Partial Identification of Linear Models Using Homophily in Network Data

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Abstract

Network endogeneity is often recognized as a threat to identification of models that involve network data, such as models of peer effects. This paper shows how endogenous networks can in fact be a source of identification. In particular, I study a linear model where network data can be used to control for unobserved heterogeneity and partially identify the parameters of the linear model. My method does not rely on a parametric model of network formation. Instead, identification is achieved by assuming that the network satisfies latent homophily — the tendency of individuals to be linked with others who are similar to themselves. I first provide two definitions of homophily: weak and strong homophily. Then, based on these definitions, I characterize the identified sets and show that they are bounded under weak conditions. Finally, to illustrate the method in an empirical setting, I estimate the effects of education on risk preferences and peer effects using social network data from 150 Chinese villages.

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1 Introduction

Homophily, the tendency to interact with others with similar traits, is a prominent feature of networks. It has been widely studied and documented across a wide array of characteristics, including ethnicity, age, profession, and religion (McPherson et al. (2001)). The ubiquity of homophily in networks led economists to study its implications for economic phenomena, such as learning and information diffusion.

An implication of homophily is that networks are endogenous; individuals choose whom to associate based on observed and unobserved preferences. This endogeneity is considered a threat for identification in empirical models that involves network data. An important example is the estimation of peer effects, where peers are defined based on friendships in the network. If network endogeneity is not accounted for, peer effect estimates will be biased. The majority of papers in the literature ignore this problem by assuming that the network is formed exogenously.

This paper proposes using homophily as a solution to network endogeneity. In particular, I develop a method that uses network data to control for endogeneity in a linear model and partially identify the parameters. The method relies on constructing moment inequalities using network data under homophily assumption. Unlike prior approaches, my approach does not impose a specific network formation model. Instead, it relies on homophily, a feature of a broad family of network formation models. In this sense, my method is robust to a misspecified network formation model as long as homophily is satisfied. My model can also be used to estimate peer effects. I provide both simulation and empirical evidence that the estimated bounds are informative.

The object of interest is the parameters of a linear model with endogenous regressors. The researcher observes a network that includes observations of the linear model. Some examples are returns to schooling estimation, where the researcher observes a social network, and cross-country regressions, where the researcher observes trade or spatial networks between countries. My approach relies on two assumptions: (i) The same unobserved variable affects both network formation, and the outcome of the linear model (ii) The network exhibits unobserved homophily conditional on the unobserved variable. Homophily implies that linked nodes in the network are closer in terms of unobserved heterogeneity than non-linked nodes. Therefore, network data provides information about the unobserved variable. This paper shows how to use this information to control for endogeneity in the linear model and set identify the parameters.

The first contribution of the paper is to provide several definitions of homophily. Unlike previous definitions in the literature, these definitions do not rely on a network formation model, but they are satisfied by commonly-used network formation models. My framework, instead, uses restrictions on the shape of the conditional link probability function or stochastic orderings of conditional latent distances. This framework gives a range of homophily definitions, which can be ordered from strongest to weakest. These model-free homophily definitions are of independent interest, even though they are not the focus of the paper. For example, researchers can use these definitions to quantify homophily in observed networks or incorporate these definitions into network formation models.

I use two of the homophily definitions, weak and strong homophily, to identify the parameters of the linear model. Weak homophily is satisfied if the expected difference between unobserved heterogeneity is smaller if two agents are linked than if they are non-linked. Strong homophily orders (in the first-order stochastic dominance sense) the distributions of distance in the unobserved space based on the presence of links. Weak homophily is implied by strong homophily.

I show that homophily in networks can be used to construct moment inequalities. Weak homophily gives a conditional moment inequality, while strong homophily gives a continuum of conditional moment inequalities. To analyze how informative these moment inequalities are, I first derive the identified sets implied by these moments inequities. Then, I characterize the conditions under which the identified sets are bounded, and the conditions under which the signs of the parameters are identified. These conditions are weak and testable. Finally, for estimation, I develop doubly robust moment inequalities and show that standard methods of moment inequality estimation can be used to estimate my model.

I use Monte Carlo simulations to analyze the identified set under different scenarios. I investigate how the extent of homophily and endogeneity affects the size of the identified set. The simulations suggest that the identified set becomes more informative as the degree of homophily in the network increases. Thus, my model is more effective for networks with large homophily, such as social networks. The simulation also suggests that the identified set gets larger as the extent of endogeneity increases. However, this effect is small in my simulations.

I demonstrate my method in an empirical application using social network data from 185 villages in rural China. I consider a peer effect model (Manski (1993)), which estimates the effects of own literacy and peer literacy on perceptions about future disasters. The estimated set excludes the OLS estimates and its confidence band, suggesting that the model has endogeneity, and my approach controls for that endogeneity using network data. The OLS estimates are close to zero, whereas my estimated set implies both own and peer literacy have statistically significant effects. However, the estimated set does not pin down the signs of these effects but suggests that both own and peer effects have the same signs. Finally, I compare the estimated sets under strong and weak homophily assumptions. As expected, the identified set is more informative under strong homophily than under weak homophily.

This paper is related to a large literature on estimation using network data. This literature overwhelmingly focuses on peer effect estimation, employing a common specification called the linear-in-means model (Manski (1993)). However, most of the literature ignores network endogeneity and assumes that the network is exogenous (Bramoullé et al. (2009), Blume et al. (2015)). Another strand of the literature tries to address network endogeneity by randomly assigning links in networks either through intervention or a quasi-experiment. However, this solution is applicable only in very controlled environments.

A small but growing literature addresses network endogeneity (Goldsmith-Pinkham and Imbens (2013), Hsieh and Lee (2016), Johnsson and Moon (2017), Arduini et al. (2015)). The common theme in these papers is a parametric network formation model. They jointly estimate the linear model and network formation model to overcome endogeneity. My approach is related to this literature in that I also assume that the linear model and network share the same unobserved heterogeneity. However, I do not impose a specific network formation model, but use an important feature of a family of network formation models. Importantly, my assumptions are satisfied in the models commonly-used in this literature. Therefore, my model is robust to deviations from a specified network formation model. This flexibility comes at a cost: I identify bounds on the parameters, whereas this literature considers point identification.

The closest paper to my paper is Auerbach (2019), which uses network data to overcome endogeneity in a partially linear model. His method relies on identifying individuals with the same unobserved heterogeneity by finding pairs with similar link distributions. He does not impose a parametric network formation model but assumes that links are formed independently in a non-strategic fashion. My paper differs from his paper in three ways. First, I consider a more general family of network formation models, with possibly dependent and strategic pairwise network formation models. Second, I use a structural assumption, homophily, to achieve identification, so my results rely on different features of networks to achieve identification. Finally, I only consider partial identification, whereas he studies point identification.

I also contribute to the network literature in economics by studying homophily in networks. The literature studies homophily either using simple statistics based on group membership (Currarini et al. (2009)), or in a network formation model (Boucher (2015), Graham (2016)). In contrast, I provide a unified and flexible framework to analyze homophily based on the statistical properties of network data rather than a fully-specified model. My framework gives rise to several definitions of homophily that can be used to investigate observed networks in economics.

In the next section, I provide a formal definition of homophily. In section 3, I investigate the identification of a linear model with an endogenous variable using weak and strong homophily and characterize the identified set. Section 4 shows how my model accommodates peer effects. Section 5 discusses estimation, and section 6 discusses several extensions. Section 7 reports the result from Monte Carlo simulations. I provide an empirical application to demonstrate my method in Section 8.

Notation. I use the notation $F_a(t)$ and $F_a(t \mid b)$ to donate the distribution of variable a and the distribution of a conditional on b, respectively. Similarly, I use $f_a(t)$ and $f_a(t \mid b)$ to denote the probability density function of random variable a and the probability density function of a conditional on b, respectively. I also use $F_{|a|}(t)$ to denote the distribution of the absolute value of random variable a. Δ is the pairwise difference operator, so $\Delta x_{ij} := x_i - x_j$.

2 Defining Homophily in Networks

This section provides a discussion on homophily, a widely observed feature of networks, and then presents a series of formal definitions of homophily in a unified framework.

Homophily is one of the fundamental patterns of networks. It is defined as the tendency of individuals to associate with others similar to themselves. Homophily has been widely studied and documented in sociology across a wide array of characteristics, including ethnicity, age, profession, and religion (McPherson et al. (2001), Shrum et al. (1988), Moody (2001), Baerveldt et al. (2004)). The ubiquity of homophily in networks also led economists to study it from different perspectives. Several papers have investigated the implications of homophily for important economic phenomena, such as learning and information diffusion (Golub and Jackson (2012), Jackson and López-Pintado (2013), Bramoullé et al. (2012)). Also, the network formation literature in economics has studied how to incorporate homophily into network formation models.[1]

There are two types of homophily: observed and unobserved. The literature mostly focuses on observed homophily as it is easy to measure and document. However, there might also be homophilic preferences for characteristics that are unobservable to researchers. This would generate unobserved (latent) homophily in networks. Although it is hard to quantify, unobserved homophily has been considered to be an important feature of networks. For example, identifying an unobserved community structure from network data often relies on the latent homophily assumption. (Copic et al. (2009)).

Although homophily has been documented across a wide range of characteristics, to the best of my knowledge, there is no consensus on how to formally define homophily in networks. The literature often relies on simple statistics to measure homophily. For categorical variables, this is often the ratio of connections within the same category, divided by the total number of connections (Jackson (2008), Currarini et al. (2009)). However, these statistics do not extend to continuous variables, and their properties are not well-known.

The literature also analyzes homophily via network formation models. This approach specifies the link formation probability as a function of the similarity between nodes. In particular, the probability of forming a link between two nodes decreases in the distance between the observed and unobserved characteristics. To give an example, consider a model where links are formed according to

$$G_{ij} = \mathbb{1}\{c_0 + c_1|\alpha_i - \alpha_j| + c_2|x_i - x_j| \leqslant u_{ij}\}, \tag{2.1}$$

where G_{ij} is an indicator variable that denotes whether i and j are connected, and u_{it} is a ran-

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[1] See Jackson et al. (2017) for a survey on the economic consequences of the structure of networks.

dom variable with known distribution, typically Extreme Value Type I. The model parameters are (c_0, c_1, c_2). In this model, α_i denotes the unobserved characteristic and x_i denotes the observed characteristics of node i.[2] Thus, both observed and unobserved homophily are captured. This model, or one of its variants, has commonly been used in the literature (Goldsmith-Pinkham and Imbens (2013), Johnsson and Moon (2017), Qu and Lee (2015), Hsieh and Lee (2017), Boucher and Mourifié (2017)). When defined this way, homophily corresponds to the relation between link formation probability and the distance between nodes' characteristics.

A drawback of defining homophily using a link formation function is that it requires a fully-specified network formation model. These models are useful for fully characterizing and analyzing the network; however, they are not ideal if the goal is to analyze and measure homophily. For example, a misspecified network formation model would lead to incorrect conclusions about homophily.

The central objective of this paper is to use homophily for identification without relying on a specific network formation model. For this reason, I present alternative definitions of homophily that do not rely on a network formation model. Instead, my definitions employ stochastic ordering of random variables. I will consider only unobserved homophily; however, the same definitions can be written in terms of observed homophily. I start with the definition of strong homophily. Define $\tilde{\mathcal{X}}$ as the support of (x_i, x_j) such that such that $\mathbb{E}[G_{ij} \mid x_i, x_j]$ is bounded below zero and above one.

Definition 2.1 ((Conditional) Strong Homophily). *A network formation model satisfies strong homophily if*

$$F_{(\Delta\alpha_{ij})^2}\big(t \mid x_i, x_j, G_{ij} = 1\big) \geqslant F_{(\Delta\alpha_{ij})^2}\big(t \mid x_i, x_j, G_{ij} = 0\big),$$

for $t \geqslant 0$ *and* $(x_i, x_j) \in \tilde{\mathcal{X}}$.

This definition specifies a stochastic ordering for the distances between latent characteristics of linked and non-linked nodes. Conditional on observed characteristics x_i and x_j, the squared distance in latent space for non-linked nodes first-order stochastically dominates the squared distance for linked nodes. An interpretation of this property is that nodes that are 'close' in the latent space are more likely to be connected than nodes that are 'away' from each other. Strong homophily is satisfied by the network formation model in Equation (2.1); therefore, it imposes less restriction than the commonly-used network formation models. Next, I provide a weaker notion of homophily.

Definition 2.2 ((Conditional) Weak Homophily). *A network formation model satisfies weak homophily if*

$$\mathbb{E}\big[(\Delta\alpha_{ij})^2 \mid x_i, x_j, G_{ij} = 0\big] \geqslant \mathbb{E}\big[(\Delta\alpha_{ij})^2 \mid x_i, x_j, G_{ij} = 1\big],$$

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[2] I assume that all parameters are scalar to simplify the analysis.

for $(x_i, x_j) \in \tilde{\mathcal{X}}$.

This definition restricts only the second moment of the distances instead of their distributions. It is nested by strong homophily. Both definitions of homophily stochastically order distances in latent space based on the existence of a link. Weak homophily orders the moments; strong homophily orders the distributions in the first-order stochastic dominance sense.

Even though this section provides two definitions, there are other ways of defining homophily using different stochastic orderings. In Appendix A, I present a range of homophily definitions that use both stochastic ordering and properties of link formation probability. I also examine the relationship between these definitions: I order them from strongest to weakest, and I show which definition nests the others. As a result, one contribution of this paper is to provide a toolkit for understanding and measuring homophily in networks. I focus on weak and strong homophily assumptions because I will only use those two to demonstrate how to address endogeneity in an empirical model.

There are several reasons why a broad range of homophily definitions is of independent interest. First, researchers can use these definitions to quantify homophily in observed networks. Since networks are present in a number of empirical contexts, different homophily definitions may be better suited for different types of networks. Also, these definitions make it possible to compare networks in terms of homophily. Second, network formation models that aim to capture homophily can incorporate these definitions.

The rest of the paper investigates how to use homophily to address endogeneity in a linear regression model.

3 Model and Assumptions

This section first presents a linear model and assumptions. Then, I show how to construct moment inequalities using network data under weak and strong homophily assumptions. Finally, I characterize the identified sets implied by moment inequalities.

The goal is to estimate the parameters of a linear model with endogeneity. The outcome, y_i, is given by the following model:

$$y_i = \beta_0 x_i + \alpha_i + \epsilon_i, \tag{3.1}$$

where x_i is an observed and α_i is an unobserved scalar random variable, and ϵ_i is orthogonal to both x_i and α_i. Thus, α_i represents unobserved heterogeneity and creates endogeneity in this model. β_0 is the parameter of interest, which gives the causal effect of x_i on the outcome. I consider a model with a scalar endogenous variable to simplify the exposition. The model can accommodate multi-dimensional endogenous variables and exogenous control variables.[3]

I also assume that the researcher observes whether each pair (i, j) is linked in a network. This situation might arise in different empirical contexts. For example, Equation (3.1) can estimate the returns to schooling, and the researcher observes a social network of individuals. Another example is a cross-country regression. In this case, the network observed by the researcher could be geography or trade networks.

To introduce the network into the model, let G_{ij} be an indicator variable that equals one if i and j are linked and zero otherwise. The model has three stages. In the first stage, variables $\{x_i, \alpha_i, \epsilon_i\}$ are drawn independently from the same distribution. In the second stage, links are formed according to an unknown, and possibly complicated, network formation model, so G_{ij} is realized.[4] In the last stage, outcomes y_i are realized according to Equation (3.1). This timing assumption implies that the outcome variable y_i does not affect link formation. This sequential structure, where the network is formed, and then outcomes are realized, is standard in the literature.[5,6]

Without further assumptions, β_0 cannot be identified, as x_i is endogenous. To overcome this non-identification problem, I will impose restrictions on the observed network and exploit these restrictions to (partially) identify β_0. The overall idea is that if unobserved heterogeneity α_i in Equation (3.1) also affects link formation, then network data are informative about α_i. This information can be used to control for α_i when estimating Equation (3.1). The particular assumption I impose is unobserved homophily, which relates link formation probability to the distance between units in latent space. To see how homophily can be useful for estimation, I take the pairwise difference of Equation (3.1) to write:

$$\Delta y_{ij} = \beta_0 \Delta x_{ij} + \Delta \alpha_{ij} + \Delta \epsilon_{ij}. \tag{3.2}$$

This model relates the differences in outcomes to the differences in endogenous variables, Δx_{ij}, and unobserved heterogeneity, $\Delta \alpha_{ij}$. The pairwise difference model is useful because it is written in terms of the difference of $\Delta \alpha_{ij}$, for which homophily provides information.[7] In particular, homophily says that $\Delta \alpha_{ij}$ should be smaller in absolute value for linked pairs than for non-linked pairs. So, one can use network data, along with Equation (3.2), to make inference about β_0.

To be able to use the homophily assumption for estimation, I first need to formally define ho-

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[3] I discuss some of these extensions in Section 6.

[4] Link formation may be affected by variables that are outside the model.

[5] Alternatively, one can assume that the second and third stages occur simultaneously and independently. However, for the peer effects model developed later, I need the three-stage timing assumption. If the second and third stages occur simultaneously, the outcome variable y_i depends on variables affected by network formation, so the second and third stage are not independent with the presence of peer effects.

[6] Another important issue in estimations with network data is whether asymptotics is based on a single large network or many networks. This is beyond the scope of this paper. The empirical application involves many networks, which allows me to do inference using the standard methods.

[7] Pairwise difference models have a long history in econometrics; see Aradillas-Lopez et al. (2007), Honoré and Powell (1994).

mophily. I use the weak and strong homophily definitions given in the previous section. To simplify notation, I drop the ij subscript from difference variables, so any variable with Δ is implicitly indexed by ij. I also drop ij from the link variable G_{ij}.

3.1 Identification under Weak Homophily

In this section, I show that a network with weak homophily provides moment inequalities for estimating β_0. Then, I characterize the identified set given by the derived moment inequalities. To be able to use weak homophily for identification, I need to impose additional restrictions on the distribution of ϵ_i. The next assumption states these restrictions.

Assumption 3.1. *Suppose that*
(i) $\mathbb{E}\big[\epsilon_i \mid \alpha_i, x_i\big] = 0$.
(ii) $\mathbb{E}\big[\epsilon_i^2 \mid \alpha_i, x_i\big] = \mathbb{E}\big[\epsilon_i^2 \mid x_i\big]$.
(iii) (ϵ_i, ϵ_j) *is jointly independent of* G *conditional on* $(\alpha_i, \alpha_j, x_i, x_j)$.
(iv) *The network satisfies weak homophily defined in Definition (2.1).*

Part (i) assumes that ϵ_i is mean independent of (x_i, α_i), so it is not a source of endogeneity. Part (ii) states that the variance of ϵ_i does not change with α_i conditional on x_i. This assumption is non-standard in linear models. I need this assumption because homophily imposes restrictions on the second moment of distance, $\Delta\alpha^2$, instead of α_i. For this reason, I need to restrict the second moment of ϵ_i. Part (iii) implies that (ϵ_i, ϵ_j) do not affect link formation once we condition on other unobservables and observables in the model. Part (iv) states that the network satisfies the weak homophily assumption. Using these assumptions, I obtain the following proposition.

Proposition 3.1. *Under the conditions of Assumption 3.1,*

$$\mathbb{E}\big[(\Delta\alpha + \Delta\epsilon)^2 \mid x_i, x_j, G = 0\big] \geqslant \mathbb{E}\big[(\Delta\alpha + \Delta\epsilon)^2 \mid x_i, x_j, G = 1\big],$$

for $(x_i, x_j) \in \tilde{\mathcal{X}}$.

Proof. See Appendix B.

This proposition establishes that weak homophily is robust to additive noise, ϵ_i, under Assumption 3.1. I need this proposition to ensure that weak homophily is preserved when α_i is contaminated by ϵ_i. By assumption (iv), weak homophily is satisfied in terms of α_i. However, the linear model in Equation (3.1) includes another unobserved variable, ϵ_i. And from data and parameters, I can recover only the sum of the unobserved variables, $\alpha_i + \epsilon_i$. So I need weak homophily for $\Delta\alpha + \Delta\epsilon$.

3.1.1 Identified Set

This section derives the moment inequalities implied by the weak homophily assumption and characterizes the identified set. The first step is to write unobservables as a function of parameters and data. The pairwise difference model in Equation (3.2) yields

$$\Delta\alpha_{ij} + \Delta\epsilon_{ij} = \Delta y_{ij} - \beta_0 \Delta x_{ij}.$$

Substituting this expression into Proposition 3.1, I obtain a conditional moment inequality:

$$\mathbb{E}[(\Delta y - \beta_0 \Delta x)^2 \mid x_i, x_j, G = 1] \leqslant \mathbb{E}[(\Delta y - \beta_0 \Delta x)^2 \mid x_i, x_j, G = 0]. \tag{3.3}$$

This inequality orders two means conditional on the existence and absence of a link. Note that it involves observed variables and parameters only, so I can use this moment inequality to partially identify β_0. I first characterize the identified set given by the conditional moment inequality in Equation (3.3). The identified set is the intersection of conditionally identified sets. Let $x_{ij} := (x_i, x_j)$. Equation (3.3) can be written as

$$\beta_0 \Delta x \big(\mathbb{E}[\Delta y \mid x_{ij}, G = 1] - \mathbb{E}[\Delta y \mid x_{ij}, G = 0]\big) \geqslant \mathbb{E}[(\Delta y)^2 \mid x_{ij}, G = 1] - \mathbb{E}[(\Delta y)^2 \mid x_{ij}, G = 0]. \tag{3.4}$$

This inequality suggests that the identified set (conditional on x_{ij}) is a half-space. Also, it shows that the direction of half-spaces depends on the sign of the conditional mean differences on the left-hand side of Equation (3.4). Using this, I characterize the identified set conditional on x_{ij} as follows:

$$\mathcal{B}(x_{ij}) = \begin{cases} \left(-\infty, \dfrac{\mathbb{E}[\Delta y^2 \mid x_{ij}, G = 1] - \mathbb{E}[\Delta y^2 \mid x_{ij}, G = 0]}{2\Delta x \left(\mathbb{E}[\Delta y \mid x_{ij}, G = 1] - \mathbb{E}[\Delta y \mid x_{ij}, G = 0]\right)} \right], & \text{if } \Delta x \left(\mathbb{E}[\Delta y \mid x_{ij}, G = 1] - \mathbb{E}[\Delta y \mid x_{ij}, G = 0]\right) < 0 \\ \Big(-\infty, \infty \Big), & \text{if } \Delta x \left(\mathbb{E}[\Delta y \mid x_{ij}, G = 1] - \mathbb{E}[\Delta y \mid x_{ij}, G = 0]\right) = 0 \\ \left[\dfrac{\mathbb{E}[\Delta y^2 \mid x_{ij}, G = 1] - \mathbb{E}[\Delta y^2 \mid x_{ij}, G = 0]}{2\Delta x \left(\mathbb{E}[\Delta y \mid x_{ij}, G = 1] - \mathbb{E}[\Delta y \mid x_{ij}, G = 0]\right)}, \infty \right), & \text{if } \Delta x \left(\mathbb{E}[\Delta y \mid x_{ij}, G = 1] - \mathbb{E}[\Delta y \mid x_{ij}, G = 0]\right) > 0 \end{cases}$$

The identified set is given by the intersection of these sets:

$$\tilde{\mathcal{B}} = \{\cap_{x_{ij} \in \tilde{\mathcal{X}}} \ \mathcal{B}(x_{ij})\},$$

Next, I investigate the conditions under which the identified set is informative.

3.1.2 Characterizing the Identified Set

I focus on the conditions under which the identified set is bounded, and the sign of β_0 is identified.

Since the identified set is given by the intersection of half-spaces, its informativeness depends on the shape of these half-spaces. To obtain a bounded identified set, there should exist two x_{ij}'s such that identified sets (conditional on the x_{ij}'s) should extend in different directions. For the sign of β_0 to be identified, we need at least one x_{ij} such that conditional on that, the identified set excludes zero. The next proposition establishes these results.

Proposition 3.2.

(i) *The identified set is bounded if there exists* $(\bar{x}_{ij}, \tilde{x}_{ij}) \in \tilde{\mathcal{X}}^2$ *such that*

$$\Delta\bar{x}\big(\mathbb{E}[\Delta y \mid \bar{x}_{ij}, G=1] - \mathbb{E}[\Delta y \mid \bar{x}_{ij}, G=0]\big) \geqslant 0 \geqslant \Delta\tilde{x}\left(\mathbb{E}[\Delta y \mid \tilde{x}_{ij}, G=1] - \mathbb{E}[\Delta y \mid \tilde{x}_{ij}, G=0]\right).$$

(ii) *The sign of* β_0 *is identified if there exists* $\tilde{x}_{ij} \in \tilde{\mathcal{X}}$ *such that*

$$\big(\mathbb{E}[(\Delta y)^2 \mid \tilde{x}_{ij}, G=1] - \mathbb{E}[(\Delta y)^2 \mid \tilde{x}_{ij}, G=0]\big) \geqslant 0. \tag{3.5}$$

The proof of this proposition is trivial, and therefore omitted. The first part of the proposition specifies the condition under which the identified set is bounded. This condition is testable because all moments in the proposition can be identified from data. However, it is also useful to interpret this condition in terms of model primitives. For this purpose, I write the condition to obtain a bounded identified set as:

$$\begin{aligned} &\Delta\bar{x}\left(\mathbb{E}[\Delta\alpha \mid \bar{x}_{ij}, G=1] - \mathbb{E}[\Delta\alpha \mid \bar{x}_{ij}, G=0]\right) + \beta_0(\Delta\bar{x})^2 \geqslant 0, \\ &\Delta\tilde{x}\left(\mathbb{E}[\Delta\alpha \mid \tilde{x}_{ij}, G=1] - \mathbb{E}[\Delta\alpha \mid \tilde{x}_{ij}, G=0]\right) + \beta_0(\Delta\tilde{x})^2 \leqslant 0. \end{aligned} \tag{3.6}$$

This reformulation is written in terms of unobserved heterogeneity $\Delta\alpha$ and does not depend on Δy. The difference of expectations in Equation (3.6) is similar to the condition given in the definition of weak homophily, except that it involves the first moment of $\Delta\alpha$, instead of its second moment. Therefore, whether the identified set is bounded depends on the expected difference in $\Delta\alpha$ of linked and non-linked nodes and how that difference varies with x_{ij}.

The second part of Proposition (4.2) concerns the identification of the sign of β_0. The sign is identified if expected $(\Delta y)^2$ for the linked nodes is greater than expected $(\Delta y)^2$ for the non-linked nodes. Note that this condition is closely related to the definition of weak homophily: to identify the sign of β_0, the network should not exhibit homophily in terms of y_i. This can happen in two ways. To explain them, I rewrite Equation (3.5) as

$$\underbrace{\big(\mathbb{E}[(\Delta\alpha)^2 \mid \tilde{x}_{ij}, G=1] - \mathbb{E}[(\Delta\alpha)^2 \mid \tilde{x}_{ij}, G=0]\big)}_{I} + 2\beta_0\Delta\tilde{x}\underbrace{\big(\mathbb{E}[\Delta\alpha \mid \tilde{x}_{ij}, G=1] - \mathbb{E}[\Delta\alpha \mid \tilde{x}_{ij}, G=0]\big)}_{II} \geqslant 0, \tag{3.7}$$

which involves two parts. Part *I* is negative by the weak homophily assumption. Thus, in order for this inequality to hold, the second summand should be positive and larger than the first summand in absolute value. Three quantities affect the second summand: (i) β_0, (ii) $\Delta\tilde{x}$ and (iii) the expression labeled as *II*. If $\beta_0 < 0$ then $\Delta\tilde{x}$ and *II* should have different signs, otherwise, they should have the same signs. Since the sign of II depends on the underlying network formation, which is not specified, it is not possible to further analyze the identification of the sign of β_0.

From Equation (3.7) we can also see that in two cases it is not possible to identify the sign of β_0: (i) $\beta_0 = 0$ and (ii) II equals zero. The first case is obvious. To rule out the second case, link formation should be related not only to $(\Delta\alpha)^2$ but also to the expected difference in unobserved heterogeneity, $\Delta\alpha$.

After analyzing identification under weak homophily, I next turn to what we can learn from networks with strong homophily.

3.2 Identification under Strong Homophily

In this section, I show how to use the strong homophily assumption to derive moment inequalities. Then, I characterize the identified set based on these moment inequalities.

Since strong homophily implies weak homophily, the identified set obtained from strong homophily is tighter than the identified set obtained from weak homophily. However, I need more conditions on the distribution of ϵ_i to exploit strong homophily for identification. In particular, I need to strengthen the restrictions on the distribution of ϵ given in Assumption 3.1.

Assumption 3.2. *Suppose that*

(i) *ϵ_i is independently distributed from α_i conditional on (x_i, G_{ij}).*

(ii) *(ϵ_i, ϵ_j) is jointly independent of G_{ij} conditional on $(\alpha_i, \alpha_j, x_i, x_j)$.*

(iii) *$f_{\Delta\epsilon}(\Delta\epsilon \mid x_i, x_j)$ is unimodal around zero for all $(x_i, x_j) \in \tilde{\mathcal{X}}$.*

(iv) *The network satisfies the strong homophily assumption.*

Part (i) of Assumption 3.2 states that two unobserved variables are independently distributed conditional on observables. This assumption strengthens the mean independence in Assumption 3.1(ii) to independence. I need this restriction on the distribution of ϵ_i because strong homophily involves distribution functions, not just moments. In Part (ii), I maintain the assumption that ϵ_i does not affect network formation after conditioning on observed and unobserved characteristics.

Part (iii) imposes a shape restriction on the distribution of $\Delta\epsilon$. I need this assumption to show that strong homophily in terms of $\Delta\alpha$ implies strong homophily in terms of $\Delta\alpha + \Delta\epsilon$. This assumption is not as strong as it seems because it requires unimodality only for $\Delta\epsilon$; the distribution of ϵ_i does not have to be unimodal. Unimodality for the distribution of the difference between two independently and identically distribution variables is a substantially weaker condition that unimodality for the distribution of both of these variables.[8] For most well-known distributions, such as those in the exponential family, the difference of two identically and independently distributed random variables has a unimodal distribution. One primitive condition ensuring unimodality is that

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[8] Note that, by construction, the probability density function of $\Delta\epsilon$ is symmetric, so we need to rule out distributions that are symmetric but not unimodal.

ϵ_i has a log-concave distribution function.

The next proposition shows that strong homophily continues to hold when ϵ_i is added to α_i.

Proposition 3.3. *Under the conditions given in Assumptions 3.2*

$$F_{|\Delta\alpha+\Delta\epsilon|}\big(t \mid x_i, x_j, G=1\big) \geqslant F_{|\Delta\alpha+\Delta\epsilon|}\big(t \mid x_i, x_j, G=0\big),$$

for $(t, x_i, x_j) \in \mathbb{R}^+ \times \tilde{\mathcal{X}}$.

Proof. See Appendix B.

According to this proposition, strong homophily is robust to additive noise.[9] Unimodality of the distribution of $\Delta\epsilon$ and independence of ϵ_i and α_i are sufficient to achieve this. The proof of this proposition uses the fact that the distribution of the sum of two independent random variables is given by a convolution. So, under the condition of Assumption 3.2(i), I can use convolution analysis to derive the distribution of $\alpha_i+\epsilon_i$ conditional on $(G=1)$ and $(G=0)$, and then establish first-order stochastic dominance. The unimodality of the distribution of $\Delta\epsilon$ ensures that the convolution is well behaved. Although these conditions are strong, they allow me to use strong homophily, which can lead to a substantially tighter identified set than weak homophily.

3.2.1 Identified Set

Proposition 3.3 gives a first-order stochastic dominance relation between two distribution functions. To use this for identification, I turn the stochastic dominance relation into moment inequalities. One way to achieve this is to write first-order stochastic dominance in terms of a continuum of moment inequalities:

$$\mathbb{E}[\mathbb{1}\{|\Delta\alpha + \Delta\epsilon| \leqslant \gamma\} \mid x_{ij}, G=1] \geqslant \mathbb{E}[\mathbb{1}\{|\Delta\alpha + \Delta\epsilon| \leqslant \gamma\} \mid x_{ij}, G=0] \tag{3.8}$$

for $(\gamma, x_i, x_j) \in \mathbb{R}^+ \times \mathbb{X}^c$. Substituting $\Delta\alpha + \Delta\epsilon$ as a function of data and parameters I obtain:

$$\mathbb{E}[\mathbb{1}\{|\Delta y - \beta_0\Delta x| \leqslant \gamma\} \mid x_{ij}, G=1] \geqslant \mathbb{E}[\mathbb{1}\{|\Delta y - \beta_0\Delta x| \leqslant \gamma\} \mid x_{ij}, G=0]. \tag{3.9}$$

This inequality says that the true parameter value satisfies a continuum of conditional moment inequalities. To see the difference between strong and weak homophily, note that FOSD implies that if A dominates B, then the expectation of any monotone transformation B is smaller than the expectation of the same monotone transformation of A. Therefore, strong homophily gives moment inequalities for any monotone transformation of $|\Delta\alpha|$. This is in contrast to weak homophily, which

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[9] FOSD is preserved under Fourier transformation for the random variables. However, we need FOSD for the difference between two random variables. This requires additional conditions on the distribution of the random variables.

gives moment inequalities only for the second moment of $|\Delta\alpha|$. Thus, strong homophily should give a more informative identified set.

To state the identified set, I turn Equation (3.9), which involves two moments, into a inequality with a single moment. Note that one can write the expectations in Equation (3.9) as

$$\mathbb{E}[\mathbb{1}\{|\Delta y - \beta_0 \Delta x| \leqslant \gamma\} \mid x_{ij}, G = 1] = \mathbb{E}\left[\frac{\mathbb{1}\{|\Delta y - \beta_0 \Delta x| \leqslant \gamma\} G}{\mathbb{E}[G \mid x_{ij}]} \;\middle|\; x_{ij}\right],$$
$$\mathbb{E}[\mathbb{1}\{|\Delta y - \beta_0 \Delta x| \leqslant \gamma\} \mid x_{ij}, G = 0] = \mathbb{E}\left[\frac{\mathbb{1}\{|\Delta y - \beta_0 \Delta x| \leqslant \gamma\}(1 - G)}{1 - \mathbb{E}[G \mid x_{ij}]} \;\middle|\; x_{ij}\right],$$

where $\mathbb{E}[G \mid x_{ij}]$ corresponds to the propensity of link formation conditional on observed characteristics. This transformation has been widely-used in the treatment effect estimation literature (Rosenbaum and Rubin (1983)). Now, define a function g that takes parameters and data:

$$g(x_i, x_j, \Delta y, G, \gamma, \beta) := \frac{\mathbb{1}\{|\Delta y - \beta_0 \Delta x| \leqslant \gamma\}(1 - G)}{1 - \mathbb{E}[G \mid x_{ij}]} - \frac{\mathbb{1}\{|\Delta y - \beta_0 \Delta x| \leqslant \gamma\} G}{\mathbb{E}[G \mid x_{ij}]}.$$

Using this function, I define the identified set.

Proposition 3.4 (Identified Set). *Assume $\beta_0 \in \tilde{B}$, a compact parameter space. The identified set B is defined as the set of parameter values that satisfy the conditional moment inequalities*

$$B := \left\{\beta \in \tilde{B} : \bigcap_{(x_i, x_j) \in \tilde{\mathcal{X}}} \bigcap_{\gamma > 0} \mathbb{E}[g(x_i, x_i, \Delta y, G, \gamma, \beta) \mid x_{ij}] \leqslant 0 \quad a.s.\right\},$$

and the identified set contains the true parameter value $\beta_0 \in B$.

Next, I analyze the identified set given in this proposition.

3.2.2 Characterization of the Identified Set

Under strong homophily, it is difficult to characterize the identified set because moment inequalities involve non-linear functions. In this section, I derive some properties of the identified set under additional regulatory conditions, which are given by the next assumption.

Assumption 3.3. *Suppose that there exists $x_{ij} \in \tilde{\mathcal{X}}$ such that*
(i) *Δy has a bounded support conditional on $x_{ij} \in \tilde{\mathcal{X}}$.*
(ii) *There exists $M \in \mathbb{R}$ such that $\mathbb{E}\big[G = 1 \mid x_{ij}, \Delta\alpha = \Delta\big] < \mathbb{E}[G = 1]$ for $\Delta z \in (-\infty, -M) \cup (M, \infty)$.*

Part (i) imposes a mild support restriction. According to Part (ii), if the distance in latent space is too large, then the conditional link formation probability is less than the unconditional link formation probability. This condition imposes a mild restriction on the shape of conditional link probability, and is consistent with, albeit not implied by, strong homophily. This is because, by definition, observations that are too far in the latent space should have a very low probability of link formation. I use the following lemma to show that the identified set is bounded under Assumption 3.3.

Lemma 3.1. *Suppose that there exists* $(t, x_i, x_j), (t', x_i, x_j) \in \mathcal{R}^+ \times \mathbb{X}^c$ *and* $t \neq t'$ *such that*

$$F_{\Delta\alpha}(t \mid x_{ij}, G = 1) - F_{\Delta\alpha}(t' \mid x_{ij}, G = 0) < 0,$$
$$F_{\Delta\alpha}(t \mid x_{ij}, G = 1) - F_{\Delta\alpha}(t' \mid x_{ij}, G = 0) > 0.$$

Then, the identified set is bounded.

Proof. See Appendix B.

This lemma rules out a stochastic ordering in $\Delta\alpha$ conditional on $(G = 1)$ and conditional on $(G = 0)$. Note that this is different from the strong homophily condition, which involves the absolute value of the difference. Since the model does impose restrictions on $(\Delta\alpha)^2$, not $(\Delta\alpha)$, it is plausible to expect that Lemma 3.1 holds. If this condition is satisfied, then it is possible to show that the strong homophily condition is violated for large and small candidate parameter values. Therefore, we can reject parameter values that are larger than $\bar{\beta}$ and smaller than $-\bar{\beta}$, where $\bar{\beta}$ is positive. This implies that the identified set is bounded.

As for the identified set under weak homophily, the difference in expectation of $\Delta\alpha$ between linked and non-linked nodes plays a critical role in the identified set. As a result, the informativeness of the identified set depends on the underlying network formation model. Next, I show that Assumption 3.3 is sufficient for the conditions of this lemma to hold.

Proposition 3.5. *Under Assumptions 3.2–3.3, the conditions of Lemma 3.1 are satisfied, and therefore, the identified set given in Proposition 4.1 is bounded.*

Proof. See Appendix B.

This proposition uses the Bayes rule for continuous variables to show that the conditions of Lemma 3.1 are satisfied.

3.3 Discussion and Relation to Literature

Exploiting network data to address endogeneity has been proposed in the literature, especially in peer effects estimation. The standard implementation of this idea is to assume a network formation model and jointly estimate a linear model of peer effects and a network formation model. To give an example, Goldsmith-Pinkham and Imbens (2013) consider the following model:[10]

$$y_i = \beta_0 x_i + \alpha_i + \epsilon_i, \qquad \epsilon_i \mid \alpha_i, x_i, G_{ij} \sim \mathcal{N}(0, \sigma_1^2). \tag{3.10}$$

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[10] Their model considers also a peer effects variable. I omit that variable to facilitate the comparison.

To address endogeneity in Equation (3.10) they consider the following network formation model:

$$G_{ij} = \mathbb{1}\{\alpha_0 + c_1|\alpha_i - \alpha_j| + c_2|x_i - x_j|\}, \quad u_{ij} \sim \text{EV II}(0, \sigma_2). \tag{3.11}$$

This network formation model incorporates both latent and observed homophily. Also, the unobserved heterogeneity, α_i, is the same in Equations (3.10) and (3.11). Therefore, one can estimate these models jointly to account for the correlation between α_i and x_i. Specifically, Goldsmith-Pinkham and Imbens (2013) take a Bayesian approach to estimate the parameters under distributional assumptions.[11] Other papers in the literature take similar approaches with slightly different network formation and estimation models (Hsieh and Lee (2016), Johnsson and Moon (2017), Arduini et al. (2015)).

My approach is related to this literature in that I also assume that the linear model and network formation model share the same unobserved variable. However, I do not impose a specific network formation model, but use an important feature of a family of network formation models. Importantly, the network formation model in Equation (3.11) satisfies both weak and strong homophily. Therefore, my model is robust to deviations from a specified network formation model as long as the true network formation model exhibits homophily. Yet this flexibility comes at a cost: I identify a bound on the parameters, whereas the existing literature considers point identification.

This paper is also related to the literature on monotone instrumental variables (Manski (1997), Manski and Pepper (2000)). This literature assumes that the expected potential outcomes are ordered based on an observed variable, which is called a monotone instrument. In my model, G_{ij} can be considered a monotone instrument for the pairwise difference model in Equation (3.2) under weak homophily. That is because, in that equation, the second moment of potential outcomes can be ordered based on G. The main difference between my model and the standard monotone instrumental variable approach is that monotonicity holds for the second moment of unobserved heterogeneity in Equation (3.2), which requires stronger assumptions than the monotone instrumental variables approach.

My paper is also related to the 'imperfect instrument approach', which assumes that the researcher has some prior information about the correlation between the endogenous variable and unobserved heterogeneity. This information is used to construct moment inequalities. See, for example; Nevo and Rosen (2012) and Conley et al. (2012).

4 A Model with Peer Effects

The most common empirical setting with network data is peer effects estimation. In this section, I show that my model accommodates peer effects. The estimation strategy is similar to the main

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[11] Goldsmith-Pinkham and Imbens (2013) study other important questions such as testing the endogeneity of the network and estimating a dynamic network formation model. This paper is not related to their other contributions.

model, but due to complications that come with peer effects, the characterization of the identified set is limited compared to the main model.

Let $\bar{x}_i$ be a scalar variable that is a function of peer characteristics. Following a common specification called the linear-in-means model, I assume that $\bar{x}_i$ equals the average characteristics of person i's peers.[12] With the addition of $\bar{x}_i$, the model in Equation (3.1) becomes

$$y_i = \beta_0 x_i + \rho_0 \bar{x}_i + \alpha_i + \epsilon_i.$$

In this model, β_0 corresponds to own effect, and ρ_0 corresponds to peer effects. Since Manski (1993), the linear-in-means model has become the workhorse of peer effects estimation and has been used to estimate peer effects in many different settings. My model, unlike Manski (1993), considers only contextual peer effects, not endogenous peer effects. That is, only peer *characteristics* influence the outcome, not peer *outcomes.* I make this restriction because, with endogenous peer effects, the model becomes a game, which requires solving for the equilibrium and deriving the implied reduced form equation (Blume et al. (2015)).[13]

This model is more difficult to analyze than the model in Equation (3.1) due to two endogenous variables: both own characteristics x_i and peer characteristics $\bar{x}_i$ are endogenous.[14] For identification, I consider the same assumptions stated for the main model, but construct the identified set only under strong homophily.[15]

4.1 Identified Set with Peer Effects

Recall that Propositions 3.1 and 3.3 state the moment inequalities under the weak and strong homophily assumptions. These propositions continue to hold with the addition of peer effects because they involve only α_i and ϵ_i, and they are affected by the linear model (by timing assumption). Thus, I can use the same moment inequalities with the addition of peer characteristics, $\bar{x}_i$, in the estimation. Specifically, under strong homophily, the true parameter vector $\theta_0 = (\beta_0, \gamma_0)$ satisfies

$$\mathbb{E}[\mathbb{1}\{|\Delta y - \beta_0 \Delta x - \rho_0 \Delta \bar{x}| \leqslant \gamma\} \mid x_{ij}, G = 1] \leqslant \mathbb{E}[\mathbb{1}\{|\Delta y - \beta_0 \Delta x - \rho_0 \Delta \bar{x}| \leqslant \gamma\} \mid x_{ij}, G = 0],$$

for $\{(t, x_i, x_j) : t \geqslant 0, (x_{ij}) \in \tilde{\mathcal{X}}\}$, which gives a continuum of conditional moment inequalities. Define a function that takes data and model parameters as

$$g^p(x_{ij}, \Delta y, G, \Delta \bar{x}, \theta) := \frac{\mathbb{1}\{|\Delta y - \beta \Delta x - \gamma \Delta \bar{x}| \leqslant \gamma\}(1-G)}{1 - \mathbb{E}[G \mid x_{ij}]} - \frac{\mathbb{1}\{|\Delta y - \beta \Delta x - \gamma \Delta \bar{x}| \leqslant \gamma\} G}{\mathbb{E}[G \mid x_{ij}]}.$$

Using this function, I define the identified set in the presence of peer effects.

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[12] In principle, $\bar{x}_i$ can be any function of peer characteristics.

[13] Extending my framework to endogenous peer effects is a subject of future work.

[14] Peer characteristics are endogenous because they are realized based on the network, which is endogenous due to the presence of α_i

[15] Identification under weak homophily is similar, and I do not repeat it here.

Proposition 4.1 (Identified Set with Peer Effects)**.** *Assume $\theta_0 \in \tilde{\Theta}$, a compact parameter space. The identified set Θ is defined as the set of parameters that satisfy the conditional moment inequalities,*

$$\Theta := \left\{\theta \in \tilde{\Theta} : \bigcap_{(x_i,x_j)\in\tilde{\mathcal{X}}} \bigcap_{\gamma>0} \mathbb{E}[g^p(x_i, x_j, \Delta y, G, \Delta\bar{x}, \theta) \mid x_{ij}] \geqslant 0 \quad a.s.\right\},$$

and the identified set contains the true parameter value $\theta_0 \in \Theta$.

With peer effects, analyzing the identified set is complicated for two reasons. First, the model involves two parameters. Second, without peer effects, homophily holds conditional on endogenous variables in the linear model. This is not the case with peer effects, as homophily does not necessarily hold conditional on $\bar{x}$. Thus, I analyze the informativeness of the identified sets under the weak homophily assumption and in some special cases.

4.2 Identification Conditional on $(x_i = x_j)$

If the object of interest is the peer effects, not the own effect, one way to simplify estimation and identification analysis is to condition on $(x_i = x_j)$. In this case, β_0 drops from the pairwise model in Equation (3.2), so only the peer effects coefficient ρ_0 can be estimated. Conditional on $(x_i = x_j)$, the moment inequality becomes

$$\mathbb{E}[(\Delta y - \rho_0\Delta\bar{x})^2 \mid x_i = x_j, G = 1] \leqslant \mathbb{E}[(\Delta y - \rho_0\Delta\bar{x})^2 \mid x_i = x_j, G = 0].$$

This is similar to the moment inequality I derived in Subsection 3.1. This moment inequality can be written as

$$\begin{aligned}\rho_0^2\big(\mathbb{E}[\Delta\bar{x}^2 \mid x_i = x_j, G = 1] - \mathbb{E}[\Delta\bar{x}^2 \mid x_i = x_j, G = 1] \leqslant \\ \mathbb{E}[\Delta y\Delta\bar{x} \mid x_i = x_j, G = 0]\big) + \big(\mathbb{E}[(\Delta y)^2 \mid x_i = x_j, G = 1] - \mathbb{E}[(\Delta y)^2 \mid x_i = x_j, G = 0]\big).\end{aligned} \tag{4.1}$$

The following proposition considers whether the identified set is bounded and whether the sign of the coefficient ρ_0 is identified.

Proposition 4.2.

(i) *The identified set is bounded if there exists $\tilde{x}_i = \tilde{x}_j$ such that*

$$\big(\mathbb{E}[\Delta\bar{x}^2 \mid \tilde{x}_i, \tilde{x}_j, G = 1] - \mathbb{E}[\Delta\bar{x}^2 \mid \tilde{x}_i, \tilde{x}_j, G = 0]\big) \geqslant 0. \tag{4.2}$$

(ii) *The identification of the sign of β_0 depends on the solution to inequality in Equation (4.1) that is quadratic in parameters.*

The proof of this proposition is trivial and therefore omitted. The conditions stated in this proposition are different from those in Equation (3.3). Notably, moment inequality (4.2) is quadratic in the parameter. The quadratic structure arises because in deriving the moment inequality (3.3) for the main model, I condition on the endogenous variable, whereas in this proposition, it is not possible to condition on $\bar{x}_i$.

Part (i) of this proposition requires an interesting condition. The expectation of the difference in peer characteristics of linked nodes must be greater than the difference in peer characteristics of non-linked nodes. In other words, the identified set is bounded if there is no homophily in terms of peer characteristics. This is a strong restriction, but it is only a sufficient condition for obtaining a bounded identified set. Part (ii) requires solving the quadratic equation in Equation (4.2). If the solution to that quadratic equation is an interval, then the identified set is bounded.

4.3 Identification Conditional on $(x_i \neq x_j)$

If the researcher is also interested in estimating β_0, we need to condition on x_{ij} such that $x_i \neq x_j$. Let $\mathbb{E}_k[Y] = \mathbb{E}[Y \mid x_{ij}, G = k]$, for $k \in \{0, 1\}$. Using this notation, I obtain

$$\begin{aligned}\big(\mathbb{E}_1[\Delta y^2] - \mathbb{E}_0[\Delta y^2]\big) + \rho_0^2\big(\mathbb{E}_1[\Delta \bar{x}^2] - \mathbb{E}_0[\Delta \bar{x}^2]\big) - 2\beta_0 \Delta x\big(\mathbb{E}_1[\Delta y] - {} \\ \mathbb{E}_0[\Delta y]\big) - 2\beta_0\rho_0\Delta x\big(\mathbb{E}_1[\Delta \bar{x}] - \mathbb{E}_0[\Delta \bar{x}]\big) - 2\rho_0\big(\mathbb{E}_1[\Delta y \Delta \bar{x}] - \mathbb{E}_0[\Delta y \Delta \bar{x}]\big) \leqslant 0.\end{aligned}$$

The parameters β_0 and ρ_0 can be partially identified from this moment inequality.

5 Estimation

This section considers estimation of a bound for the parameters. In particular, I show how to apply the standard estimation methods of moment inequalities to my empirical model.

The previous section derived moment inequalities from homophily assumptions. For estimation, it is convenient to turn these conditional moment inequalities into unconditional moment inequalities. To do this, I first define the propensity of link formation conditional on observables:

$$m(x_{ij}) = \mathbb{E}[G = 1 \mid x_{ij}].$$

I can write the moments in Equation (3.8) using $m(x_{ij})$

$$\begin{aligned}\mathbb{E}[\mathbb{1}\{|\Delta y - \beta_0 \Delta x| \leqslant \gamma\} \mid x_{ij}, G = 1] &= \mathbb{E}\left[\frac{\mathbb{1}\{|\Delta y - \beta_0 \Delta x| \leqslant \gamma\} G}{m(x_{ij})} \;\middle|\; x_{ij}\right], \\ \mathbb{E}[\mathbb{1}\{|\Delta y - \beta_0 \Delta x| \leqslant \gamma\} \mid x_{ij}, G = 0] &= \mathbb{E}\left[\frac{\mathbb{1}\{|\Delta y - \beta_0 \Delta x| \leqslant \gamma\}(1 - G)}{1 - m(x_{ij})} \;\middle|\; x_{ij}\right].\end{aligned}$$

Using these expectations, I write the conditional moment inequality as

$$\mathbb{E}\left[\frac{\mathbb{1}\{|\Delta y-\beta_0\Delta x|\leqslant\gamma\}(1-G)}{1-m(x_{ij})}-\frac{\mathbb{1}\{|\Delta y-\beta_0\Delta x|\leqslant\gamma\}G}{m(x_{ij})}\;\Big|\;x_{ij}\right]\leqslant 0, \tag{5.1}$$

which contains a single conditional moment. As a result, one can use the standard estimation methods of conditional moment inequalities after accounting for $m(x_{ij})$. To avoid the indicator function in the moment inequality and ease implementation, I write the moment inequalities as

$$\mathbb{E}\left[\frac{t\big(|\Delta y-\beta_0\Delta x|\big)(1-G)}{1-m(x_{ij})}-\frac{t\big(|\Delta y-\beta_0\Delta x|\big)G}{m(x_{ij})}\;\Big|\;x_{ij}\right]\geqslant 0, \tag{5.2}$$

where $t(x)$ is a monotone function. For example, $t(x)=x^2$ corresponds to the moment inequality obtained under the weak homophily assumption in Equation (3.3). For the rest of this section, I present an estimation procedure for $t(x)=x^2$. However, the procedure can be applied to other monotone functions. The estimation relies on a doubly robust version of the moment inequality in Equation (5.2). Rearranging Equation (5.2) and using $t(x)=x^2$, I obtain

$$\mathbb{E}\left[\frac{\big((\Delta y)^2-2\beta\Delta x\Delta y\big)(1-G)}{1-m(x_{ij})}-\frac{\big((\Delta y)^2-2\beta\Delta x\Delta y\big)G}{m(x_{ij})}\;\Big|\;x_{ij}\right]\geqslant 0.$$

Next, I define some nuisance functions:

$$\begin{aligned} f^k(x_{ij}) &:= \mathbb{E}[(\Delta y)^2\mid x_{ij},G=k]\\ h^k(x_{ij}) &:= \mathbb{E}[\Delta y\mid x_{ij},G=k]\end{aligned}$$

for $k\in\{0,1\}$. The moment inequality can be written in a doubly robust form as:

$$\begin{aligned}\mathbb{E}\Bigg[\Big(f^0(x_{ij})-2\beta\Delta x h^0(x_{ij})\Big)+\frac{\Big(\big((\Delta y)^2-f^0(x_{ij})\big)-2\beta\Delta x\big(\Delta y-h^0(x_{ij})\big)\Big)(1-G)}{1-m(x_{ij})}-\\ \Big(f^1(x_{ij})-2\beta\Delta x h^1(x_{ij})\Big)-\frac{\Big(\big((\Delta y)^2-f^1(x_{ij})\big)-2\beta\Delta x\big(\Delta y-h^1(x_{ij})\big)\Big)G}{m(x_{ij})}\;\Big|\;x_{ij}\Bigg]\geqslant 0.\end{aligned}$$

For doubly robust moments, the inequality holds if either of the nuisance functions is correct, so this estimation strategy is robust to misspecification in one of the nuisance functions. It also has other appealing properties, as studied by Chernozhukov et al. (2018a). Estimation of moment inequalities with doubly robust moments has been studied by Semenova (2017). She shows that using doubly robust moments, one can estimate nuisance functions with machine learning methods and obtain uniformly consistent estimates.

If x_i is a continuous variable, a straightforward way of estimation would be choosing a finite number of monotone $t(x)$ functions and integrating over x_{ij} to obtain unconditional moment inequalities. Then, one can use the method proposed by Semenova (2017). An alternative approach would be to use estimation methods for many moment inequalities. This approach could capture more information from the continuum of moment inequalities given by first-order stochastic dominance. For estimating many moment inequalities, see Chernozhukov et al. (2018b) and Andrews and Shi (2013).

If x_i is a discrete variable, it is also possible to estimate the set by inverting a hypothesis test. For weak homophily, one can test mean inequality using the standard two-sample t-test and invert the test to obtain the estimated set. For strong homophily, one can use the available first-order stochastic dominance test and invert the test to obtain the estimated set (Linton et al. (2005), Barrett and Donald (2003), Horváth et al. (2006)). I use this approach in my empirical application since my endogenous variables are binary.

6 Extensions

In this section, I briefly discuss two extensions of my main model by showing how to account for (i) exogenous control variables and (ii) nonlinear models.

6.1 Model with Controls

My main model does not include control variables. In this section, I incorporate the control variables into the model as:

$$y_i = \beta_0 x_i + \lambda_0 z_i + \alpha_i + \epsilon_i,$$

where z_i is a vector of exogenous control variables. To accommodate controls in identification, I modify the strong homophily assumption.

Definition 6.1 ((Conditional) Strong Homophily with Controls)**.** *Network formation satisfies*

$$F_{|\Delta\alpha|}\big(t \mid x_i, x_j, z_i, z_j, G=1\big) \leqslant F_{|\Delta\alpha|}\big(t \mid x_i, x_j, z_i, z_j, G=0\big),$$

for $(t, z_i, z_j, x_i, x_j) \in \mathbb{R}^+ \times \tilde{\mathcal{X}}^c$.

$\tilde{\mathcal{X}}^c$ is defined as the support of (z_i, z_j, x_i, x_j) such that $\mathbb{E}[G_{ij} \mid z_i, z_j, x_i, x_j]$ is bounded below zero and above one. In this definition, latent homophily holds conditional on all control variables, which accounts for the possibility that z_i and z_j might affect network formation. I also need to alter other assumptions to accommodate control variables.

Assumption 6.1. *Suppose that*

(i) $\epsilon_i \perp\!\!\!\perp \alpha_i, x_i, z_i, G_{ij}$.

(ii) *$\Delta\epsilon$ has a unimodal distribution.*

(iii) $\mathbb{E}[z_i(\alpha_i + \epsilon_i)] = 0$.

(iv) *The network satisfies strong homophily with controls.*

This assumption differs from Assumption (3.2) in that the conditions hold conditional on control variables, and also it assumes that z_i is exogenous. Since control variables are endogenous, I can partial out z_i and rewrite the model as

$$\tilde{y}_i = \beta_0 \tilde{x}_i + \alpha_i + \epsilon_i,$$

where $\tilde{x}_i := x_i - z_i \mathbb{E}\big[z_i' z_i\big]^{-1} \mathbb{E}\big[z_i' x_i\big]^{-1}$ and $\tilde{y}_i := y_i - z_i \mathbb{E}\big[z_i' z_i\big]^{-1} \mathbb{E}\big[z_i' y_i\big]^{-1}$.

After partialing out, α_i and ϵ_i are still in the model. This suggests that having exogenous controls in the model does not affect my identification results significantly. It is easy to show that Propositions 3.1 and 3.3 hold when x_i and x_j are replaced with $\tilde{x}_i$ and $\tilde{x}_j$. After satisfying these conditions, I can follow the same procedure from Section (5). Moreover, since the homophily assumption holds conditional on z_i, it is possible to obtain a tighter identified set. Also, including the control variables is important for homophily, as homophily might hold only conditional on some observables.

6.2 Deviations from the Linear Model

My identification strategy does not rely on a linear model. The linear function in Equation (3.1) can be replaced with a known nonlinear function up to a finite dimensional parameter vector. To demonstrate this extension, consider the model

$$y_i = r(\theta_0, x_i) + \alpha_i + \epsilon_i,$$

where $r(\theta_0, x_i)$ is a known function up to the parameter vector θ_0. For this model, I can obtain

$$\mathbb{E}[(\Delta y - r(\theta_0, x_i) + r(\theta_0, x_j) \mid x_i, x_j, G = 1] \leqslant \mathbb{E}[(\Delta y - r(\theta_0, x_i) + r(\theta_0, x_j) \mid x_i, x_j, G = 0].$$

This moment inequality can be used to partially identify θ_0.

7 Monte Carlo Simulations

I use Monte Carlo simulations to analyze the identified set under different scenarios.

7.1 Simulation Design I

The first simulation examines how the model features affect the size of the identified set. I consider two simulation designs. The first design looks at how the identified set changes with the degree of homophily. Intuitively, stronger homophily should lead to a more informative identified set. In the limit where there is no homophily, the identified set is not informative at all. The purpose of the second design is to understand the impact of endogeneity on the identified set. This is important because the characterization of the identified set does not provide guidance about how endogeneity affects the identified set. For these two exercises, I consider the following outcome and link formation models:

$$y_i = \beta_0 x_i + \alpha_i + \epsilon_i, \tag{7.1}$$

$$G_{ij} = 1\{\gamma|\alpha_i - \alpha_j| \leqslant \eta\}. \tag{7.2}$$

The data generating process is given by

$$\begin{pmatrix}\alpha_i \\ x_i\end{pmatrix} \sim N\left[\begin{pmatrix}0 \\ 0\end{pmatrix}, \begin{pmatrix}1 & p \\ p & 1\end{pmatrix}\right], \tag{7.3}$$

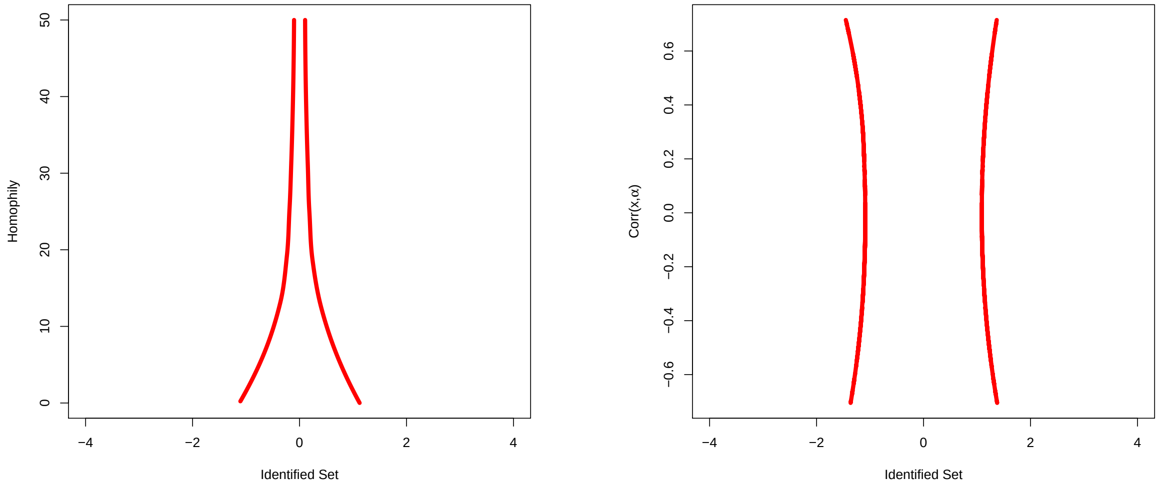
where $x_i = 1\{\tilde{x}_i > 0\}$, $\eta \sim U[-1, 5]$, $\epsilon \sim N[0, 1]$ and $\beta_0 = 0$. The network formation model in Equation (7.2) is simple and does not include observables. It incorporates homophily since the link formation probability decreases with the distance in latent space. Two parameters in this model control the features I aim to study. p equals the correlation between x_i and α_i, so it controls the degree of endogeneity in the model. The second parameter, γ, controls for the degree of homophily in the network formation model. As γ increases, the impact of the distance in latent space on link formation increases. My goal is to understand how these two parameters affect the length of the identified set. For this purpose, I investigate the identified sets for different values of p and γ.

I set the number of observations to ten million to reduce the impact of estimation error and focus on the identified set. Since x_i is an indicator variable, the model provides a single conditional moment inequality. I derive the identified set under the strong homophily assumption. Since my focus is on the identified set, I simulate this model only once.

Figure 1 reports the identified sets from Monte Carlo simulations. Panel (a) displays the relationship between the size of the identified set and the degree of homophily as controlled by γ. As expected, the size of the identified set becomes smaller as the degree of homophily increases. At a very large value of γ, the identified set is very informative and converges to a point. This result suggests that in networks with a high degree of homophily, the identified set should be more informative. Social networks are a good example of networks with a high degree of homophily (McPherson et al. (2001), Shrum et al. (1988), Moody (2001)).

In Panel (b), I report the identified set for different values of p, which controls the extent of endogeneity. The size of the identified set is negatively related to the degree of endogeneity: The identified set is narrower when there is no endogeneity, and it gets wider as endogeneity increases. However, the effect of endogeneity is small, as we see an only slight change in the size of the identified

Figure 1: Identified Set-Simulation Design I



(a) Degree of Homophily and Identified Set (b) Degree of Homophily and Identified Set

Note: The left panel shows the width of the identified set as the degree of homophily, governed by γ in Equation (7.2), changes. The left panel shows the width of the identified set as the degree of endogeneity, governed by γ in Equation (7.3), changes.

set.

7.2 Simulation Design II

My second simulation design considers a data generating process with two endogenous variables, and a network formation model with both observed and unobserved homophily. I assume the following model:

$$\begin{aligned} y_i &= \beta_1 x_{1i} + \beta_2 x_{2i} + \alpha_i + \epsilon_i \\ G_{ij} &= 1\{|\alpha_i - \alpha_j| + |x_{1i} - x_{1j}| + |x_{2i} - x_{2j}| \leqslant \eta\}. \end{aligned}$$

This simulation design is more realistic in the sense that the network formation model includes both observed and unobserved homophily. To generate the variables, I first simulate $(\alpha, \tilde{x}_1, \tilde{x}_2)$ from a multivariate normal distribution:

$$\begin{pmatrix} \alpha \\ \tilde{x}_1 \\ \tilde{x}_2 \end{pmatrix} \sim N \left[\begin{pmatrix} 0 \\ 0 \\ 0 \end{pmatrix}, \begin{pmatrix} 1 & 0.5 & 0.5 \\ 0.5 & 1 & 0.5 \\ 0.5 & 0.5 & 1 \end{pmatrix} \right],$$

and generate (x_1, x_2) as $x_1 = 1\{\tilde{x}_1 > 0\}$, $x_2 = 1\{\tilde{x}_2 > 0\}$. The other random variables are distributed $\eta \sim U[-1, 5]$, $\epsilon \sim N(0, 1)$ with true parameter values $\beta_1 = -1$, $\beta_2 = 1$. In this simulation, I report the estimated set with the number of observations equal to 500. Also, this

Figure 2: Simulation with Two Endogenous Variables - Estimated Set

Note: The estimated set obtained from the simulation design in section (7.2). The reported set shown in red covers the true parameter with a 95% probability, and the black point shows the true parameter values.

simulation allows me to examine the identified set with two endogenous variables, which I have not analyzed in Section 3.1.1.

I report the results in Figure 2. The reported set shown in red covers the true parameter with a 95% probability, and the black point shows the true parameter values. The results suggest that the identified set is bounded and quite informative, even though the number of observations is small. For example, the identified set excludes $(0, 0)$, rejecting the null hypothesis of no effects. Another interesting point worth noting is the shape of the identified set. This shape arises because the two variables are positively correlated.

8 Empirical Application

I demonstrate my method in an empirical setting using social network data from villages in rural China. This dataset was collected and used by Cai et al. (2015) to study the influence of social networks on weather insurance adoption. The authors conduct a randomized control trial where households are randomly assigned to information sessions about insurance products. Their paper combines this randomized control trial with network data to understand how information diffusion through the network affects insurance purchases. In my empirical application, I do not use insurance adoption or treatment variables, so my empirical setting is not affected by the experiment.

The data are collected from two surveys: a social network survey carried out before the experiment, and a household survey completed after households had made their insurance purchase decisions. The household survey includes questions on demographics, income, experience in purchasing any insurance, risk attitudes, and perception about future disasters. The dataset provides a census of the population of 185 villages with a total number of 5,335 households surveyed.

In my empirical application, I consider a peer effects model. The model includes both own effect and peer effects:

$$y_i = \theta x_i + \gamma \bar{x}_i + \lambda z_i + \alpha_i + \epsilon_i. \tag{8.1}$$

The outcome variable, y_i, is perceptions about future disasters, x_i is an indicator variable for literacy, and the controls, z_i, include age, gender, and village fixed effects.[16] I choose these variables because they are the most suitable variables in the dataset for my empirical application.[17,18] Since the endogenous variable is an indicator variable, the estimation gives a single moment inequality. I estimate the model under both the weak homophily and strong homophily assumptions.

We should expect that disaster perception and literacy are related to each other. A literate individual should acquire information from sources that an illiterate individual cannot. Also, we should also expect that unobservables affecting risk perception have an effect on whether an individual is literate. My objective is not to draw a definite conclusion about the relationship between perception of disaster and literacy, but to understand how my approach helps solve the endogeneity problem.

The goal of this empirical application is twofold. First and most important, I look at whether the identified set is informative. Since the data is a social network, there should be some degree of homophily, but whether this homophily is informative is an empirical question. My second goal is to compare my results with the OLS estimates. Excluding the OLS estimates would suggest that the model has endogeneity, and my approach controls for that endogeneity using network data.

I present the estimation results in Figure (3). The black region shows the estimated set (with 95% coverage) from my method. The blue points show the OLS estimates, and the red regions are 95% confidence bands for the OLS estimates. The panel on the left reports estimates under the weak homophily assumption and the panel on the right reports results for the strong homophily assumption. We observe that under both assumptions, the identified excludes the OLS estimates and their confidence bands. The OLS estimates suggest no effect of education and peer education

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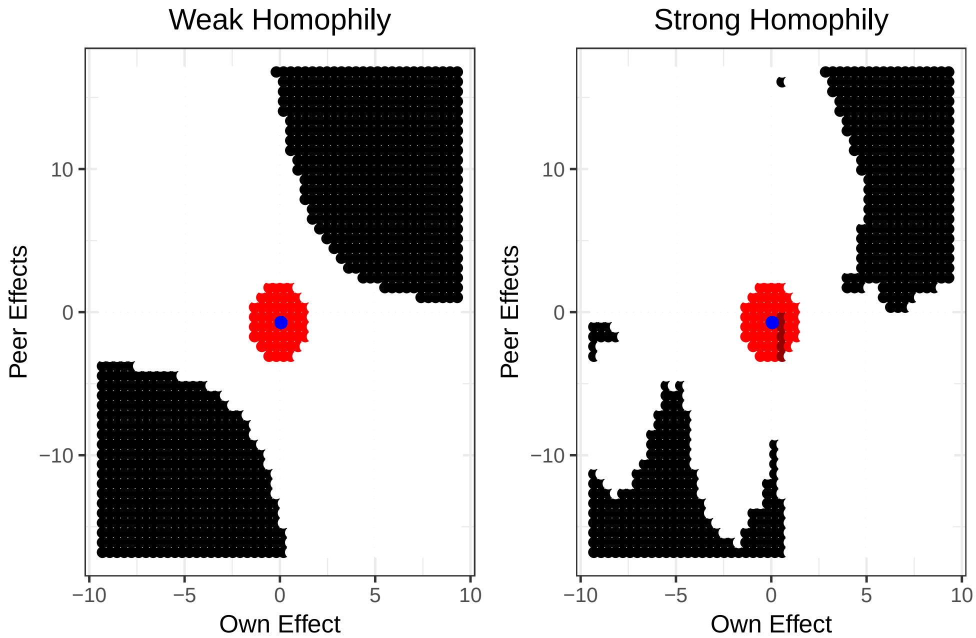
[16] The perceived probability of future disasters was elicited by asking, 'What do you think is the probability of a disaster that leads to a more than 30 percent loss in yield next year?'.

[17] Most outcome variables in the dataset are binary, which is not covered in my model.

[18] In a future iteration of this project, I will use data from AddHealth, which provides a richer set of variables and a larger number of observations.

Figure 3: Own and Peer Effects



Note: Estimated set for the parameters θ and γ in Equation (8.1) under weak and strong homophily assumptions. The regions in black cover the true parameter value with 95% probability. The blue points show the OLS estimates, and the red regions are 95% confidence bands for the OLS estimates.

on risk perception. In contrast, my estimated set excludes null effects.

Even though my estimates exclude the OLS estimates from the identified set, they do not give a definite answer on the sign of the effects. Under both the strong and weak homophily assumptions, my estimates suggest either positive or negative own and peer effects. Their signs are not identified, but we learn that the own effect and peer effects cannot have different signs. Finally, I compare the estimated sets from strong and weak homophily assumptions. As expected, the identified set is tighter under strong homophily than under weak homophily. Also, the identified set given by strong homophily is less well-behaved than the one given by weak homophily. This might be due to non-linearities in the moment inequalities under the strong homophily assumption.

9 Conclusion

This paper provides set identification results for the parameters of a linear model using homophily in networks. The model assumes that unobserved heterogeneity in the linear model also affects network formation. Using this assumption, I show that the homophily in unobservables, which is recognized as an essential feature of networks, provides information about unobserved heterogeneity in the linear model. I show how to use this information in the form of moment inequalities and make inferences about the parameters.

I analyze the identified set under two weak and strong homophily assumptions. Weak homophily gives a conditional moment inequality, while strong homophily gives a continuum of conditional moment inequalities. To analyze the informativeness of these moment inequalities, I derive the identified sets implied by these moments inequities and characterize the conditions under which the identified sets are bounded, and the conditions under which the signs of the parameters are identified. These conditions are weak and testable.

Importantly, my identification strategy is agnostic about the network formation model. I exploit a feature, homophily, that exists in a broad class of network formation models, rather than relying on a correctly specified network formation model. This makes my approach robust to misspecifications in the network formation model.

Finally, an empirical application and Monte Carlo simulations show that the identified set is informative about the parameters. Estimating own effect and peer effects of education on risk perception using social network data from villages in rural China, I find that my identified set excludes the OLS estimate and its confidence band, pointing to an endogeneity problem. The simulation exercise suggests that the identified set becomes more informative as the degree of homophily in the network increases. Therefore, my method is more effective to address endogeneity in networks with high degree of homophily, such as in social networks.

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A Alternative Definitions of Homophily

In this section, I provide several definitions of homophily and discuss the implication of these definitions. The definition relies on two features: (i) the shape of conditional link probability, and (ii) stochastic ordering of distance measures. I show that my definitions provide a range of homophily structures that might be of independent interest. I analyze these structures by showing that they are often nested with each other, so they can be ordered from strongest to weakest. I also argue that using stochastic ordering, which has not been used before, provides a flexible framework to characterize and study homophily in networks. Finally, this section also comments on how model-based homophily is related to my definitions.

Consistent with the empirical framework, this section considers unobserved homophily conditional on observed variables. However, these definitions can easily be extended to observed homophily. Let α_i denote an unobserved and scalar characteristic, and x_i denote a vector of observed features. G_{ij} is an indicator variable that equals one if i and j are connected. First, I define a function that characterizes the link formation probability,

$$h(\Delta, x_i, x_j) = \Pr(G_{ij} = 1 \mid \Delta\alpha_{ij} = \Delta, x_i, x_j). \tag{A.1}$$

This function specifies the link formation probability conditional on the distance in the latent space and observed characteristics. Next, I define a representative network formation model, which nests the commonly used network formation models. Assume that there exists $g(\cdot)$ such that links are formed according to:

$$G_{ij} = \mathbb{1}(g(\Delta\alpha_{ij}, x_i, x_j) \geqslant u_{ij}), \tag{A.2}$$

where u_{ij} is independent and identically distributed random variable with strictly increasing cumulative distribution function. The main difference between this model and Equation (A.1) is that this model imposes a structural model, whereas Equation (A.1) just a function of the unknown data generating process. For example, according to Equation (A.2), the links are independently formed, whereas, $h(\Delta, x_i, x_j)$ might exist when network is generated from a more complicated model. I start with the strongest definition of homophily.

A.1 Symmetric and Unimodal Network Formation - (SUF)

According to this definition, the network is formed based on Equation (A.2) and

$$g(\Delta\alpha_{ij}, x_i, x_j)$$

is symmetric and unimodal around zero with respect to its first argument for all x_i and x_j. The standard models in the literature assumes that g has a known form (possibly up to a parameter vector). This homophily definition is strong because it imposes a particular network formation structure and functional form restriction.

A.2 Symmetric and Unimodal Link Formation Probability- (SUP)

This definition states that

$$h(\cdot, x_i, x_j)$$

is symmetric and unimodal around zero. This differs from SUF in that it does not impose a particular network formation structure. As a result, it covers a broader network formation model and data generating processes. For example, this definition does not rule out interdependent link formation and multiple equilibria. I only require that $h(\cdot, x_i, x_j)$ exists.

A.3 Unimodal Link Formation Probability - (UP)

According to this definition

$$h(\cdot, x_i, x_j)$$

is unimodal around zero. This is similar to the previous definition but does not impose symmetry. This can happen, for example, when the links are not symmetric, and the nodes in the network are not exchangeable.

A.4 Decreasing Link Formation Probability - (DP)

This definition states that

$$\Pr\big(G_{ij} = 1 \mid (\Delta\alpha_{ij})^2 = \Delta, x_i, x_j\big)$$

is decreasing in Δ for all (x_i, x_j). This definition concerns how link formation probability changes with the squared distance. It is slightly weaker than the previous definitions in that it does restrict the entire shape link formation function.

A.5 Monotone Likelihood Ratio based Homophily Definition - (MLRP)

This definition states that

$$\frac{f_{(\Delta\alpha_{ij})^2}(\Delta \mid x_i, x_j, G_{ij} = 0)}{f_{(\Delta\alpha_{ij})^2}(\Delta \mid x_i, x_j, G_{ij} = 1)}$$

is increasing in Δ for all x_i and x_j. This definition is based on stochastic ordering of the distribution of $\Delta\alpha^2$ conditional on a link and no link. Using stochastic ordering is important because it provides a flexible framework to define homophily based on other stochastic orderings implied by MLRP.

A.6 Monotone Hazard Rate based Homophily Definition - (MHR)

This definition states that

$$\frac{f_{(\Delta\alpha_{ij})^2}(\Delta \mid x_i, x_j, G_{ij}=0)}{1-F_{(\Delta\alpha_{ij})^2}(\Delta \mid x_i, x_j, G_{ij}=0)} \geqslant \frac{f_{(\Delta\alpha_{ij})^2}(\Delta \mid x_i, x_j, G_{ij}=1)}{1-F_{(\Delta\alpha_{ij})^2}(\Delta \mid x_i, x_j, G_{ij}=1)}$$

for all Δ, x_i and x_j. Monotone Hazard Rate is an implication of MLRP and based on a weaker notion of stochastic ordering.

A.7 First Order Stochastic Dominance based Homophily Definition - (FOSD)

This definition imposes a first order stochastic ordering. In particular, it says that

$$F_{(\Delta\alpha_{ij})^2}(\Delta \mid x_i, x_j, G_{ij}=0) \geqslant F_{(\Delta\alpha_{ij})^2}(\Delta \mid x_i, x_j, G_{ij}=1)$$

for all Δ, x_i and x_j. This corresponds to the strong homophily definition I use to identify the linear model in the main text. First order stochastic dominance is an implication of MHR and based on a weaker notion of stochastic ordering.

A.8 Moment Inequality based Homophily Definition - (MI)

This definition states that

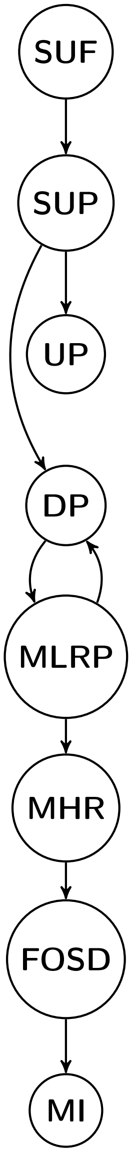
$$\mathbb{E}[(\Delta\alpha_{ij})^2 \mid x_i, x_j, G_{ij}=0] \geqslant \mathbb{E}[(\Delta\alpha_{ij})^2 \mid x_i, x_j, G_{ij}=1]$$

for all x_i and x_j. This definition corresponds to the weak homophily definition I use to identify the linear model in the main text. This is again an implication of first order stochastic dominance. This is the weakest homophily definition.

Figure 4 compares the homophily definitions given above. An arrow from definition A to definition B shows that if a network satisfies definition A, then it also satisfies the definition B. We see that SUF, the model-based definition, is the strongest notion of homophily. In contrast, MI is the weakest. Among all definitions, only DP and MLRP are equivalent. Also, definitions that impose restrictions on the shape of the conditional probability of link (SUF, SUP, UP and DP) in general impose stronger restrictions than the ones that are based on stochastic ordering (MLRP, MHR, FOSD, MI). The equivalence of MLRP and DP relates the two concepts of homophily.

The proofs that show that the relationships between homophily definitions are given in the next section.

Figure 4: Relationship between Hompohily Definitions



A.9 Proofs

In this section, I present the proofs for the relationship between homophily definitions presented in this section. I omit the trivial proofs that SUF implies SUP, SUP implies UP, MLRP implies MHR, MHR implies FOSD, FOSD implies MI.

SUP implies DP

Assume that I condition on x_i and x_j in all expectations and probability distribution functions

$$\begin{aligned}
\Pr(G_{ij}=1 \mid (\Delta\alpha_{ij})^2=\Delta) &= \frac{\Pr(G_{ij}=1 \mid \Delta\alpha_{ij}=-\sqrt{\Delta})f_{\Delta\alpha_{ij}}(-\sqrt{\Delta})+\Pr(G_{ij}=1 \mid \Delta\alpha_{ij}=\sqrt{\Delta})f_{\Delta\alpha_{ij}}(\sqrt{\Delta})}{f_{\Delta\alpha_{ij}}(\sqrt{\Delta})+f_{\Delta\alpha_{ij}}(-\sqrt{\Delta})}, \\
&= \frac{\Pr(G_{ij}=1 \mid \Delta\alpha_{ij}=\sqrt{\Delta})\big(\Delta f_{\alpha_{ij}}(-\sqrt{\Delta})+f_{\Delta\alpha_{ij}}(\sqrt{\Delta})\big)}{\big(f_{\Delta\alpha_{ij}}(-\sqrt{\Delta})+f_{\Delta\alpha_{ij}}(\sqrt{\Delta})\big)}, \\
&= \Pr(G_{ij}=1 \mid \Delta\alpha_{ij}=\sqrt{\Delta}),
\end{aligned}$$

which is decreasing in Δ by unimodality of $\Pr(G_{ij}=1 \mid \Delta\alpha_{ij}=\Delta)$ and monotonicity of $\sqrt{\Delta}$ in Δ.

UP Does not Imply DP

I condition on x_i and x_j throughout. Take $\Delta_1 > \Delta_2 \geqslant 0$ Network formation according DP should satisfy

$$\Pr(G_{ij}=1 \mid (\Delta\alpha_{ij})^2=\Delta_2) \geqslant \Pr(G_{ij}=1 \mid (\Delta\alpha_{ij})^2=\Delta_1).$$

I will show a counterexample where this does not hold when UP holds. The probabilities above can be computed as

$$\begin{aligned}
\Pr(G_{ij}=1 \mid (\Delta\alpha_{ij})^2=\Delta_1) &= \frac{\Pr(G_{ij}=1 \mid \Delta\alpha_{ij}=-\sqrt{\Delta_1})f_{\alpha_{ij}}(-\sqrt{\Delta_1})+\Pr(G_{ij}=1 \mid \Delta\alpha_{ij}=\sqrt{\Delta_1})f_{\alpha_{ij}}(\sqrt{\Delta_1})}{f_{\alpha_{ij}}(\sqrt{\Delta_1})+f_{\alpha_{ij}}(-\sqrt{\Delta_1})}, \\
\Pr(G_{ij}=1 \mid (\Delta\alpha_{ij})^2=\Delta_2) &= \frac{\Pr(G_{ij}=1 \mid \Delta\alpha_{ij}=-\sqrt{\Delta_2})f_{\alpha_{ij}}(-\sqrt{\Delta_2})+\Pr(G_{ij}=1 \mid \Delta\alpha_{ij}=\sqrt{\Delta_2})f_{\alpha_{ij}}(\sqrt{\Delta_2})}{f_{\alpha_{ij}}(\sqrt{\Delta_2})+f_{\alpha_{ij}}(-\sqrt{\Delta_2})}
\end{aligned}$$

Unimodal link formation probability according to UP implies

$$\begin{gathered}
\Pr(G_{ij}=1 \mid \Delta\alpha_{ij}=-\sqrt{\Delta_2}) \geqslant \Pr(G_{ij}=1 \mid \Delta\alpha_{ij}=-\sqrt{\Delta_1}), \\
\Pr(G_{ij}=1 \mid \Delta\alpha_{ij}=\sqrt{\Delta_2}) \geqslant \Pr(G_{ij}=1 \mid \Delta\alpha_{ij}=\sqrt{\Delta_1}).
\end{gathered}$$

To see a counterexample assume that

$$\begin{gathered}
m=\Pr(G_{ij}=1 \mid \Delta\alpha_{ij}=-\sqrt{\Delta_2}) \geqslant \Pr(G_{ij}=1 \mid \Delta\alpha_{ij}=-\sqrt{\Delta_1})=0, \\
\Pr(G_{ij}=1 \mid \Delta\alpha_{ij}=\sqrt{\Delta_2})=\Pr(G_{ij}=1 \mid \Delta\alpha_{ij}=\sqrt{\Delta_1})=k,
\end{gathered}$$

which satisfies the unimodal network formation probability. Substituting these

$$
\begin{aligned}
\Pr(G_{ij} = 1 \mid (\Delta\alpha_{ij})^2 = \Delta_1) &= \frac{m f_{\alpha_{ij}}(\sqrt{\Delta_1})}{f_{\alpha_{ij}}(\sqrt{\Delta_1}) + f_{\alpha_{ij}}(-\sqrt{\Delta_1})} \\
\Pr(G_{ij} = 1 \mid (\Delta\alpha_{ij})^2 = \Delta_2) &= \frac{\epsilon f_{\alpha_{ij}}(-\sqrt{\Delta_2}) + k f_{\alpha_{ij}}(\sqrt{\Delta_2})}{f_{\alpha_{ij}}(\sqrt{\Delta_2}) + f_{\alpha_{ij}}(-\sqrt{\Delta_2})}
\end{aligned}
$$

For any values of m and $f_{\alpha_{ij}}(\sqrt{\Delta_2})$, $f_{\alpha_{ij}}(\sqrt{\Delta_1})$ and k there exists large enough $f_{\Delta\alpha_{ij}}(-\sqrt{\Delta_1})$ such that

$$
\frac{m f_{\alpha_{ij}}(-\sqrt{\Delta_2}) + k f_{\alpha_{ij}}(\sqrt{\Delta_2})}{f_{\alpha_{ij}}(\sqrt{\Delta_2}) + f_{\alpha_{ij}}(-\sqrt{\Delta_2})} \geqslant \frac{k f_{\alpha_{ij}}(\sqrt{\Delta_1})}{f_{\alpha_{ij}}(\sqrt{\Delta_1}) + f_{\alpha_{ij}}(-\sqrt{\Delta_1})},
$$

which violates the condition given in definition of DP.

DP holds if and only if MLRP Holds

Using the Bayes Rule for continuous random variables gives

$$
\begin{aligned}
f_{\Delta\alpha^2_{ij}}(\Delta \mid x_i, x_j, G_{ij} = 1) &= \frac{\Pr(G_{ij} = 1 \mid \Delta, x_i, x_j) f_{\Delta\alpha_{ij}}(\Delta \mid x_i, x_j) f(x_i, x_j)}{\Pr(G_{ij} = 1 \mid x_i, x_j) f(x_i, x_j)}, \\
&= \frac{\Pr(G_{ij} = 1 \mid \Delta, x_i, x_j) f_{\Delta\alpha_{ij}}(\Delta \mid x_i, x_j)}{\Pr(G_{ij} = 1 \mid x_i, x_j)}.
\end{aligned}
$$

And similarly for $f_{\Delta\alpha^2_{ij}}(\Delta \mid x_i, x_j, G_{ij} = 0)$. By taking the ratio of the two

$$
\begin{aligned}
\frac{f_{\Delta\alpha^2_{ij}}(\Delta \mid x_i, x_j, G_{ij} = 0)}{f_{\Delta\alpha^2_{ij}}(\Delta \mid x_i, x_j, G_{ij} = 1)} &= \frac{\Pr(G_{ij} = 0 \mid \Delta, x_i, x_j) \Pr(G_{ij} = 1 \mid x_i, x_j)}{\Pr(G_{ij} = 1 \mid \Delta, x_i, x_j) \Pr(G_{ij} = 0 \mid x_i, x_j)}, \\
&= \frac{\big(1 - \Pr(G_{ij} = 1 \mid \Delta, x_i, x_j)\big) \Pr(G_{ij} = 1 \mid x_i, x_j)}{\Pr(G_{ij} = 1 \mid \Delta, x_i, x_j)\big(1 - \Pr(G_{ij} = 1 \mid x_i, x_j)\big)}.
\end{aligned}
$$

Since the numerator is decreasing in $\Pr(G_{ij} = 1 \mid \Delta, x_i, x_j)$ and denominator is increasing in $\Pr(G_{ij} = 1 \mid \Delta, x_i, x_j)$ the right hand side is decreasing in $\Pr(G_{ij} = 1 \mid \Delta, x_i, x_j)$. Pick $\Delta_1 \geqslant \Delta_2$, MLRP implies

$$
\Pr(G_{ij} = 1 \mid \Delta_2, x_i, x_j) \geqslant \Pr(G_{ij} = 1 \mid \Delta_1, x_i, x_j).
$$

Using this, it is easy to see that

$$
\frac{f_{\Delta\alpha^2_{ij}}(\Delta_1 \mid x_i, x_j, G_{ij} = 0)}{f_{\Delta\alpha^2_{ij}}(\Delta_1 \mid x_i, x_j, G_{ij} = 1)} \geqslant \frac{f_{\Delta\alpha^2_{ij}}(\Delta_2 \mid x_i, x_j, G_{ij} = 0)}{f_{\Delta\alpha^2_{ij}}(\Delta_2 \mid x_i, x_j, G_{ij} = 1)}.
$$

Therefore, MLRP follows. Pick Δ_1 and Δ_2 such that $\Delta_1 \geqslant \Delta_2$, DP implies

$$
\frac{\big(1 - \Pr(G_{ij} = 1 \mid \Delta_1, x_i, x_j)\big) \Pr(G_{ij} = 1 \mid x_i, x_j)}{\Pr(G_{ij} = 1 \mid \Delta_1, x_i, x_j)\big(1 - \Pr(G_{ij} = 1 \mid x_i, x_j)\big)} \geqslant \frac{\big(1 - \Pr(G_{ij} = 1 \mid \Delta_2, x_i, x_j)\big) \Pr(G_{ij} = 1 \mid x_i, x_j)}{\Pr(G_{ij} = 1 \mid \Delta_2, x_i, x_j)\big(1 - \Pr(G_{ij} = 1 \mid x_i, x_j)\big)},
$$

which further gives

$$\frac{\big(1-\Pr(G_{ij}=1\mid\Delta_1,x_i,x_j)\big)}{\Pr(G_{ij}=1\mid\Delta_1,x_i,x_j)}\geqslant\frac{\big(1-\Pr(G_{ij}=1\mid\Delta_2,x_i,x_j)\big)}{\Pr(G_{ij}=1\mid\Delta_2,x_i,x_j)},$$

and

$$\Pr(G_{ij}=1\mid\Delta_2,x_i,x_j)\geqslant\Pr(G_{ij}=1\mid\Delta_1,x_i,x_j).$$

Therefore MLRP implies that the link formation probability is decreasing in Δ.

B Proofs

B.1 Proof of Proposition 3.1

In this proof, I show that weak homophily is robust to an additive noise that satisfies the conditions in Assumption 3.1. To simplify notation, I condition on x_i and x_j throughout the proof, and drop them from the conditioning set. Expectation of $(\Delta\alpha + \Delta\epsilon)^2$ conditional on G is given by:

$$\begin{aligned}
\mathbb{E}\big[(\Delta\alpha + \Delta\epsilon)^2 \mid G = i\big] &= \mathbb{E}\big[(\Delta\alpha)^2 \mid G = i\big] + \mathbb{E}\big[\Delta\alpha\Delta\epsilon \mid G = i\big] + \mathbb{E}\big[(\Delta\epsilon)^2 \mid G = i\big],\\
&= \mathbb{E}\big[(\Delta\alpha)^2 \mid G = i\big] + \mathbb{E}\big[\Delta\alpha\mathbb{E}\big[\Delta\epsilon \mid \alpha_i, \alpha_j, G = i\big] \mid G = i\big] + \mathbb{E}\big[(\Delta\epsilon)^2 \mid G = i\big],\\
&= \mathbb{E}\big[(\Delta\alpha)^2 \mid G = i\big] + \mathbb{E}\big[\Delta\alpha\mathbb{E}\big[\Delta\epsilon \mid \alpha_i, \alpha_j\big] \mid G = i\big] + \mathbb{E}\big[(\Delta\epsilon)^2 \mid G = i\big],\\
&= \mathbb{E}\big[(\Delta\alpha)^2 \mid G = i\big] + \mathbb{E}\big[(\Delta\epsilon)^2 \mid G = i\big],
\end{aligned}$$

where I use the law of iterated expectations and Assumption 3.1(i, iii, v). To complete the proof I need to show that

$$\mathbb{E}[(\Delta\epsilon)^2 \mid G = 1] = \mathbb{E}[(\Delta\epsilon)^2 \mid G = 0].$$

Using Assumption 3.1(ii, iii), I obtain

$$\begin{aligned}
\mathbb{E}[(\Delta\epsilon)^2 \mid G = i] &= \mathbb{E}\big[\mathbb{E}[(\Delta\epsilon)^2 \mid \alpha_i, \alpha_j, G = i] \mid G = i],\\
&= \mathbb{E}\big[\mathbb{E}[(\Delta\epsilon)^2 \mid \alpha_i, \alpha_j] \mid G = i],\\
&= \mathbb{E}\big[\mathbb{E}[(\Delta\epsilon)^2] \mid G = i],\\
&= \mathbb{E}[(\Delta\epsilon)^2].
\end{aligned}$$

This, along with Assumption 3.1 (iv) gives

$$\mathbb{E}\big[(\Delta\alpha + \Delta\epsilon)^2 \mid x_i, x_j, G = 0\big] \geqslant \mathbb{E}\big[(\Delta\alpha + \Delta\epsilon)^2 \mid x_i, x_j, G = 1\big].$$

B.2 Proof of Proposition 3.3

First, I introduce additional notation to simplify the exposition. Throughout the proof, I condition on (x_i, x_j) and define

$$\Delta z := \Delta\alpha + \Delta\epsilon, \qquad F_{\Delta z^i}(t) := F_{\Delta z^i}(t \mid G = i).$$

For a continuously distributed random variable w, we have

$$F_{|w|}(t) = \Pr(-t \leqslant w \leqslant t) = F_w(t) - F_w(-t), \quad \text{for} \quad t \geqslant 0.$$

Therefore, Assumption 3.2 implies that

$$F_{\Delta\alpha^0}(t) - F_{\Delta\alpha^0}(-t) - F_{\Delta\alpha^1}(t) + F_{\Delta\alpha^1}(-t) \leqslant 0, \quad \text{for} \quad t \geqslant 0. \tag{B.1}$$

To prove this proposition, I need to show, using Equation (B.1) and Assumption 3.2, that

$$g(t) := F_{\Delta z^0}(t) - F_{\Delta z^0}(-t) - F_{\Delta z^1}(t) + F_{\Delta z^1}(-t) \leqslant 0, \quad \text{for} \quad t \geqslant 0.$$

By Assumption 3.2 (i) I can write conditional distribution of Δz using convolution as follows:

$$F_{\Delta z^i}(t) = \int_{-\infty}^{\infty} F_{\Delta \alpha^i}(t-u) f_{\Delta \epsilon^i}(u) du.$$

This is because, under Assumption (3.2)(i), $\Delta\alpha$ and $\Delta\epsilon$ are conditionally independent from each other and the sum of two independent random variables has a distribution function given by a convolution. Substituting this, I can obtain $g(t)$ as

$$\begin{aligned}
g(t) &= \int_{-\infty}^{\infty} \Big(F_{\Delta\alpha^0}(t-u) - F_{\Delta\alpha^0}(-t-u)\Big) f_{\Delta\epsilon^0}(u)du - \int_{-\infty}^{\infty} \Big(F_{\Delta\alpha^1}(t-u) - F_{\Delta\alpha^1}(-t-u)\Big) f_{\Delta\epsilon^1}(u)du \\
&= \int_{-\infty}^{\infty} \Big(F_{\Delta\alpha^0}(t-u) - F_{\Delta\alpha^0}(-t-u)\Big) f_{\Delta\epsilon}(u)du - \int_{-\infty}^{\infty} \Big(F_{\Delta\alpha^1}(t-u) - F_{\Delta\alpha^1}(-t-u)\Big) f_{\Delta\epsilon}(u)du \\
&= \int_{-\infty}^{\infty} \Big(F_{\Delta\alpha^0}(t-u) - F_{\Delta\alpha^1}(t-u) f_{\Delta\epsilon}(u)du + \int_{-\infty}^{\infty} \Big(F_{\Delta\alpha^1}(-t-u) - F_{\Delta\alpha^0}(-t-u) f_{\Delta\epsilon}(u)du \\
&= \int_{-\infty}^{\infty} \Big(F_{\Delta\alpha^0}(t-u) - F_{\Delta\alpha^1}(t-u)\Big) f_{\Delta\epsilon}(u)du + \int_{-\infty}^{\infty} \Big(F_{\Delta\alpha^1}(-t+\tilde{u}) - F_{\Delta\alpha^0}(-t+\tilde{u})\Big) f_{\Delta\epsilon}(-\tilde{u})d\tilde{u} \\
&= \int_{-\infty}^{\infty} \Big(F_{\Delta\alpha^0}(t-u) - F_{\Delta\alpha^1}(t-u)\Big) f_{\Delta\epsilon}(u)du + \int_{-\infty}^{\infty} \Big(F_{\Delta\alpha^1}(-t+\tilde{u}) - F_{\Delta\alpha^0}(-t+\tilde{u})\Big) f_{\Delta\epsilon}(\tilde{u})d\tilde{u} \\
&= \int_{-\infty}^{\infty} \Big(F_{\Delta\alpha^0}(t-u) - F_{\Delta\alpha^0}(-t+u)\Big) - \Big(F_{\Delta\alpha^1}(z-u) - F_{\Delta\alpha^1}(-t+u)\Big) f_{\Delta\epsilon}(u)du,
\end{aligned}$$

where the second line follows from $f_{\Delta\epsilon^1} = f_{\Delta\epsilon^0} = f_{\Delta\epsilon}$ and the third line rearranges integrals. The fourth line is obtained using the change of variable, $\tilde{u} = -\tilde{u}$. The following line uses the fact that $f_{\Delta\epsilon}$ is symmetric around zero. Symmetry holds because the convolution of two independent and identically distributed random variables is symmetric about zero. Next, define $m(t)$ as

$$m(t) := F_{\Delta\alpha^0}(t) - F_{\Delta\alpha^0}(-t) - F_{\Delta\alpha^1}(t) + F_{\Delta\alpha^1}(-t).$$

Note that $m(t)$ is an odd function by definition, $m(t)+m(-t)=0$, it is negative for $t>0$ and $m(0)=0$. Using $m(t)$ we can obtain $g(t)$ as

$$\begin{aligned} g(t) &= \int_{-\infty}^{\infty} \Big(F_{\Delta\alpha^0}(t-u) - F_{\Delta\alpha^0}(-t+u)\Big) - \Big(F_{\Delta\alpha^1}(t-u) - F_{\Delta\alpha^1}(-t+u)\Big) f_{\Delta\epsilon}(u)du, \\ &= \int_{-\infty}^{\infty} m(t-u) f_{\Delta\epsilon}(u)du. \end{aligned}$$

I need to show that this integral is non-negative for $t \geqslant 0$. First note that for $t=0$

$$g(0) = \int_{-\infty}^{\infty} m(-u) f_{\epsilon}(u)du = 0,$$

by symmetry of $f_{\Delta\epsilon}(u)$ and the fact that m is an odd function. For $t>0$ we can write

$$\begin{aligned} \int_{-\infty}^{\infty} m(t-u) f_{\Delta\epsilon}(u)du = \int_{-\infty}^{\infty} m(u) f_{\Delta\epsilon}(t-u)du &= \int_{0}^{\infty} m(u) f_{\Delta\epsilon}(t-u)du + \int_{-\infty}^{0} m(u) f_{\Delta\epsilon}(t-u)du, \\ &= \int_{0}^{\infty} m(u) f_{\Delta\epsilon}(t-u)du + \int_{0}^{\infty} m(-u) f_{\Delta\epsilon}(t+u)du, \\ &= \int_{0}^{\infty} m(u) f_{\Delta\epsilon}(t-u)du - \int_{0}^{\infty} m(u) f_{\Delta\epsilon}(t+u)du, \\ &= \int_{0}^{\infty} m(u)\big(f_{\Delta\epsilon}(t-u) - f_{\Delta\epsilon}(t+u)\big)du. \end{aligned}$$

The second line is obtained from a change of variable $\tilde{u} = -u$ and the third line uses the fact that $m(t)$ is an odd function. This derivation suggests that a sufficient condition for this integral to be negative is

$$f_{\Delta\epsilon}(t-u) - f_{\Delta\epsilon}(t+u) \geqslant 0, \quad \text{for} \quad (t,u) \in \mathbb{R}_+ \times \mathbb{R}_+.$$

Since $f_{\Delta\epsilon}(u)$ is symmetric around zero and unimodal by Assumption 3.2, this condition is satisfied. This completes the proof.

B.3 Proof of Proposition 3.5

In this proof, I will show that the condition given in Lemma 3.1 is satisfied under Assumption 3.3. Define $\Delta z := \Delta\alpha + \Delta\epsilon$ and let $f_{\Delta z}(t)$ be the corresponding probability density function. Using the Bayes rule for continuous random variables we have

$$f_{\Delta z^1}(t) = \frac{\mathbb{E}[G \mid \Delta z] f_{\Delta z}(t)}{E[G]}, \qquad f_{\Delta z^0}(t) = \frac{(1-\mathbb{E}[G \mid \Delta z] f_{\Delta z}(t)}{1-E[G]}.$$

I can write the differences of two distribution functions using these as

$$\begin{aligned}
g(t) &:= F_{\Delta z}(t \mid G=1) - F_{\Delta z}(t \mid G=0) \\
&= \int_{-\infty}^{t} f_{\Delta z^1}(u)du - \int_{-\infty}^{t} f_{\Delta z^0}(u)du = \int_{-\infty}^{t} \frac{\mathbb{E}[G \mid \Delta\alpha] f_{\Delta\alpha}(u)}{\mathbb{E}[G]}du - \int_{-\infty}^{t} \frac{\big(1-\mathbb{E}[G \mid \Delta\alpha_{ij}]\big) f_{\Delta\alpha}(u)}{1-\mathbb{E}[G]}du, \\
&= \int_{-\infty}^{t} \left(\frac{\mathbb{E}[G \mid \Delta\alpha] f_{\Delta\alpha}(u)}{\mathbb{E}[G]} - \frac{\big(1-\mathbb{E}[G \mid \Delta\alpha]\big) f_{\Delta\alpha}(u)}{1-\mathbb{E}[G]} \right) du, \\
&= \int_{-\infty}^{t} \left(\frac{\mathbb{E}[G \mid \Delta\alpha]}{\mathbb{E}[G]} - \frac{\big(1-\mathbb{E}[G \mid \Delta\alpha]\big)}{1-\mathbb{E}[G]} \right) f_{\Delta\alpha}(u)du, \\
&= \frac{1}{\mathbb{E}[G](1-E[G])} \int_{-\infty}^{t} \left(\mathbb{E}[G \mid \Delta\alpha] - E[G]\right) f_{\Delta\alpha}(u)du.
\end{aligned}$$

By my assumptions we have

$$\lim_{t\to\infty} g(t) = \lim_{t\to-\infty} g(t) = 0.$$

There exists M such that

$$\begin{aligned}
\frac{1}{\mathbb{E}[G](1-E[G])} \int_{-\infty}^{-M} \left(\mathbb{E}[G \mid \Delta\alpha] - E[G]\right) f_{\Delta\alpha}(u)du < 0, \\
\frac{1}{\mathbb{E}[G](1-E[G])} \int_{M}^{\infty} \left(\mathbb{E}[G \mid \Delta\alpha] - E[G]\right) f_{\Delta\alpha}(u)du < 0.
\end{aligned}$$

This implies that $g(t)$ should take positive and negative values. Therefore there exists t, t' such that $g(t) > 0$ and $g(t') > 0$. Therefore, the condition given in Lemma 3.1 is satisfied and I conclude that identified set is bounded.

B.4 Proof of Lemma 3.1

Without loss of generality set $x_i = 1$ and $x_j = 0$. By Assumption 3.3 (i) there exists $M \in \mathbb{R}$ such that $\operatorname{supp}(\Delta y \mid x_i, x_j) \subseteq [-M, M]$. We will show that identified set satisfies

$$B \subseteq (-2M - \beta_0, 2M - \beta_0).$$

The identification condition states that β_0 satisfies

$$\mathbb{E}[\mathbb{1}\{|\Delta y - \beta_0| \leqslant \gamma\} \mid x_{ij}, G=1] \geqslant \mathbb{E}[\mathbb{1}\{|\Delta y - \beta_0| \leqslant \gamma\} \mid x_{ij}, G=0], \qquad \text{for all} \quad \gamma \geqslant 0.$$

By substituting Δy from our model this condition can be written as

$$\mathbb{E}[\mathbb{1}\{|\Delta z + (\beta_0 - \beta)| \leqslant \gamma\} \mid x_{ij}, G=1] \geqslant \mathbb{E}[\mathbb{1}\{|\Delta z + (\beta_0 - \beta)| \leqslant \gamma\} \mid x_{ij}, G=0] \qquad \text{for all} \quad \gamma \geqslant 0$$

Assume, as a contradiction, that $(-\infty, -2M - \beta_0) \cap B = S \neq \emptyset$. Take $\tilde{\beta} \in S$ which satisfies

$$\mathbb{E}[\mathbb{1}\{|\Delta z + (\beta_0 - \tilde{\beta})| \leqslant \gamma\} \mid x_{ij}, G = 1] \geqslant \mathbb{E}[\mathbb{1}\{|\Delta z + (\beta_0 - \tilde{\beta})| \leqslant \gamma\} \mid x_{ij}, G = 0], \qquad \text{for all} \quad \gamma \geqslant 0,$$

where $\Delta z := \Delta\alpha + \Delta\epsilon$. This equation can be written as

$$\mathbb{E}[\mathbb{1}\{\Delta z \leqslant \gamma - (\beta_0 - \beta)\} \mid x_{ij}, G = 1] \geqslant \mathbb{E}[\mathbb{1}\{\Delta z \leqslant \gamma - (\beta_0 - \beta)\} \mid x_{ij}, G = 0], \qquad \text{for all} \quad \gamma \geqslant 0$$

However, this violates the condition stated in the lemma. Thus I conclude that $(2M, +\infty)$ is not in the identified set. Similarly, assume as a contradiction that $(2M - \beta_0, \infty) \cap B = S \neq \emptyset$. Take $\tilde{\beta} \in S$ which satisfies

$$\mathbb{E}[\mathbb{1}\{|\Delta z + (\beta_0 - \tilde{\beta})| \leqslant \gamma\} \mid x_{ij}, G = 1] \geqslant \mathbb{E}[\mathbb{1}\{|\Delta z + (\beta_0 - \tilde{\beta})| \leqslant \gamma\} \mid x_{ij}, G = 0],$$

which can be written as

$$\mathbb{E}[\mathbb{1}\{-\Delta z - (\beta_0 - \tilde{\beta}) \leqslant \gamma\} \mid x_{ij}, G = 1] \geqslant \mathbb{E}[\mathbb{1}\{-\Delta z - (\beta_0 - \tilde{\beta}) \leqslant \gamma\} \mid x_{ij}, G = 0],].$$

This gives

$$\mathbb{E}[\mathbb{1}\{-\Delta z \leqslant \gamma + (\beta_0 - \tilde{\beta})\} \mid x_{ij}, G = 1] \geqslant \mathbb{E}[\mathbb{1}\{-\Delta z \leqslant \gamma + (\beta_0 - \tilde{\beta})\} \mid x_{ij}, G = 0].$$

This again violates the condition given in Lemma 3.1. Therefore I conclude that

$$\beta \subseteq (-2M - \beta_0, 2M - \beta_0),$$

and the identified set is bounded.