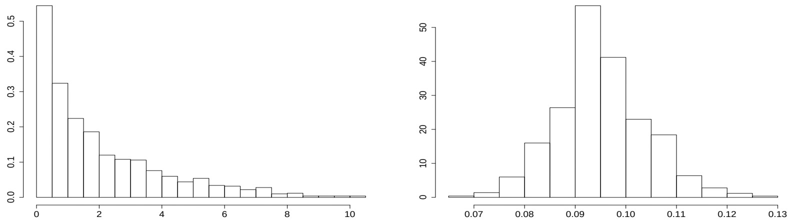


(a) n=25 (b) n=50



(c) n=100 (d) n=200

Figure C.71: Co-evolution Model With Normal Attribute Pseudo-Wald and Entropy Tests - 3 Cycles



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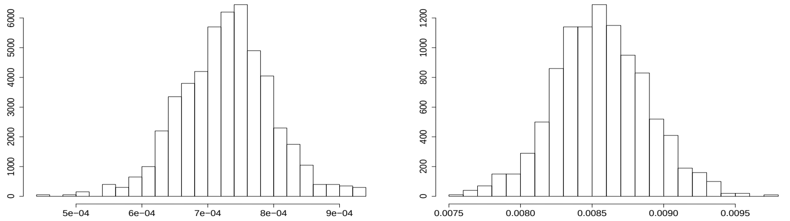
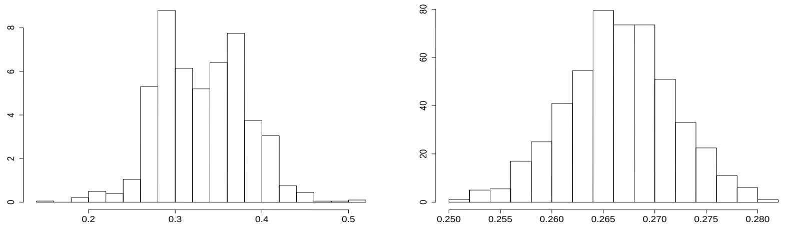
(b) n=50



(c) n=100

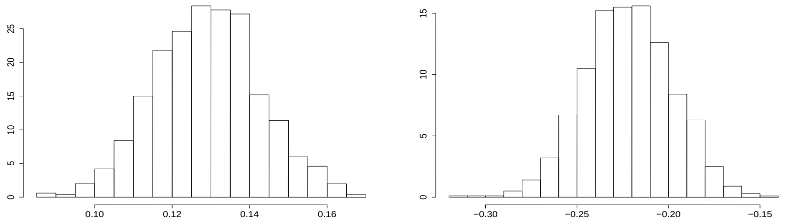
(d) n=200

Figure C.72: Co-evolution Model With Normal Attribute Pseudo-Wald and Entropy Tests - 3 Cycles SE



(a) n=25

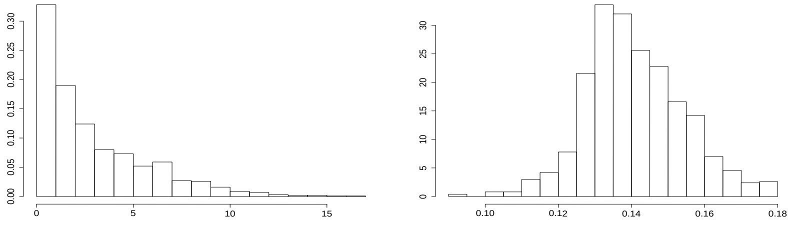
(b) n=50



(c) n=100

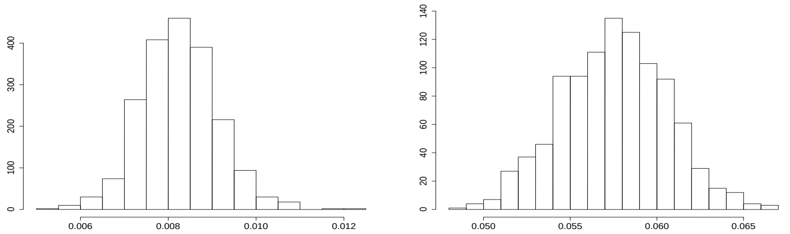
(d) n=200

Figure C.73: Co-evolution Model With Normal Attribute Pseudo-Wald and Entropy Tests - Transitive Ties



(a) n=25

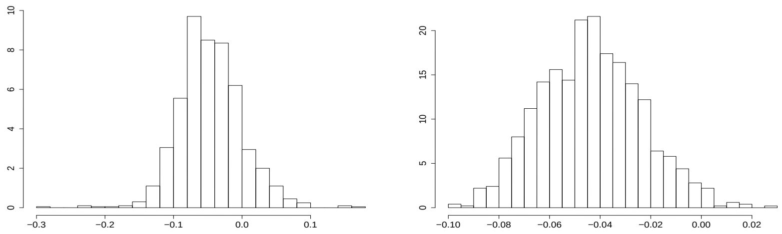
(b) n=50



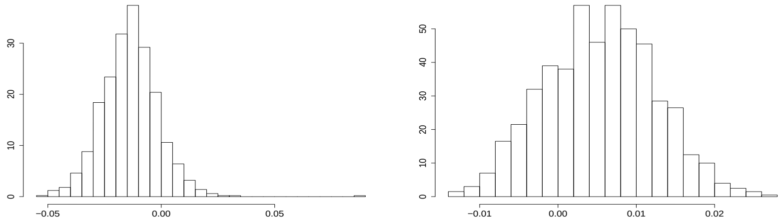
(c) n=100

(d) n=200

Figure C.74: Co-evolution Model With Normal Attribute Pseudo-Wald and Entropy Tests - Transitive Ties SE

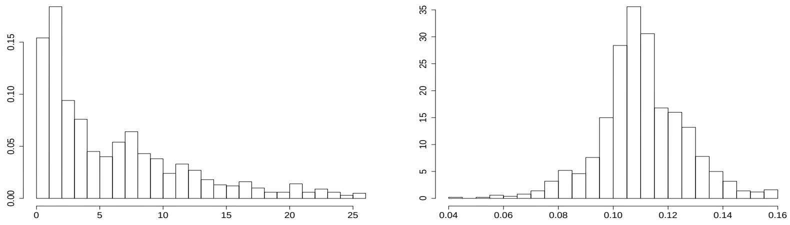


(a) n=25 (b) n=50



(c) n=100 (d) n=200

Figure C.75: Co-evolution Model With Normal Attribute Pseudo-Wald and Entropy Tests - Outdegree-Popularity (Square Root)



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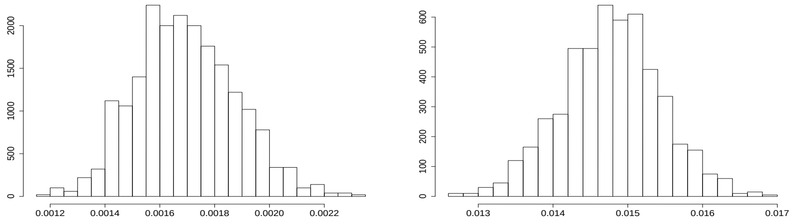
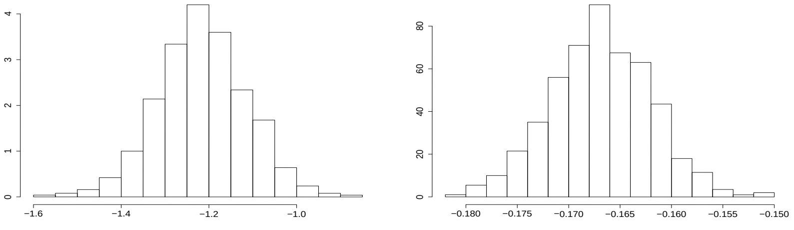


(c) n=100 (d) n=200

Figure C.76: Co-evolution Model With Normal Attribute Pseudo-Wald and Entropy Tests - Outdegree-Popularity (Square Root) SE



(a) n=25

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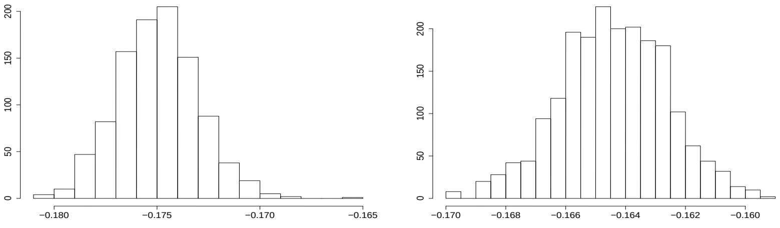
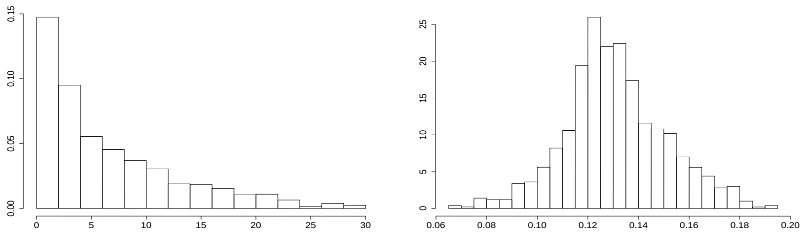


(c) n=100

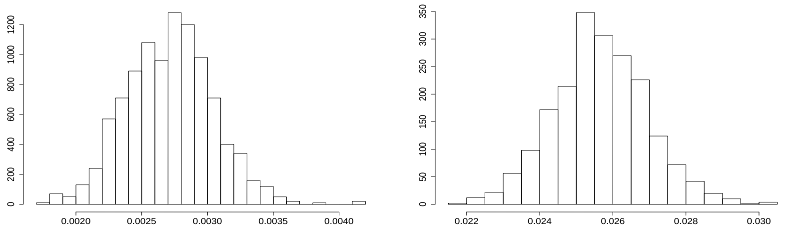
(d) n=200

Figure C.77: Co-evolution Model With Normal Attribute Pseudo-Wald and Entropy Tests - Attribute Alter



(a) n=25

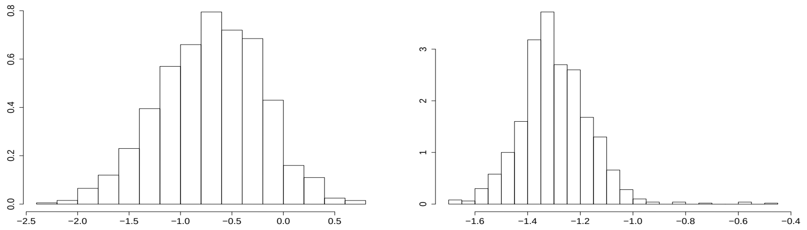
(b) n=50



(c) n=100

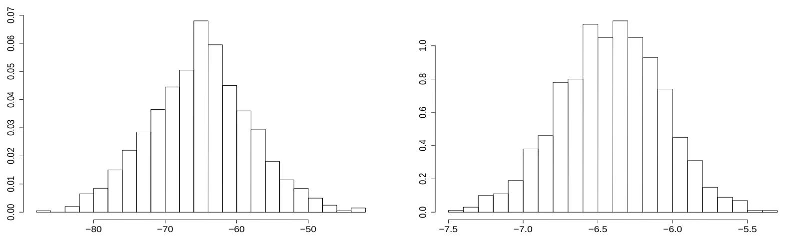
(d) n=200

Figure C.78: Co-evolution Model With Normal Attribute Pseudo-Wald and Entropy Tests - Attribute Alter SE



(a) n=25

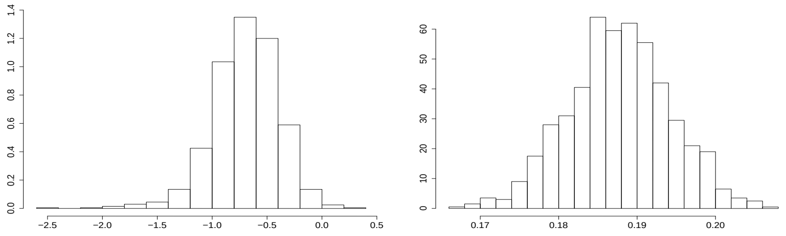
(b) n=50



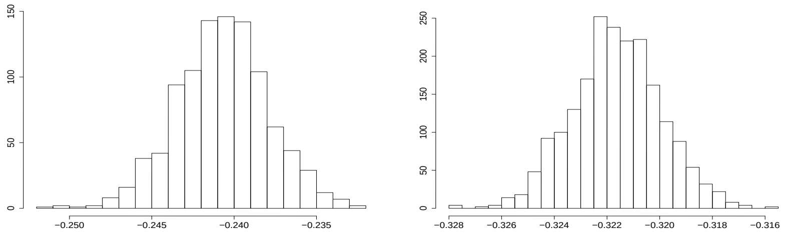
(c) n=100

(d) n=200

Figure C.79: Co-evolution Model With Normal Attribute Pseudo-Wald and Entropy Tests- Attribute Alter t-Test

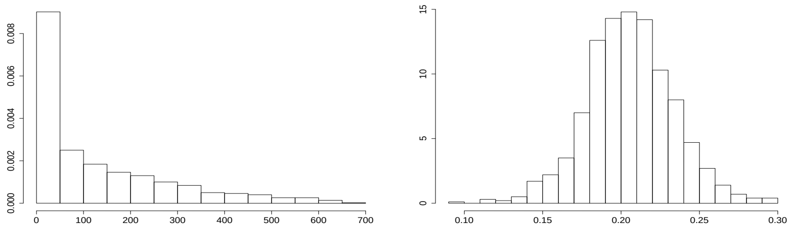


(a) n=25 (b) n=50

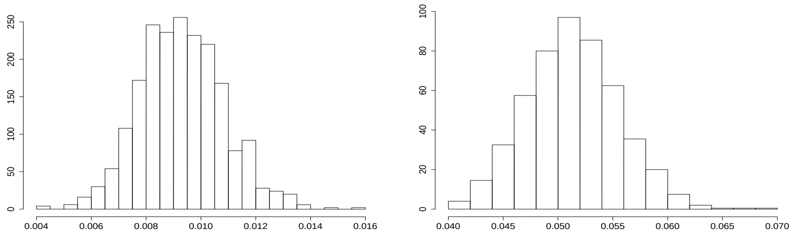


(c) n=100 (d) n=200

Figure C.80: Co-evolution Model With Normal Attribute Pseudo-Wald and Entropy Tests - Attribute Ego

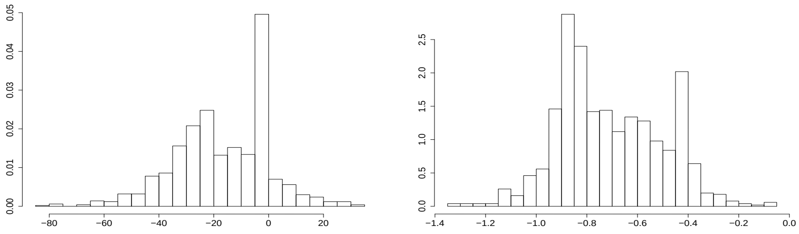


(a) n=25 (b) n=50



(c) n=100 (d) n=200

Figure C.81: Co-evolution Model With Normal Attribute Pseudo-Wald and Entropy Tests - Attribute Ego SE



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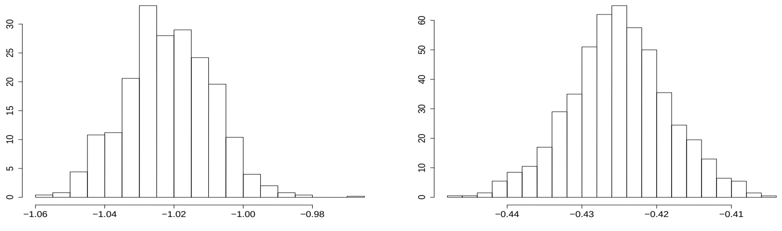
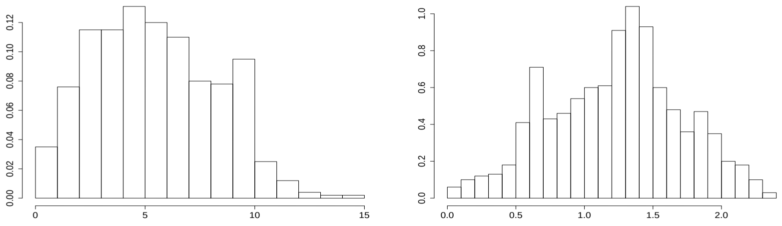
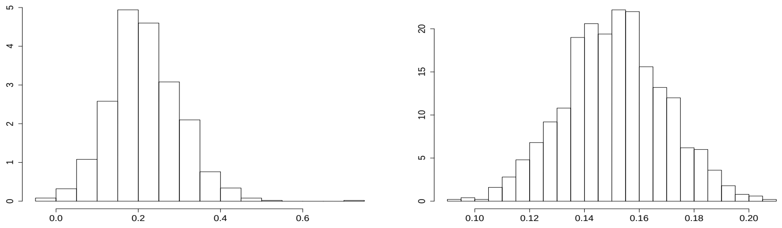


(c) n=100 (d) n=200

Figure C.82: Co-evolution Model With Normal Attribute Pseudo-Wald and Entropy Tests - Attribute Same

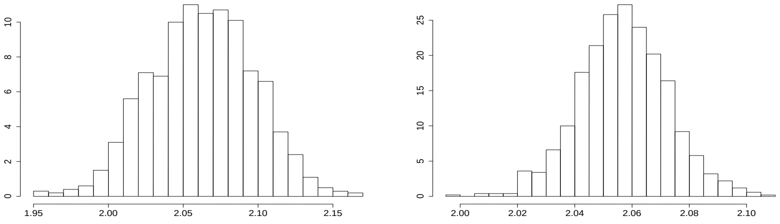


(a) n=25 (b) n=50

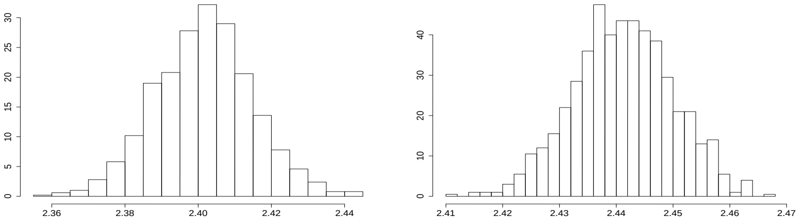


(c) n=100 (d) n=200

Figure C.83: Co-evolution Model With Normal Attribute Pseudo-Wald and Entropy Tests - Attribute Same SE

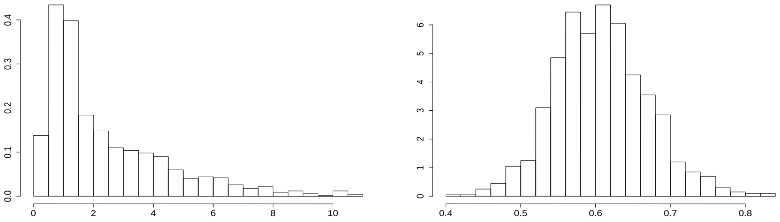


(a) n=25 (b) n=50

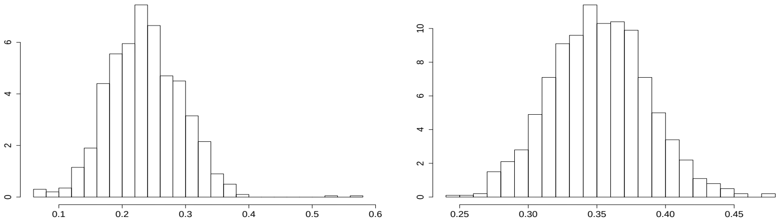


(c) n=100 (d) n=200

Figure C.84: Co-evolution Model With Normal Attribute Pseudo-Wald and Entropy Tests - Attribute Rate Time 1

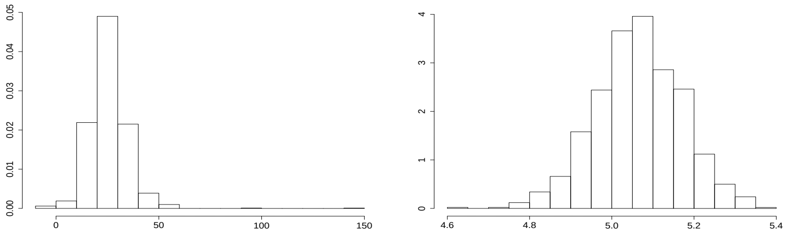


(a) n=25 (b) n=50

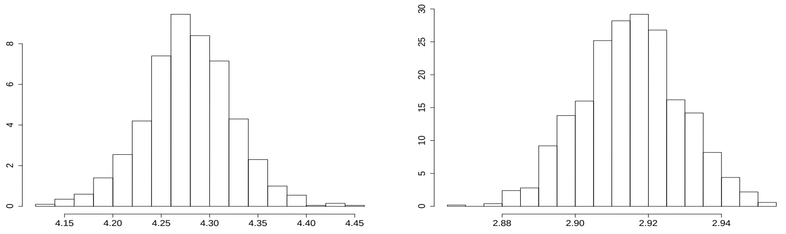


(c) n=100 (d) n=200

Figure C.85: Co-evolution Model With Normal Attribute Pseudo-Wald and Entropy Tests - Attribute Rate Time 1 SE

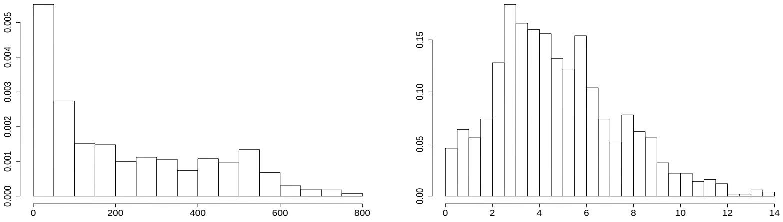


(a) n=25 (b) n=50



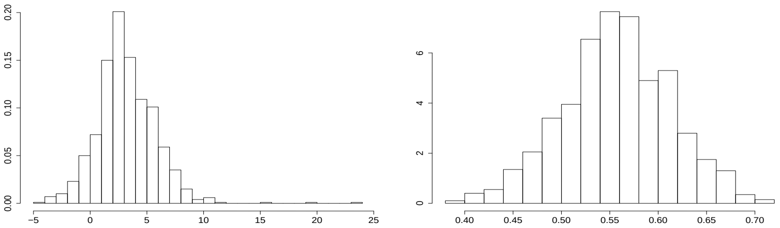
(c) n=100 (d) n=200

Figure C.86: Co-evolution Model With Normal Attribute Pseudo-Wald and Entropy Tests - Attribute Rate Time 2



(a) n=25

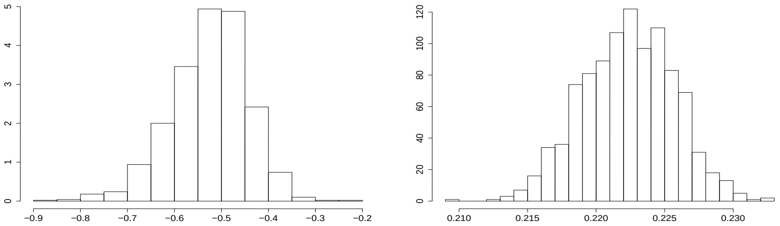
(b) n=50



(c) n=100

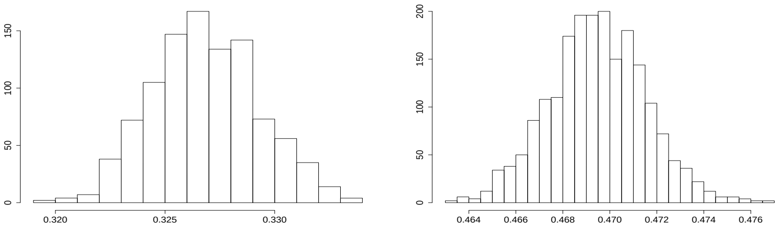
(d) n=200

Figure C.87: Co-evolution Model With Normal Attribute Pseudo-Wald and Entropy Tests - Attribute Rate Time 2 SE



(a) n=25

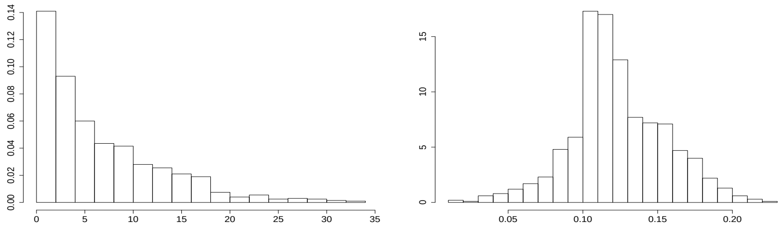
(b) n=50



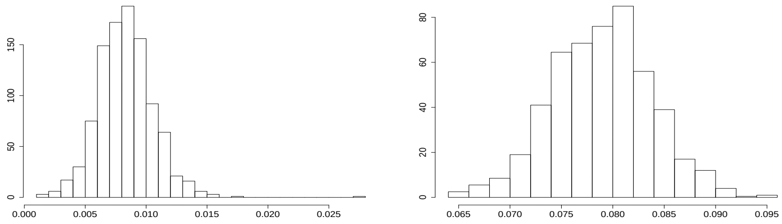
(c) n=100

(d) n=200

Figure C.88: Co-evolution Model With Normal Attribute Pseudo-Wald and Entropy Tests - Linear Shape

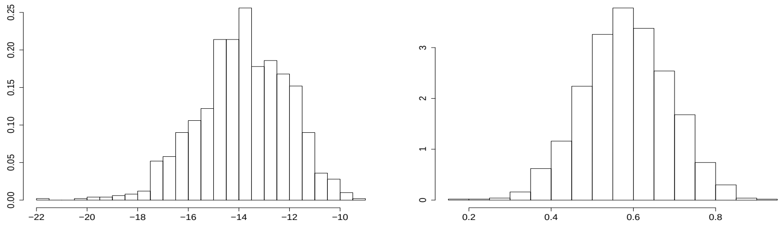


(a) n=25 (b) n=50

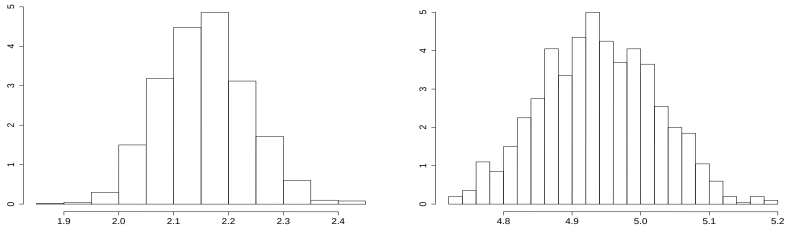


(c) n=100 (d) n=200

Figure C.89: Co-evolution Model With Normal Attribute Pseudo-Wald and Entropy Tests - Linear Shape SE

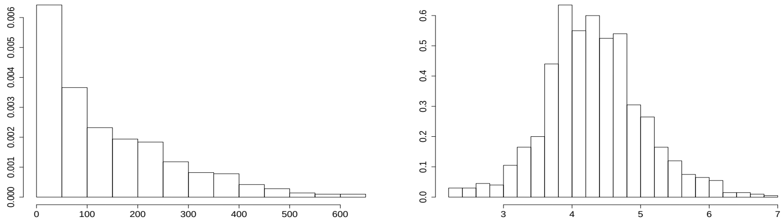


(a) n=25 (b) n=50

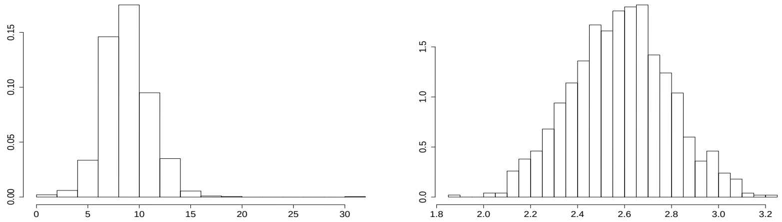


(c) n=100 (d) n=200

Figure C.90: Co-evolution Model With Normal Attribute Pseudo-Wald and Entropy Tests - Average Similarity

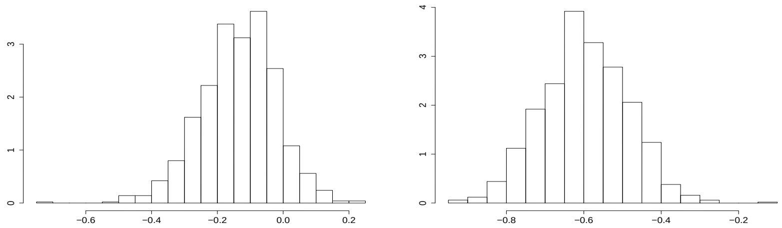


(a) n=25 (b) n=50

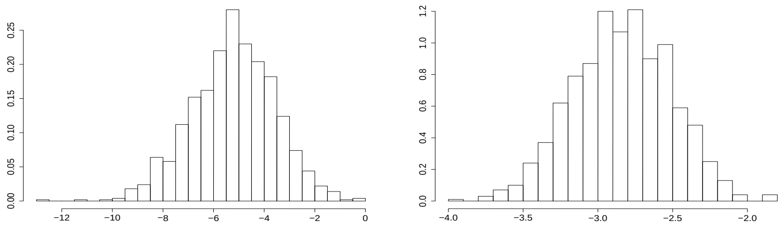


(c) n=100 (d) n=200

Figure C.91: Co-evolution Model With Normal Attribute Pseudo-Wald and Entropy Tests - Average Similarity SE

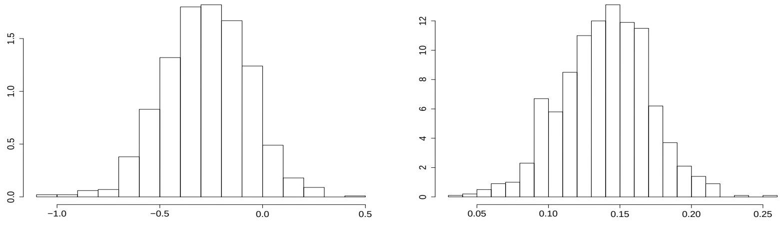


(a) n=25 (b) n=50



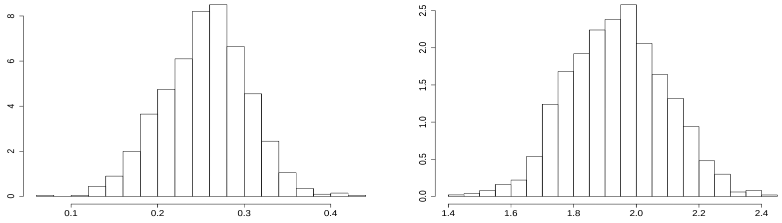
(c) n=100 (d) n=200

Figure C.92: Co-evolution Model With Normal Attribute Pseudo-Wald - Same Attribute t-Test



(a) n=25

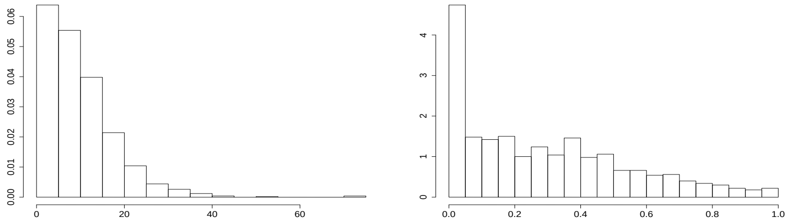
(b) n=50



(c) n=100

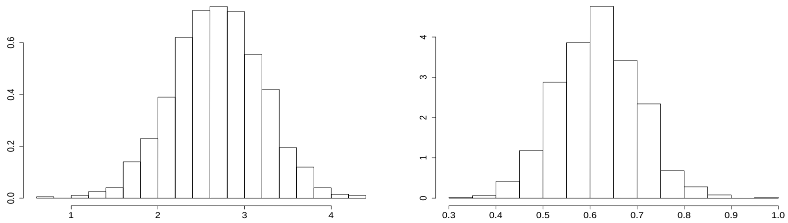
(d) n=200

Figure C.93: Co-evolution Model With Normal Attribute Pseudo-Wald - Average Similarity Attribute t-Test



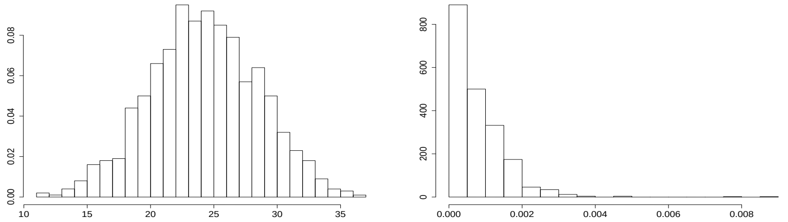
(a) Pseudo-Wald Test Statistic n=25

(b) Pseudo-Wald P-value n=25



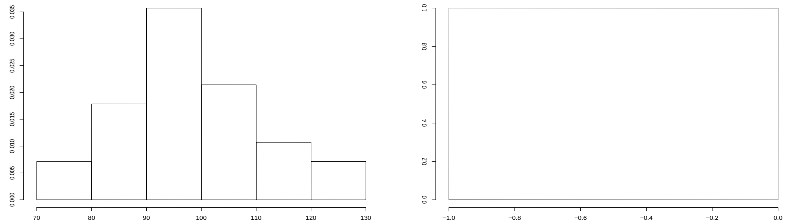
(c) Pseudo-Wald Test Statistic n=50

(d) Pseudo-Wald P-value n=50



(e) Pseudo-Wald Test Statistic n=100

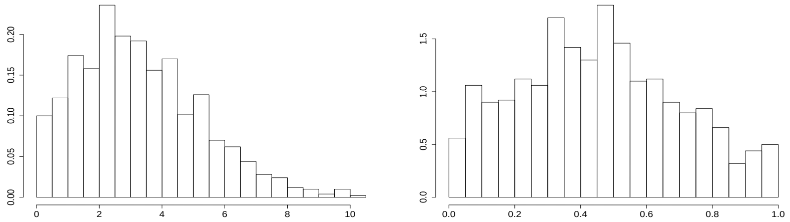
(f) Pseudo-Wald P-value n=100



(g) Pseudo-Wald Test Statistic n=200

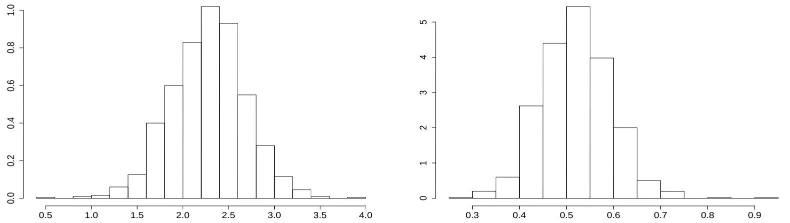
(h) Pseudo-Wald P-value n=200

Figure C.94: Co-evolution Model With Normal Attribute - Pseudo-Wald for Outdegree-Popularity (Square Root), Attribute Alter, Attribute Ego, and Attribute Same



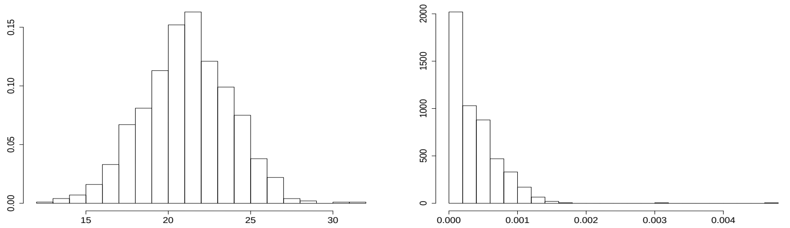
(a) Pseudo-Wald Test Statistic n=25

(b) Pseudo-Wald P-value n=25



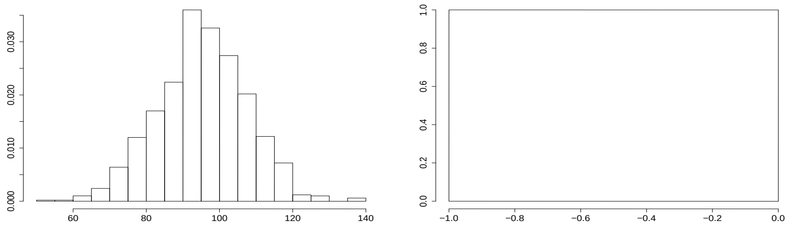
(c) Pseudo-Wald Test Statistic n=50

(d) Pseudo-Wald P-value n=50



(e) Pseudo-Wald Test Statistic n=100

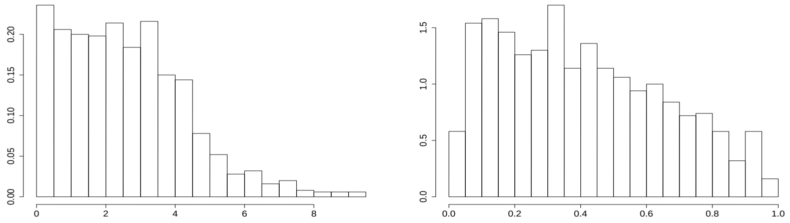
(f) Pseudo-Wald P-value n=100



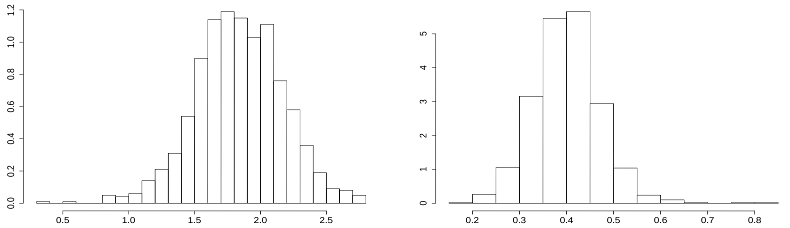
(g) Pseudo-Wald Test Statistic n=200

(h) Pseudo-Wald P-value n=200

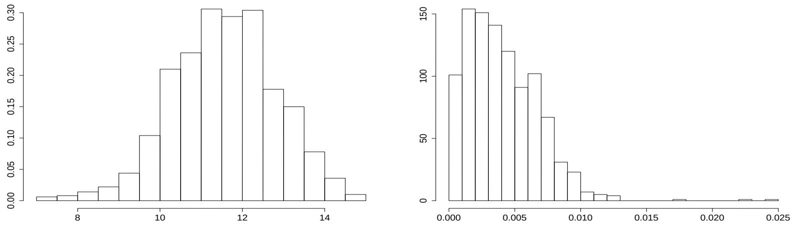
Figure C.95: Co-evolution Model With Normal Attribute - Pseudo-Wald for Outdegree-Popularity (Square Root), Attribute Alter, and Attribute Ego



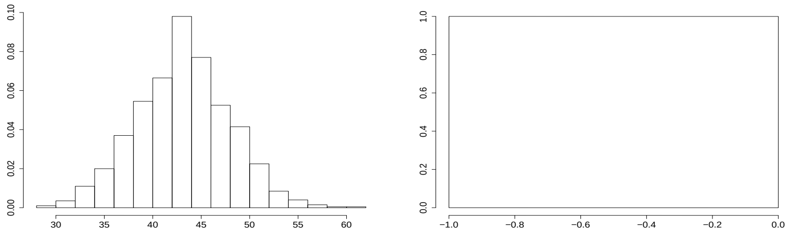
(a) Pseudo-Wald Test Statistic n=25 (b) Pseudo-Wald P-value n=25



(c) Pseudo-Wald Test Statistic n=50 (d) Pseudo-Wald P-value n=50

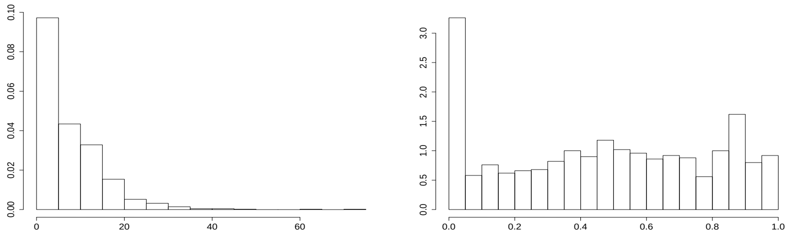


(e) Pseudo-Wald Test Statistic n=100 (f) Pseudo-Wald P-value n=100

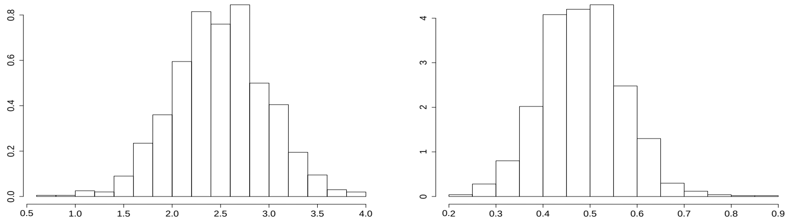


(g) Pseudo-Wald Test Statistic n=200 (h) Pseudo-Wald P-value n=200

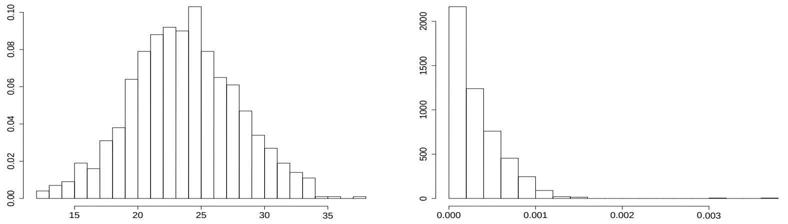
Figure C.96: Co-evolution Model With Normal Attribute - Pseudo-Wald for Outdegree-Popularity (Square Root) and Attribute Alter



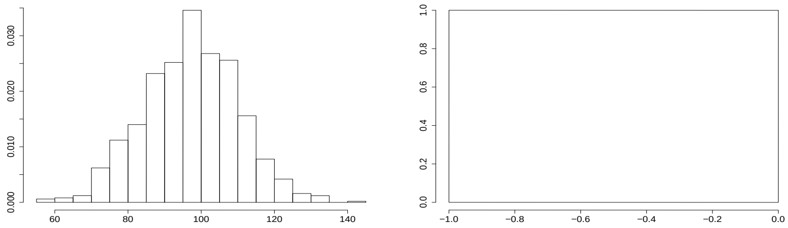
(a) Pseudo-Wald Test Statistic n=25 (b) Pseudo-Wald P-value n=25



(c) Pseudo-Wald Test Statistic n=50 (d) Pseudo-Wald P-value n=50

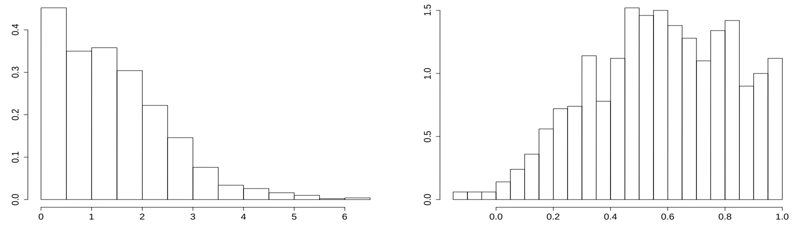


(e) Pseudo-Wald Test Statistic n=100 (f) Pseudo-Wald P-value n=100

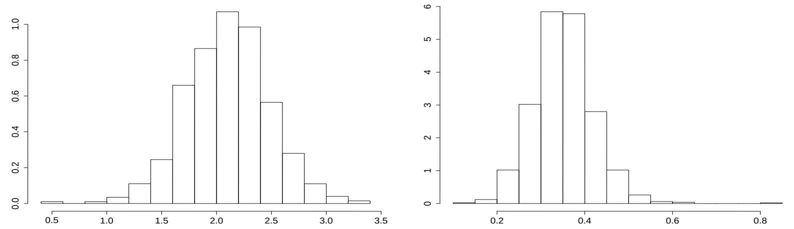


(g) Pseudo-Wald Test Statistic n=200 (h) Pseudo-Wald P-value n=200

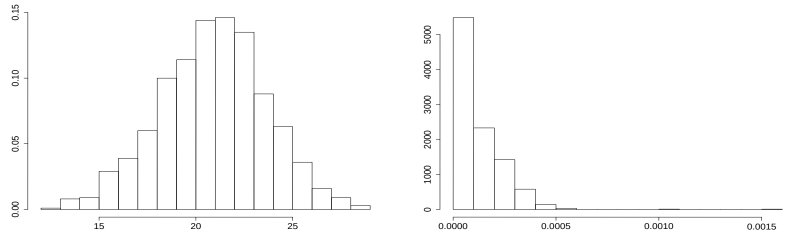
Figure C.97: Co-evolution Model With Normal Attribute - Pseudo-Wald for Attribute Alter, Attribute Ego and Attribute Same



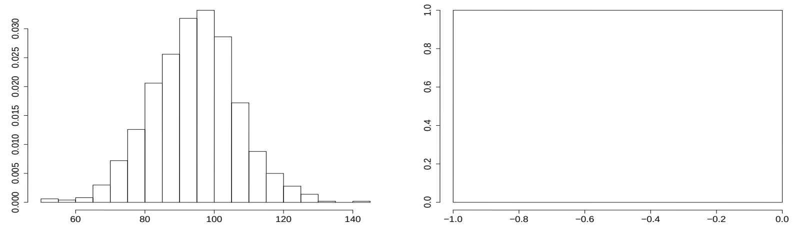
(a) Pseudo-Wald Test Statistic n=25 (b) Pseudo-Wald P-value n=25



(c) Pseudo-Wald Test Statistic n=50 (d) Pseudo-Wald P-value n=50

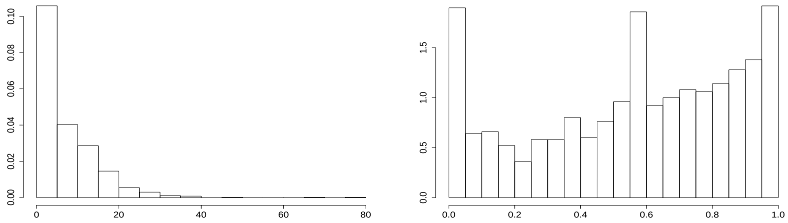


(e) Pseudo-Wald Test Statistic n=100 (f) Pseudo-Wald P-value n=100

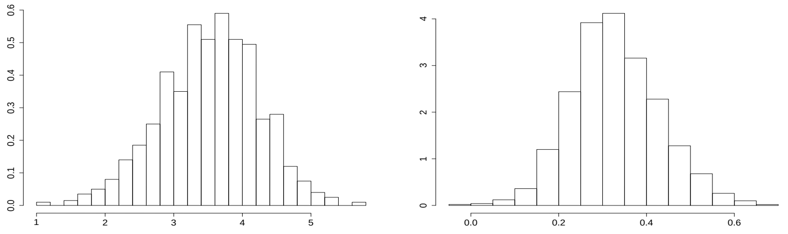


(g) Pseudo-Wald Test Statistic n=200 (h) Pseudo-Wald P-value n=200

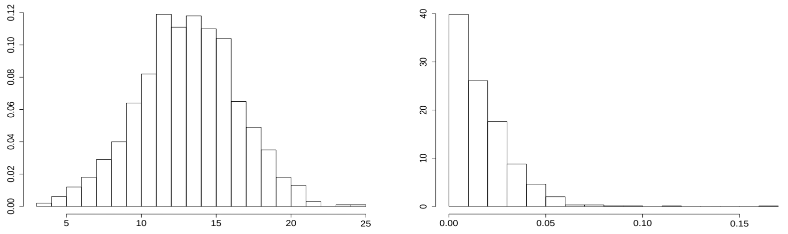
Figure C.98: Co-evolution Model With Normal Attribute - Pseudo-Wald for Attribute Alter and Attribute Ego



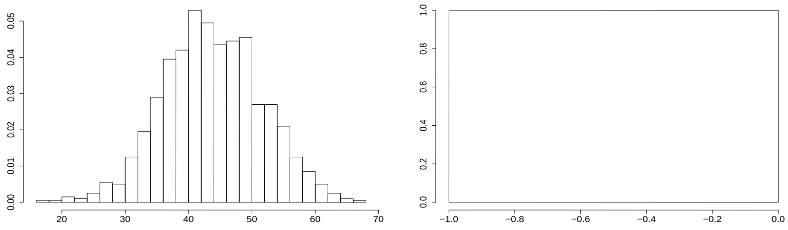
(a) Pseudo-Wald Test Statistic n=25 (b) Pseudo-Wald P-value n=25



(c) Pseudo-Wald Test Statistic n=50 (d) Pseudo-Wald P-value n=50

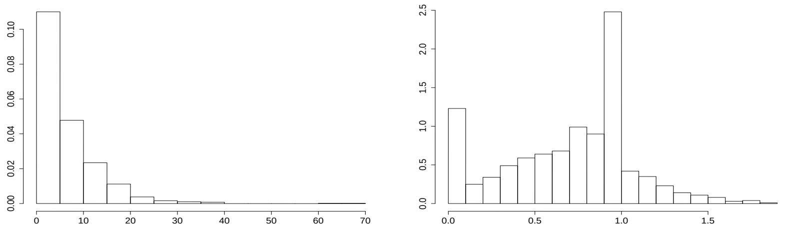


(e) Pseudo-Wald Test Statistic n=100 (f) Pseudo-Wald P-value n=100



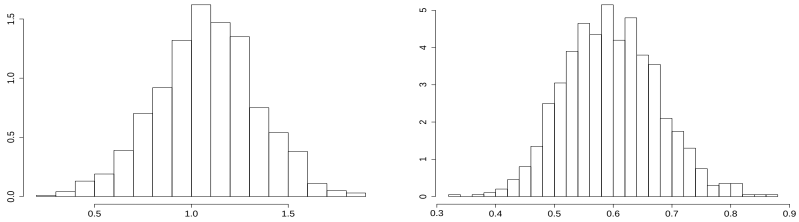
(g) Pseudo-Wald Test Statistic n=200 (h) Pseudo-Wald P-value n=200

Figure C.99: Co-evolution Model With Normal Attribute - Pseudo-Wald for Attribute Ego, Attribute Same, and Average Similarity



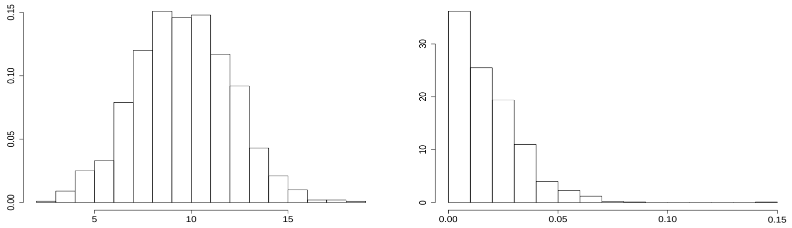
(a) Pseudo-Wald Test Statistic n=25

(b) Pseudo-Wald P-value n=25



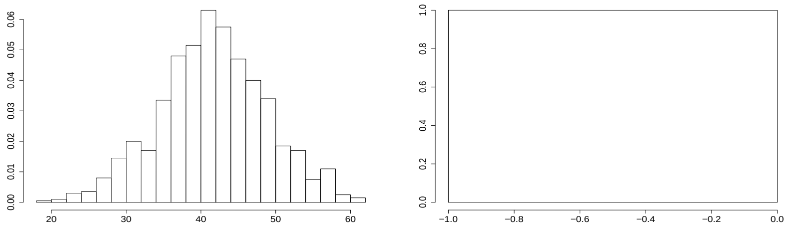
(c) Pseudo-Wald Test Statistic n=50

(d) Pseudo-Wald P-value n=50



(e) Pseudo-Wald Test Statistic n=100

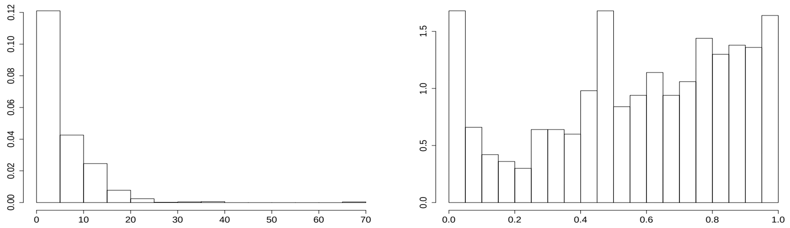
(f) Pseudo-Wald P-value n=100



(g) Pseudo-Wald Test Statistic n=200

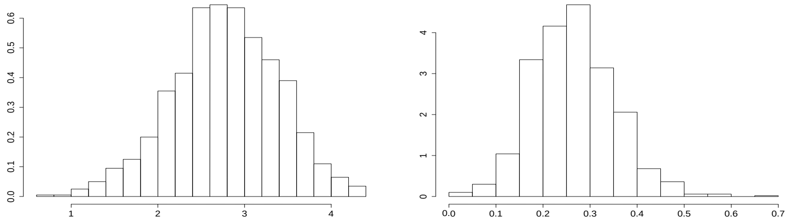
(h) Pseudo-Wald P-value n=200

Figure C.100: Co-evolution Model With Normal Attribute - Pseudo-Wald for Attribute Ego and Attribute Same



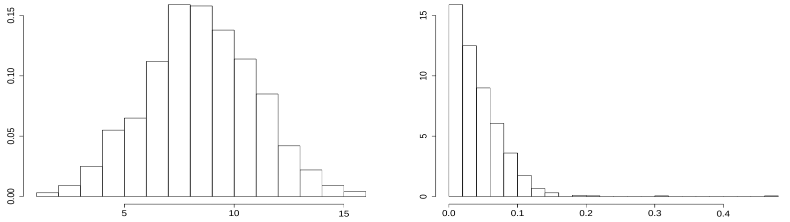
(a) Pseudo-Wald Test Statistic n=25

(b) Pseudo-Wald P-value n=25



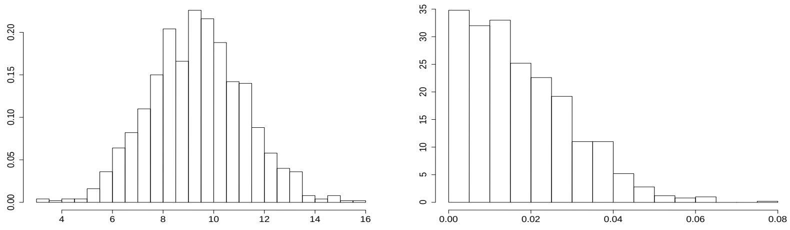
(c) Pseudo-Wald Test Statistic n=50

(d) Pseudo-Wald P-value n=50



(e) Pseudo-Wald Test Statistic n=100

(f) Pseudo-Wald P-value n=100



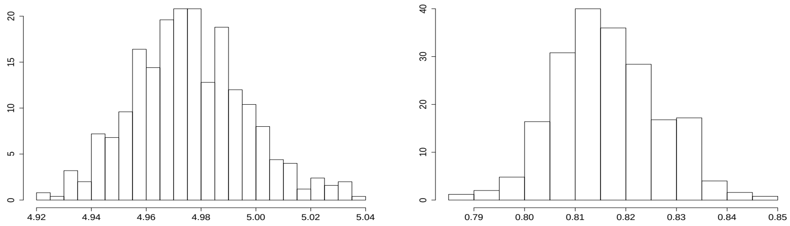
(g) Pseudo-Wald Test Statistic n=200

(h) Pseudo-Wald P-value n=200

Figure C.101: Co-evolution Model With Normal Attribute - Pseudo-Wald for Attribute Same and Average Similarity

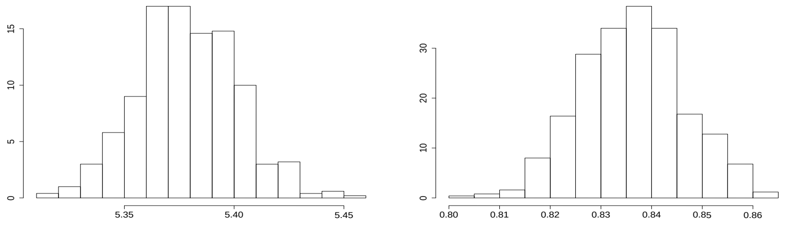
D Knecht's Friendship Data

D.1 Score Test



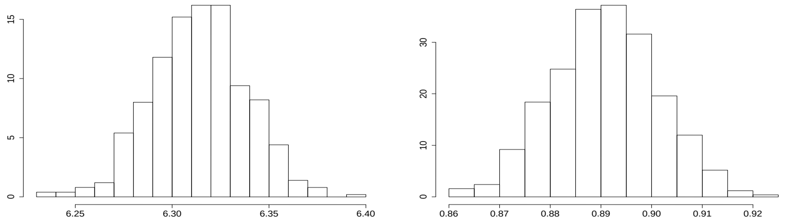
(a) Rate Time 1

(b) Rate Time 1 SE



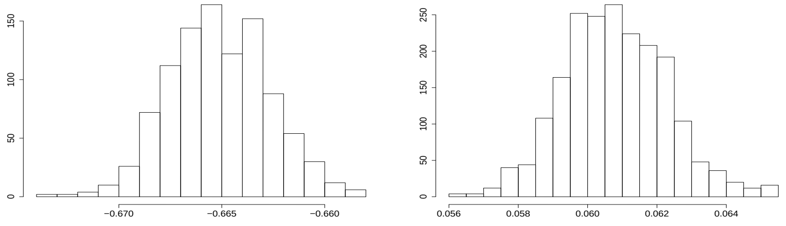
(c) Rate Time 2

(d) Rate Time 2 SE



(e) Rate Time 3

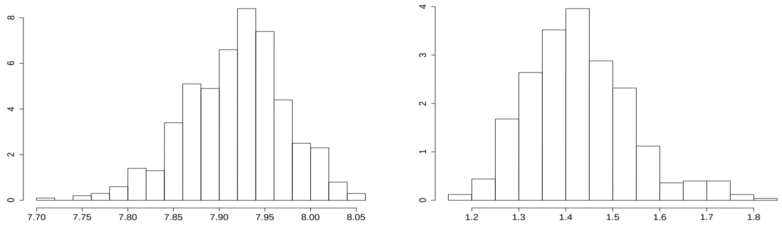
(f) Rate Time 3 SE



(g) Density

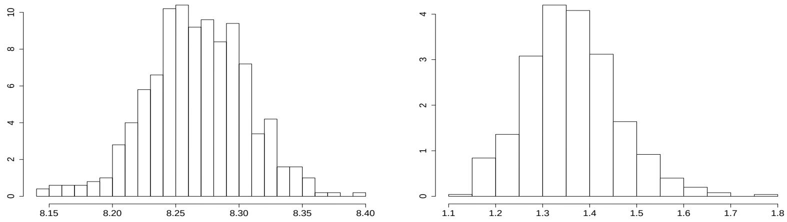
(h) Density SE

Figure D.1: Structural Model Score - Knecht Data



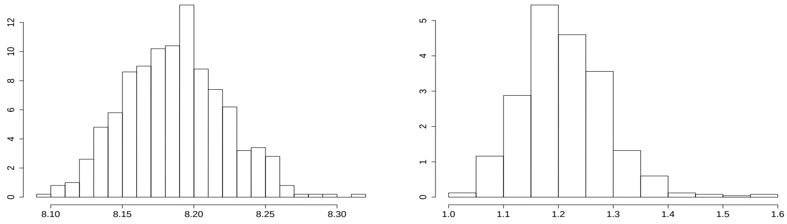
(a) Rate Time 1

(b) Rate Time 1 SE



(c) Rate Time 2

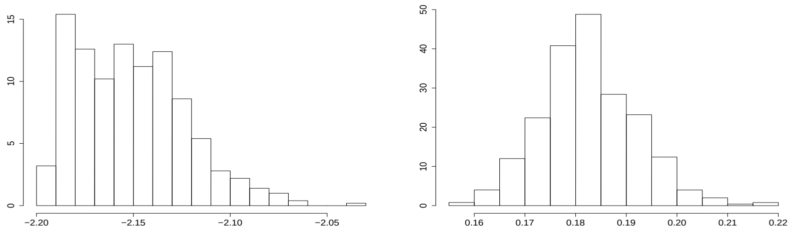
(d) Rate Time 2 SE



(e) Rate Time 3

(f) Rate Time 3 SE

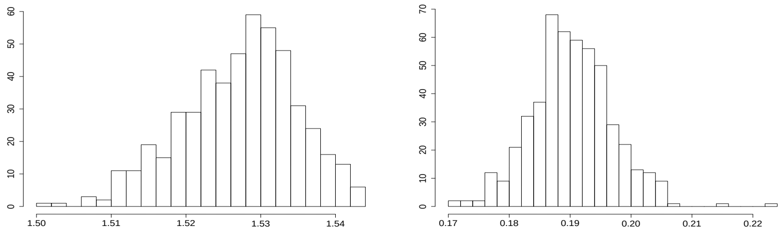
Figure D.2: Co-evolution Model Score - Knecht Data - Network Rate



(a) Density

(b) Density SE

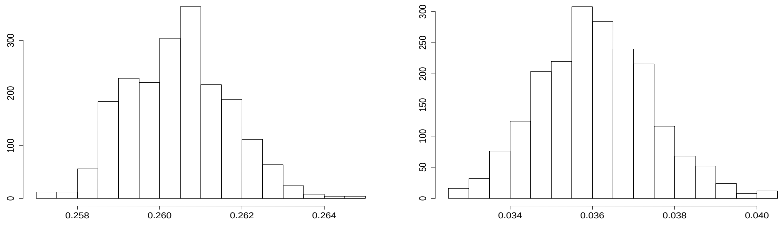
Figure D.3: Co-evolution Model Score -Knecht Data - Density



(a) Reciprocity

(b) Reciprocity SE

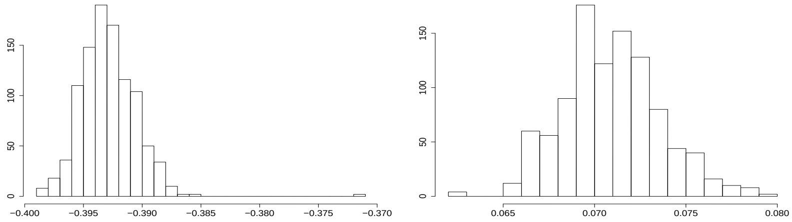
Figure D.4: Co-evolution Model Score -Knecht Data - Reciprocity



(a) Transitive Triplets

(b) Transitive Triplets SE

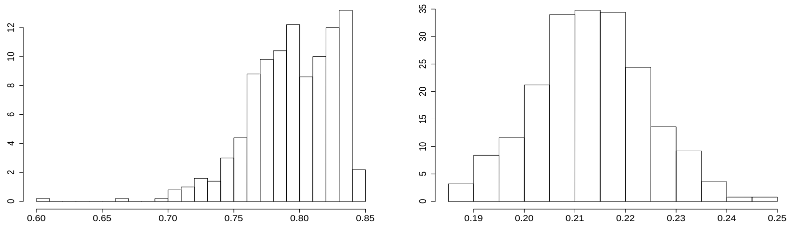
Figure D.5: Co-evolution Model Score - Knecht Data - Transitive Triplets



(a) 3-cycles

(b) 3-cycles SE

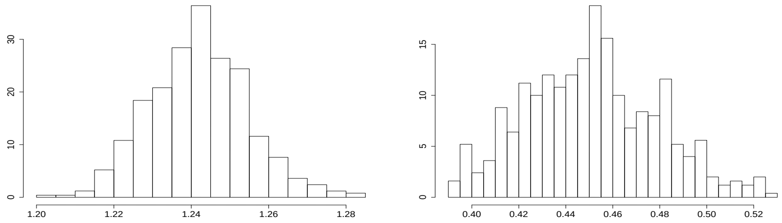
Figure D.6: Co-evolution Model Score - Knecht Data - 3-cycles



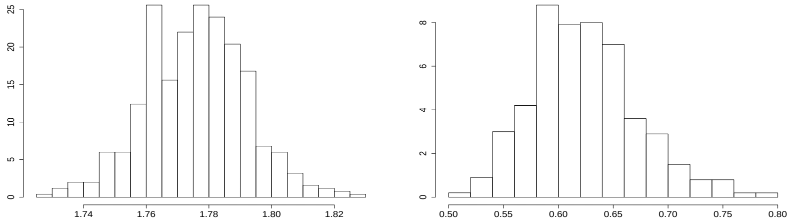
(a) Transitive Ties

(b) Transitive Ties SE

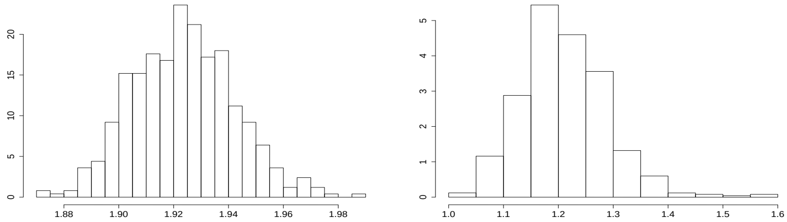
Figure D.7: Co-evolution Model Score - Knecht Data - Transitive Ties



(a) Rate Time 1 (b) Rate Time 1 SE

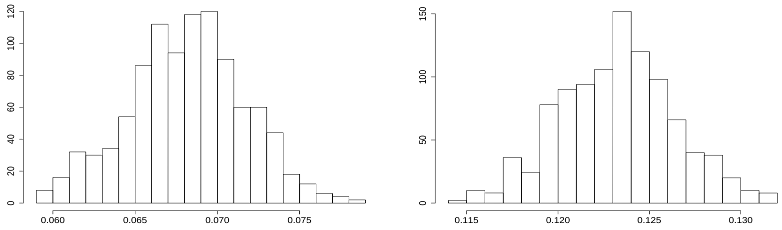


(c) Rate Time 2 (d) Rate Time 2 SE



(e) Rate Time 3 (f) Rate Time 3 SE

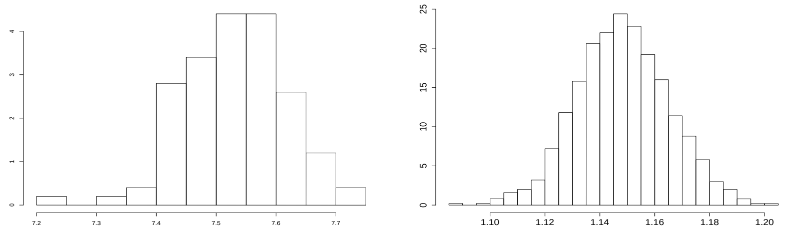
Figure D.8: Co-evolution Model Score - Knecht Data - Attribute Rate



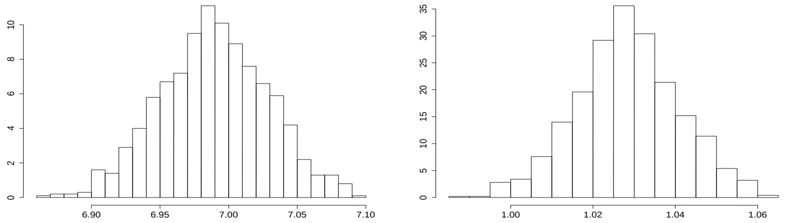
(a) Linear (b) Linear SE

Figure D.9: Co-evolution Model Score - Knecht Data - Linear Shape

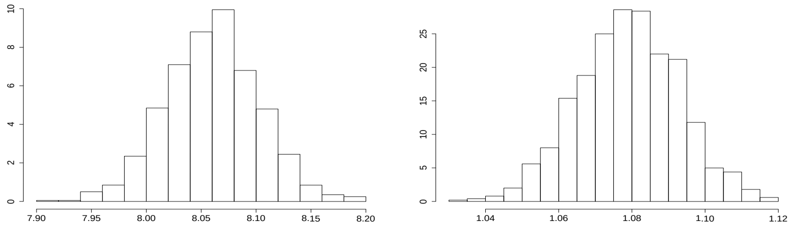
D.2 Pseudo-Wald and Entropy Tests



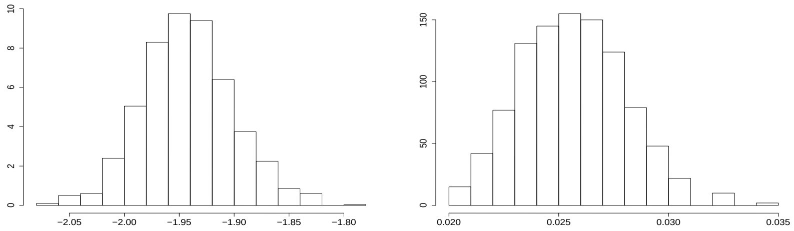
(a) Rate Time 1 (b) Rate Time 1 SE



(c) Rate Time 2 (d) Rate Time 2 SE

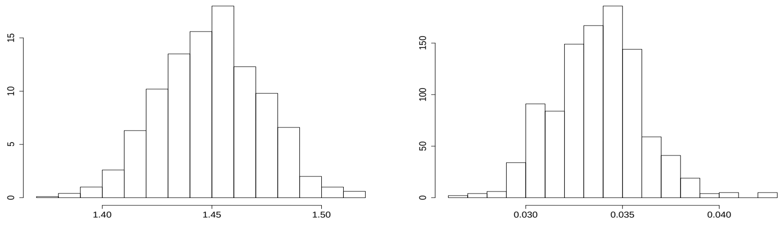


(e) Rate Time 3 (f) Rate Time 3 SE



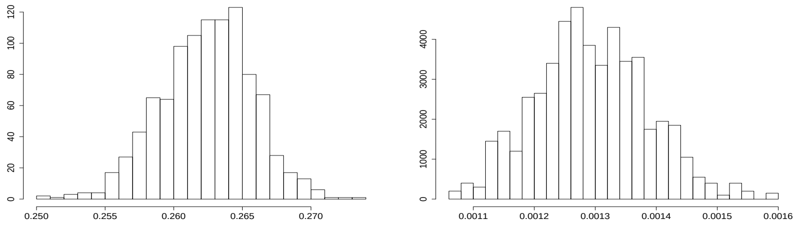
(g) Density (h) Density SE

Figure D.10: Structural Model Pseudo-Wald and Entropy Tests - Knecht Data - Network Rates and Density



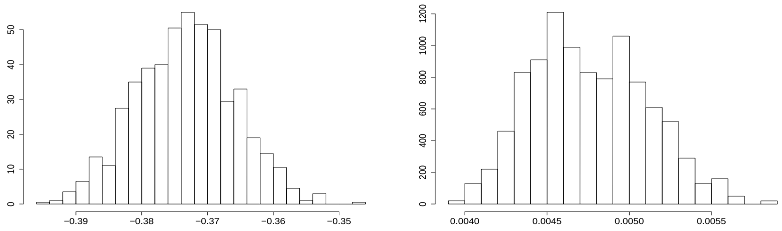
(a) Reciprocity (b) Reciprocity SE

Figure D.11: Structural Model Pseudo-Wald and Entropy Tests -Knecht Data - Reciprocity



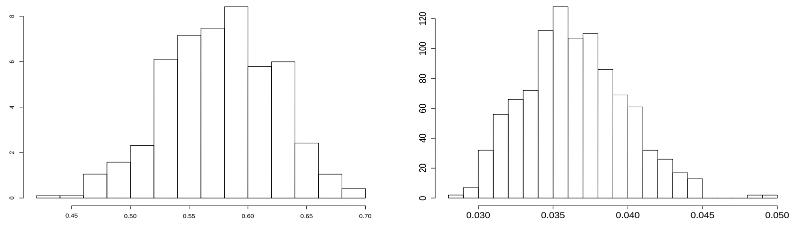
(a) Transitive Triplets (b) Transitive Triplets SE

Figure D.12: Structural Model Pseudo-Wald and Entropy Tests - Knecht Data - Transitive Triplets



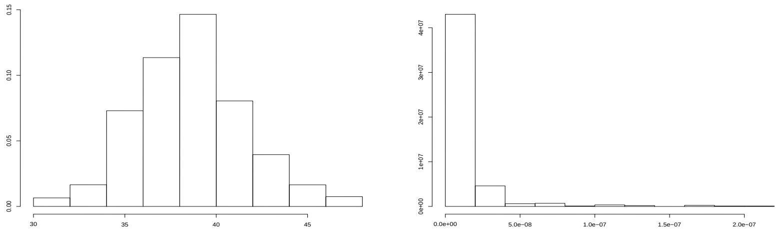
(a) 3-cycles (b) 3-cycles SE

Figure D.13: Structural Model Pseudo-Wald and Entropy Tests - Knecht Data - 3-cycles



(a) Transitive Ties (b) Transitive Ties SE

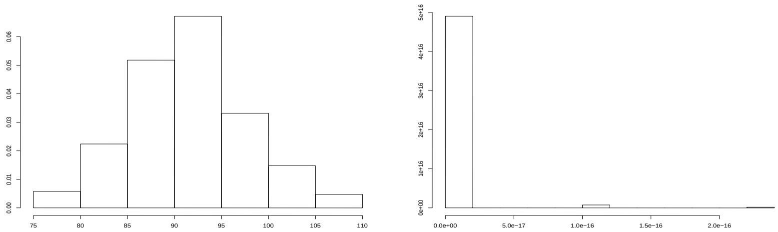
Figure D.14: Structural Model Pseudo-Wald and Entropy Tests - Knecht Data - Transitive Ties



(a) Pseudo-Wald Test Statistic

(b) Pseudo-Wald P-value

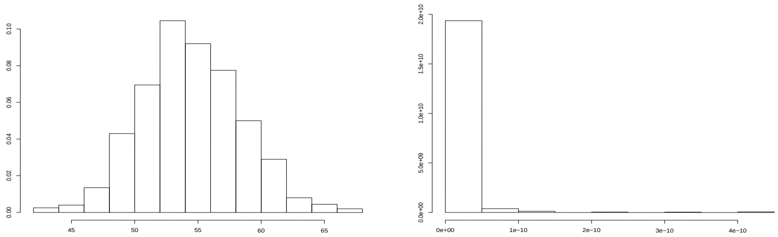
Figure D.15: Structural Model Pseudo-Wald - Knecht Data - 3-cycles, and Transitive Ties



(a) Pseudo-Wald Test Statistic

(b) Pseudo-Wald P-value

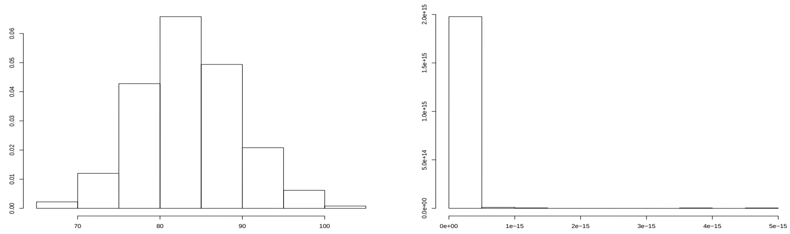
Figure D.16: Structural Model Pseudo-Wald - Knecht Data - Reciprocity, Transitive Triplets, and 3-cycles



(a) Pseudo-Wald Test Statistic

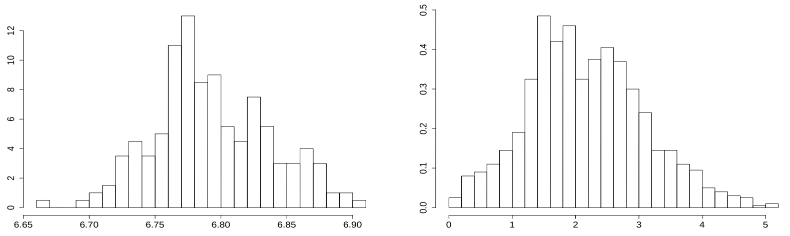
(b) Pseudo-Wald P-value

Figure D.17: Structural Model Pseudo-Wald - Knecht Data - Transitive Triplets, and 3-cycles

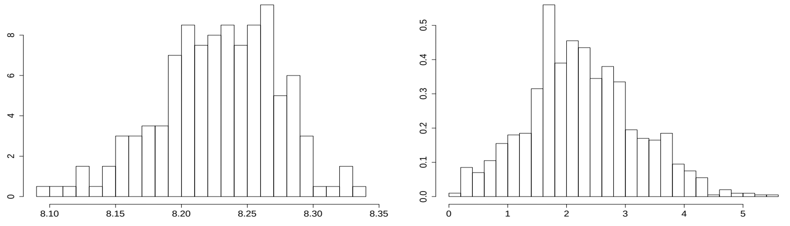


(a) Pseudo-Wald Test Statistic (b) Pseudo-Wald P-value

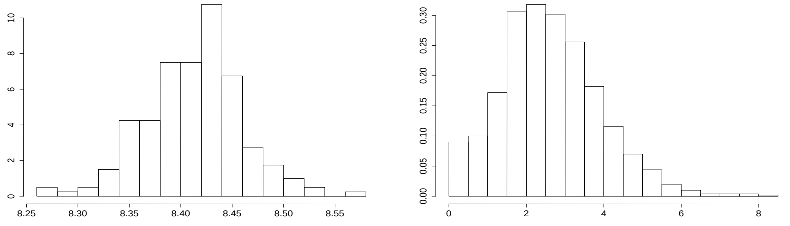
Figure D.18: Structural Model Pseudo-Wald - Knecht Data - Reciprocity, and Transitive Triplets



(a) Rate 1 (b) Rate 1 SE

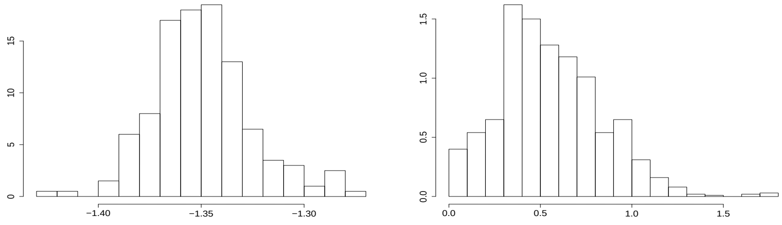


(c) Rate 2 (d) Rate 2 SE



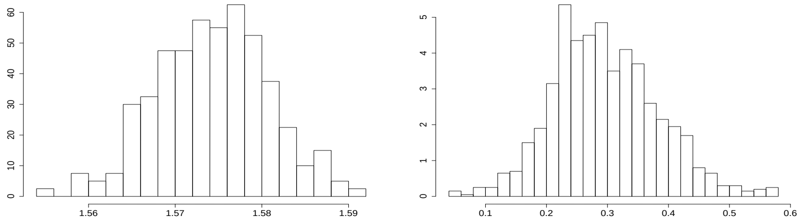
(e) Rate 3 (f) Rate 3 SE

Figure D.19: Co-evolution Model Pseudo-Wald - Knecht Data - Network Rates



(a) Density

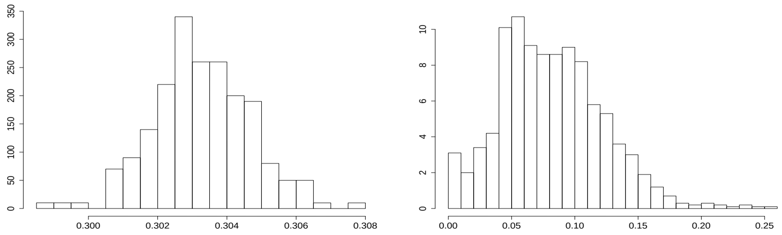
(b) Density SE



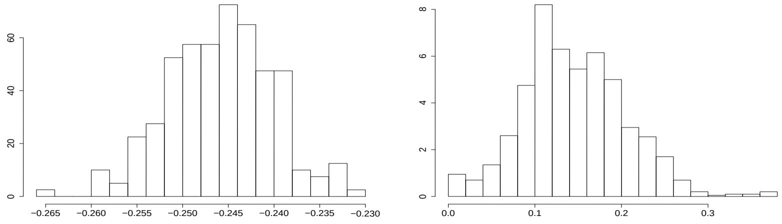
(c) Reciprocity

(d) Reciprocity SE

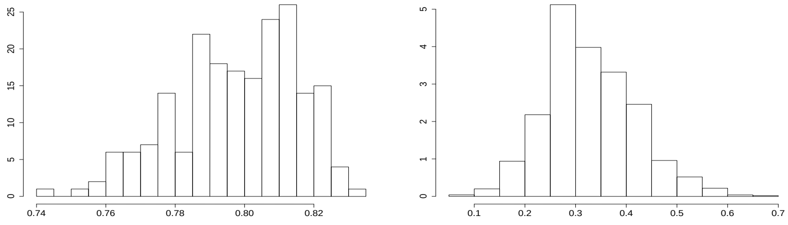
Figure D.20: Co-evolution Model Pseudo-Wald - Knecht Data - Density and Reciprocity



(a) Transitive Triplets (b) Transitive Triplets SE

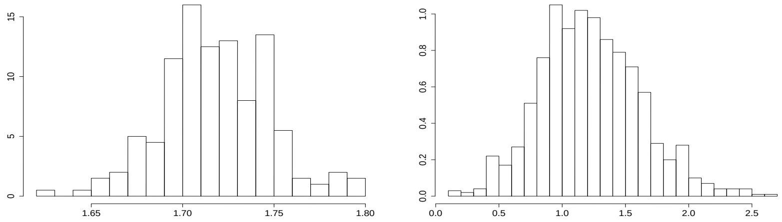


(c) 3-cycles (d) 3-cycles SE



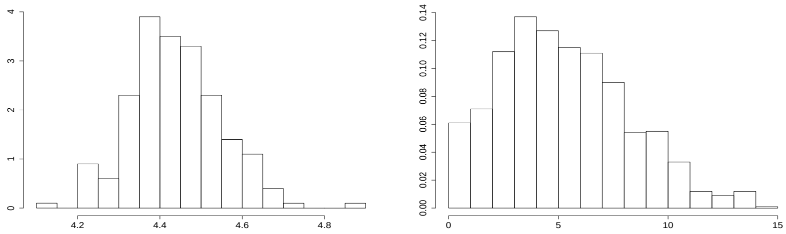
(e) Transitive Ties (f) Transitive Ties SE

Figure D.21: Co-evolution Model Pseudo-Wald - Knecht Data - Transitive Triplets, 3-cycles, and Transitive Ties



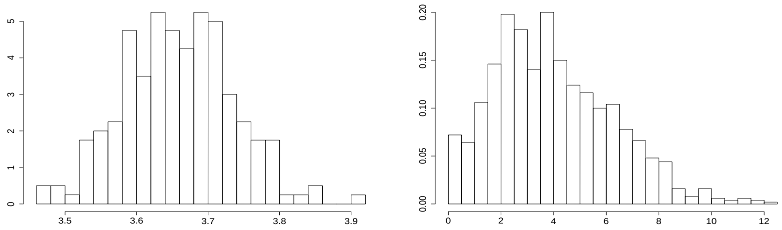
(a) Attribute Rate 1

(b) Attribute Rate 1 SE



(c) Attribute Rate 2

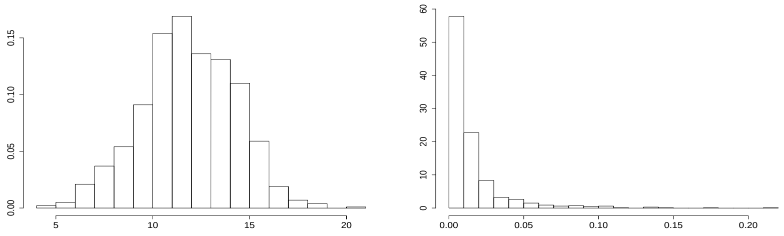
(d) Attribute Rate 2 SE



(e) Attribute Rate 3

(f) Attribute Rate 3 SE

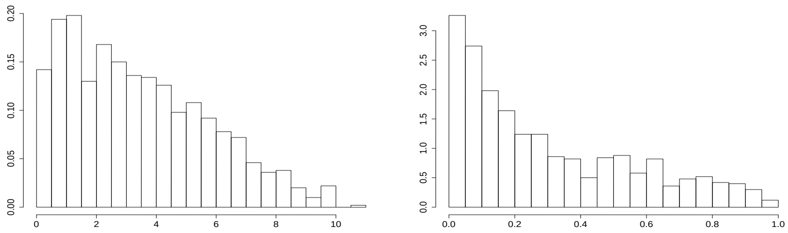
Figure D.22: Co-evolution Model Pseudo-Wald - Knecht Data - Attribute Network Rate



(a) Pseudo-Wald Test Statistic

(b) Pseudo-Wald P-value

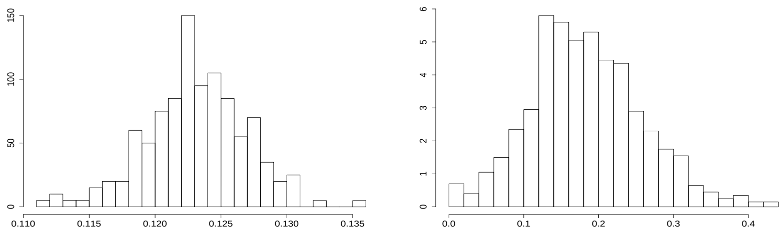
Figure D.23: Co-evolution Model - Knecht Data - Pseudo-Wald for Similarity on Delinquency, Quadratic Shape, and Average Similarity on Delinquency



(a) Pseudo-Wald Test Statistic

(b) Pseudo-Wald P-value

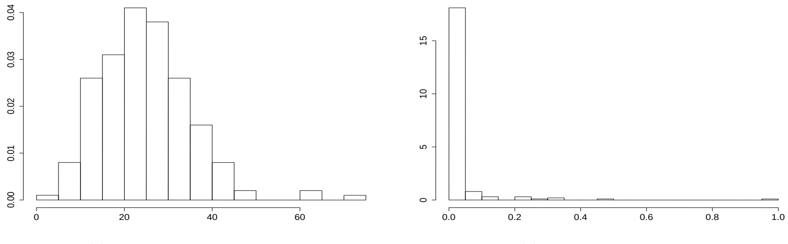
Figure D.24: Co-evolution Model - Knecht Data - Pseudo-Wald for Quadratic Shape and Average Similarity on Delinquency



(a) Linear

(b) Linear SE

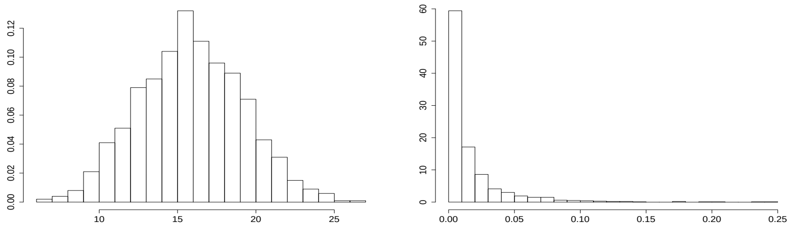
Figure D.25: Co-evolution Model Pseudo-Wald - Knecht Data - Linear



(a) Pseudo-Wald Test Statistic

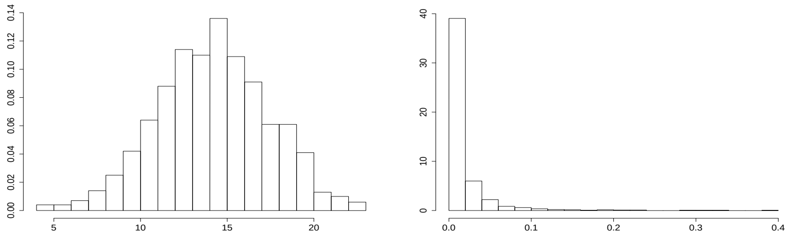
(b) Pseudo-Wald P-value

Figure D.26: Co-evolution Model - Knecht Data - Pseudo-Wald for Outdegree-Popularity, Gender Alter, Gender Ego, Same Gender, Similarity on Delinquency, and Quadratic Shape



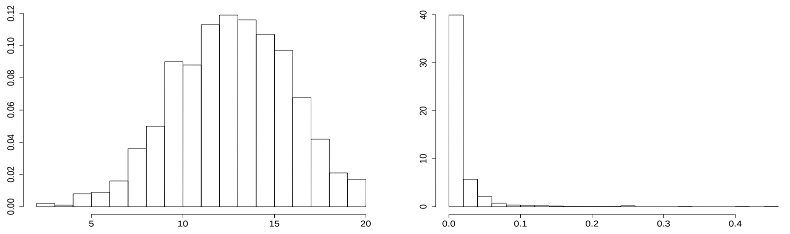
(a) Pseudo-Wald Test Statistic (b) Pseudo-Wald P-value

Figure D.27: Co-evolution Model - Knecht Data - Pseudo-Wald for Outdegree-Popularity, Gender Alter, Gender Ego, Same Gender, and Similarity on Delinquency



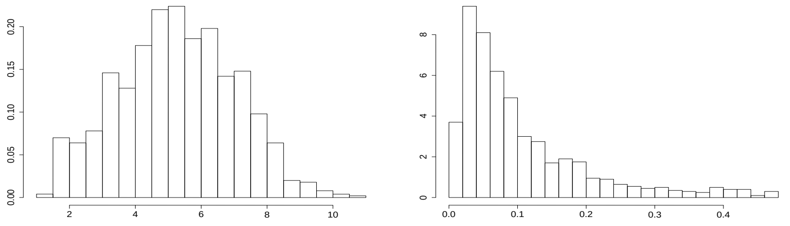
(a) Pseudo-Wald Test Statistic (b) Pseudo-Wald P-value

Figure D.28: Co-evolution Model - Knecht Data - Pseudo-Wald for Outdegree-Popularity, Gender Alter, Gender Ego, and Same Gender



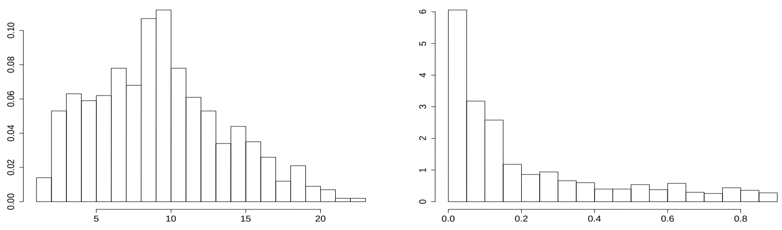
(a) Pseudo-Wald Test Statistic (b) Pseudo-Wald P-value

Figure D.29: Co-evolution Model - Knecht Data - Pseudo-Wald for Outdegree-Popularity, Gender Alter, and Gender Ego



(a) Pseudo-Wald Test Statistic (b) Pseudo-Wald P-value

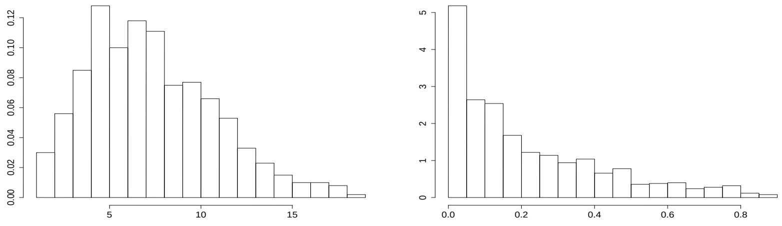
Figure D.30: Co-evolution Model - Knecht Data - Pseudo-Wald for Gender Alter, and Gender Ego



(a) Pseudo-Wald Test Statistic

(b) Pseudo-Wald P-value

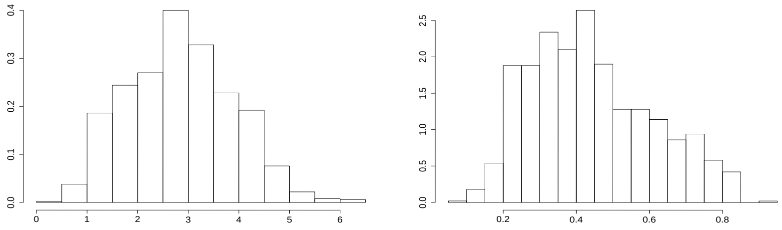
Figure D.31: Co-evolution Model - Knecht Data - Pseudo-Wald for Gender Ego, Same Gender, Similarity on Delinquency, Quadratic Shape, and Average Similarity on Delinquency



(a) Pseudo-Wald Test Statistic

(b) Pseudo-Wald P-value

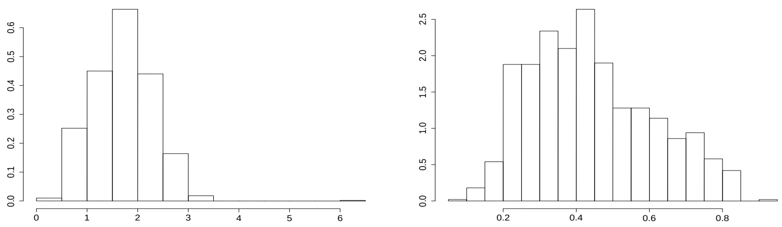
Figure D.32: Co-evolution Model - Knecht Data - Pseudo-Wald for Gender Ego, Same Gender, Similarity on Delinquency, and Quadratic Shape



(a) Pseudo-Wald Test Statistic

(b) Pseudo-Wald P-value

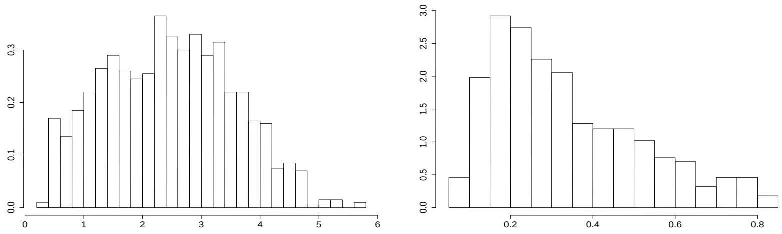
Figure D.33: Co-evolution Model - Knecht Data - Pseudo-Wald for Gender Ego, Same Gender, and Similarity on Delinquency



(a) Pseudo-Wald Test Statistic

(b) Pseudo-Wald P-value

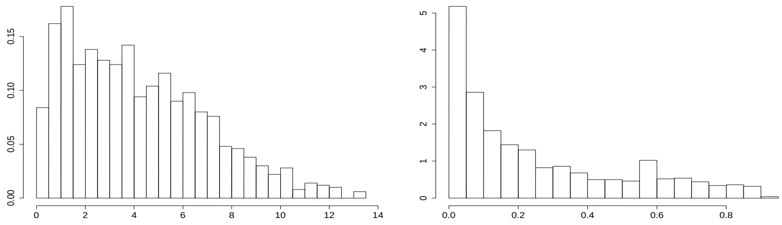
Figure D.34: Co-evolution Model - Knecht Data - Pseudo-Wald for Gender Ego and Same Gender



(a) Pseudo-Wald Test Statistic

(b) Pseudo-Wald P-value

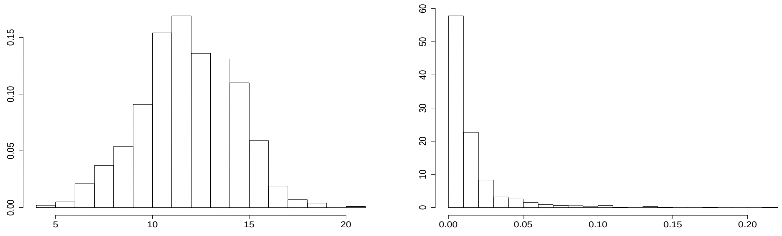
Figure D.35: Co-evolution Model - Knecht Data - Pseudo-Wald for Same Gender and Similarity on Delinquency



(a) Pseudo-Wald Test Statistic

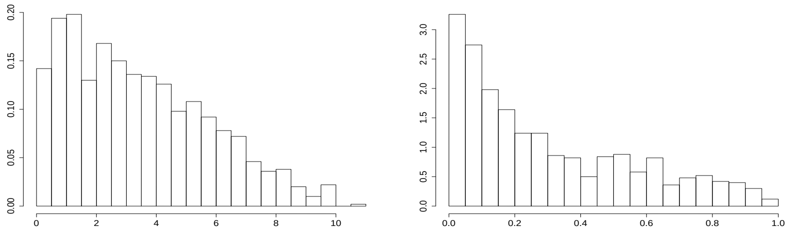
(b) Pseudo-Wald P-value

Figure D.36: Co-evolution Model - Knecht Data - Pseudo-Wald for Similarity on Delinquency and Quadratic Shape



(a) Pseudo-Wald Test Statistic (b) Pseudo-Wald P-value

Figure D.37: Co-evolution Model - Knecht Data - Pseudo-Wald for Similarity on Delinquency, Quadratic Shape, and Average Similarity on Delinquency



(a) Pseudo-Wald Test Statistic (b) Pseudo-Wald P-value

Figure D.38: Co-evolution Model - Knecht Data - Pseudo-Wald for Quadratic Shape and Average Similarity on Delinquency

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