

# Spillover Effects with Nonrandom Sample Selection\*

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## Abstract

This paper proposes a method to estimate spillover effects of a random treatment using a non-random sample of individuals for whom the analyst can observe their outcomes, i.e., *nonrandom sample selection*. Although randomized experiments facilitate comparisons between treated and control groups at the baseline, they cannot guarantee that the groups are comparable when there is endogenous sample selection. The proposed method employs an exposure monotonicity assumption that extends the conventional Lee bounds to general exposures to treatment. Under this assumption, we show how to compute the bounds for a spillover estimand that allows for the inclusion of covariate adjustments and network dependence, where statistical inference follows a design-based approach. The framework is extended with a conditional exposure monotonicity assumption that allows for the inclusion of high dimensional covariates via machine learning. The empirical application presents the new method to analyze spillover effects of a randomized experiment on computer utilization in students from public schools.

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# 1 Introduction

Spillover effects denote the impact of a treatment or intervention on individuals not directly targeted by the treatment. Estimating the magnitude of spillovers allows researchers to grasp the broader impacts of interventions and shed light on their effects beyond the treated group. However, in certain scenarios where researchers seek to estimate causal effects using nonrandom selected samples, treatment randomization is not enough to uniquely identify widely used causal estimands such as average treatment effects and average spillover effects (Heckman, 1979; Horowitz and Manski, 2000). For example, survey and sample attrition create missing outcome data, leading to an endogenous sample selection issue unless outcomes are assumed to be missing at random. Another common situation in empirical research involves analyzing extensive versus intensive margins. As discussed in Chen and Roth (2023), point-identification of the intensive margin becomes challenging when the extensive margin is of significance. Without imposing strong assumptions, the intensive margin is only partially identified. When the focus shifts to the estimation of spillover effects, the widely used Lee bounds for bounding treatment effects become inapplicable (Lee, 2009).

This paper presents a novel estimator designed to bound spillover effects in scenarios of endogenous sample selection. The method relies on an *exposure monotonicity* condition that restricts how individuals select into the sample through their exposures to treatment. Using the approach discussed in Lee (2009), we construct new bounds by trimming the outcome distribution under the worst-case scenario. The proposed spillover bounds are designed to account for the possible misspecification of the exposure mapping in the spirit of Leung (2022). Essentially, researchers do not need to know precisely how the treatment is transmitted through the network, as long as interference levels decline with network distance. Similar assumptions are imposed on the selection mechanism. Monte Carlo simulations show that the proposed estimator performs well in finite samples and is robust to misspecification of both the outcome and selection models.

The estimator uses a weighted least squares approach, leveraging the propensity score of the exposure mapping, which is numerically equivalent to the Hajek-based representation (Aronow and Samii, 2017). This approach allows for easy incorporation of covariates, improving precision in the outcome equation (Gao and Ding, 2023). The design also accommodates covariates in the selection equation, extracting information that can tighten the bounds. It supports the inclusion of regularized high-dimensional semiparametric estimators and flexible nonlinear methods to predict the probability of always being observed and conditional quantiles of the outcome. To avoid overfitting bias, it employs Neyman orthogonal moment conditions derived from the weighted least squares form and cross-fitting (Chernozhukov et al., 2018). A Python package, `spillover-effects`, implementing this method with post-lasso and automatic machine learning options is available for general use.

Understanding how to identify and estimate treatment effects under nonrandom sample selection has progressed significantly. Seminal work by Heckman (1974) addressed the classical sample selection problem where point-identification relies on functional form and valid instruments. Chernozhukov et al. (2023) examined a semiparametric generalization of the Heckman selection model

using distribution regressions and [Bia et al. \(2024\)](#) controlled for potentially high-dimensional covariates using double machine learning. These flexible frameworks allow for patterns of heterogeneity and separates from normality on the error structure but still requires exclusion restrictions or selection-on-observables. Seminal work on partial identification due to sample selection was introduced by [Horowitz and Manski \(1998\)](#). [Zhang and Rubin \(2003\)](#) and [Lee \(2009\)](#) proposed worst-case scenario bounds of the average treatment effect among individuals that always select into the sample (always-observed). The primary assumption, called monotonicity, restricts the treatment from inducing selection in some individuals, while simultaneously preventing others from being selected. Under this assumption, [Huber and Mellace \(2015\)](#) also derived sharp bounds for the compliers, defiers, and observed population.

More recently, [Semenova \(2023\)](#) expanded the Lee bounds by introducing conditional monotonicity to address diverse responses in selection. Leveraging regularization techniques, Semenova enables the incorporation of potentially high-dimensional covariates, thereby tightening the bounds on the causal parameter. Similarly, [Samii et al. \(2023\)](#) used generalized random forests to narrow nonparametric bounds on treatment effects. On the other hand, [Heiler \(2023\)](#) focused on establishing bounds for heterogeneous causal effects for always-observed individuals. For continuous treatments, [Lee \(2024\)](#) established a sufficient monotonicity condition to bound the effect of treatment intensity. [Olma \(2021\)](#) analyzed, more generally, how to estimate truncated outcomes treating the conditional quantile function as a nuisance parameter. [Bartalotti et al. \(2023\)](#) instead studied identification of marginal treatment effects when there is sample selection.

The literature considering the identification and estimation of spillover effects has focused on estimating spillovers that are robust to exposure mapping misspecification. [Leung \(2022\)](#), [Savje \(2023\)](#), and [Aronow and Samii \(2017\)](#) study identification and estimation of effects from an exposure mapping similar to the effective treatment definition of [Manski \(2013\)](#). [Hoshino and Yanagi \(2021\)](#) extend Leung’s framework to incorporate non-compliance and interference, while [Gao and Ding \(2023\)](#) explore Leung’s framework with covariate adjustment. However, none of the existing spillover effect estimators can handle scenarios involving endogenous sample selection. This paper contributes to the literature by introducing the first approach to partially identify and estimate network effects under nonrandom sample selection.

We apply the method using data from [Beuermann et al. \(2015\)](#) to demonstrate its effectiveness. They implemented a randomized controlled trial that provided laptops to students and analyzed the effects on computer utilization and other educational outcomes. When analyzing the intensive margin effect of the program, the selected sample of interest is students with a positive number of minutes of computer use. The previous analysis of the intervention suggests an increase in computer utilization at the intensive margin when students are directly treated, but no evidence of spillovers. The estimated spillover bounds instead show evidence of positive direct and spillover effects. Across different specifications, we consistently find positive direct effects among students with friends who won the lottery. In addition, the spillover bounds and their confidence intervals show positive effects of the intervention. Particularly, having also a friend who won the laptop

lottery increases computer use by 24 to 33 percent, using post-lasso.

In addition to the main contribution of introducing an estimator for bounding spillover effects with nonrandom selected samples, this paper contributes to the literature in two additional ways. First, the proposed estimator offers an alternative design-based inference for the popular Lee bounds under the assumption of no interference. Second, the proposed spillover bounds provide a framework for extending the Lee bounds to accommodate multiple treatments. The monotonicity assumption employed in this paper is related to the recent literature of instrumental variables with multiple instruments (Mogstad et al., 2021; Goff, 2023; Hoff et al., 2023).

The subsequent sections are structured as follows. Section 2 sets the groundwork for defining the estimand of interest. Section 3 outlines the assumptions under which the estimand becomes partially identified. Section 4 details the estimation and inference procedures. Section 5 shows numerical results from Monte Carlo experiments while Section 6 demonstrates the application of our method to a field experiment. Section 7 concludes and discusses the implications of our findings.

## 2 Spillover Effects

In this section, we define spillover effects within a finite population model where the treatment vector is the sole stochastic component. The model considers nonrandom sample selection and network interference, incorporating exposure mappings to reduce the dimensionality of treatments and the network into a vector, which is crucial for specifying potential outcomes. The framework allows for potential misspecification of this exposure mapping, so potential outcomes do not necessarily align with their respective exposure representations. Additionally, the framework accommodates sample selection with network interference, defining expected potential selection when the sample selection mechanism is specified correctly or incorrectly.

The core estimand of interest is the average spillover effect for subjects selected into the sample irrespective of treatment exposure. We introduce a sample selection model with network interference that extends Heckman’s model, incorporating social interactions in both the outcome and selection equations. This model of peer effects captures how individuals’ outcomes and self-selections are influenced by their network connections. This model is used to analyze the implications of the assumptions and to identify the proportion of individuals selected into the sample regardless of treatment exposure. This analysis provides the foundation for deriving sharp bounds for the spillover estimand.

### 2.1 Setup

Consider a finite population model where  $D$  is the realized treatment vector and the only stochastic component. Let  $d = (d_i)_{i=1}^n \in \{0, 1\}^n$  be the potential treatment vector and  $Y_i(d)$  the potential outcome which is a mapping from  $\{0, 1\}^n$  to  $\mathbb{R}$ . To model the presence of spillover effects under nonrandom sample selection, let  $S_i(d)$  be a sample selection indicator that depends on the potential treatment vector and takes value 1 if unit  $i$  is selected into the sample and 0 otherwise. We

denote the realization of the selection indicator and the outcome for individual  $i$  as  $S_i = S_i(D)$  and  $Y_i = Y_i(D)$ , respectively. As an example, [Chen and Roth \(2023\)](#) define sample selection as  $S_i = \mathbf{1}\{Y_i > 0\}$  when analyzing the intensive margin of a treatment.

There is a single network represented by an adjacency matrix  $\mathbf{A}$  with entry  $A_{ij} = 1$  if  $i$  and  $j$  are connected and 0 otherwise. If there are no strategic interactions with respect to the realized treatment vector  $D$ , the network, the potential outcomes, and the potential selection functions are fixed in the finite population framework. Following the network interference literature ([Aronow and Samii, 2017](#); [Manski, 2013](#)), define an exposure mapping  $T(\cdot)$  that maps network and treatments into a low-dimensional vector. The following empirical examples illustrate two specific ways to define an exposure mapping.

**Example 1.** *Effect of savings programs on asset ownership.* [Brune et al. \(2021\)](#) study the effect of a deferred wages savings scheme on downstream outcomes like asset ownership. They define the exposure mapping as  $T_i = (D_i, \sum A_{ij}D_j)$ , which contains the treatment status of worker  $i$  and the number of treated coworkers.

**Example 2.** *Effect of input subsidies on agricultural productivity.* [Carter et al. \(2021\)](#) study the effect of input subsidy programs on maize yields. They define the exposure mapping as  $T_i = (D_i, \mathbf{1}\{\sum A_{ij}D_j > \text{med}(\mathbf{A}D)\})$ , which contains the treatment status of farmer  $i$  and an indicator for when the total treated network contacts of farmer  $i$  is greater than the median of total treated network contacts for all farmers ( $\text{med}(\mathbf{A}D)$ ).

The definitions of exposure mapping in the two examples above take the  $n \times 1$  vector of potential treatments and the  $n \times n$  adjacency matrix representing the network into a two-dimensional exposure vector. Correct specification of the exposure mapping requires that  $Y_i(d) = \tilde{Y}_i(t)$  for  $t \in \mathcal{T}$ , where  $\tilde{Y}_i(t)$  maps the low-dimensional exposure to potential outcomes and  $\mathcal{T}$  represents the range of  $T_i$ . Following [Leung \(2022\)](#) and [Savje \(2023\)](#), we use a more robust definition of exposure that captures misspecification. In general, the expected potential outcome from exposure  $t$  is

$$\bar{Y}_i(t) = \sum_{d \in \{0,1\}^n} Y_i(d) \Pr(D = d | T_i = t).$$

This framework also allows for spillovers in the sample selection mechanism. We then define analogs for the expected potential selection  $\bar{S}_i(t)$  when the sample selection mechanism is misspecified and  $\tilde{S}_i(t)$  when properly specified. When the expected potential selection  $\bar{S}_i$  does not depend on the exposure mapping  $T_i$ , the outcomes are missing at random. The estimand of interest is the average spillover effect for subjects who are selected into the sample regardless of treatment *exposure*

$$\tau(t, t') = E[\bar{Y}_i(t) - \bar{Y}_i(t') | \bar{S}_i(t) = 1, \bar{S}_i(t') = 1]. \quad (1)$$

The average spillover effect for the *always-observed* group generalizes the estimand of interest discussed by [Zhang and Rubin \(2003\)](#) and [Lee \(2009\)](#) for any exposure mapping  $T_i$ . When the exposure mapping is correctly specified as the direct treatment effect  $T_i = D_i$  with exposures  $t = 1, t' = 0$ ; then  $\tau(t, t')$  reduces to the average treatment effect for always-observed individuals.

Furthermore, equation (1) can be interpreted as a generalization of the previous estimand to multiple treatments. Before discussing identification of  $\tau(t, t')$ , we introduce a model of sample selection with homogeneous treatment effects in the presence of network interference.

## 2.2 A Sample Selection Model with Network Interference

We provide an explicit model that determines sample selection when individuals interact with each other through a network. Partial identification of the spillover estimand  $\tau(t, t')$  does not require a model of sample selection, but this model serves to illustrate the assumptions that are needed. We extend Heckman’s conventional model of sample selection (Heckman, 1974, 1979) to account for social interactions on the outcome and selection equations. The model is as follows:

$$\begin{aligned} Y_i^* &= \alpha_1 + \beta_1 \frac{\sum_{j=1}^n A_{ij} Y_j^*}{\sum_{j=1}^n A_{ij}} + \gamma_1 D_i + U_i, \\ S_i^* &= \alpha_2 + \beta_2 \frac{\sum_{j=1}^n A_{ij} S_j^*}{\sum_{j=1}^n A_{ij}} + \gamma_2 D_i + V_i, \\ Y_i &= \mathbf{1}\{S_i^* > 0\} \cdot Y_i^*, \end{aligned}$$

where  $Y_i^*$  and  $S_i^*$  are latent variables for the outcome and the propensity to be selected,  $D_i$  is the realized treatment,  $X_i$  is a vector of covariates, and  $U_i$  and  $V_i$  are error terms. Due to the censored selection process, only outcomes  $Y_i$  are observed.

This particular model of sample selection features a linear-in-means specification<sup>1</sup>, which is very common in the literature of peer effects (Boucher et al., 2024). As an example, let outcomes represent wages, treatment refers to participation on a job training program, selection denotes employment status, and the network describes friendships. This model expresses individual wages as a function of the average wages of her friends and her own participation in the program (Cornelissen et al., 2017). The difference with the traditional Heckman model is that SUTVA does not hold since outcomes and selection feature network dependence. This is clear from the reduced form of the linear-in-means sample selection model:

$$\begin{aligned} \mathbf{Y}^* &= \frac{\alpha_1}{1 - \beta_1} \boldsymbol{\iota} + \gamma_1 \mathbf{D} + \gamma_1 \beta_1 \sum_{k=0}^{\infty} \beta_1^k \bar{\mathbf{A}}^{k+1} \mathbf{D} + \sum_{k=0}^{\infty} \beta_1^k \bar{\mathbf{A}}^k \mathbf{U}, \\ \mathbf{S}^* &= \frac{\alpha_2}{1 - \beta_2} \boldsymbol{\iota} + \gamma_2 \mathbf{D} + \gamma_2 \beta_2 \sum_{k=0}^{\infty} \beta_2^k \bar{\mathbf{A}}^{k+1} \mathbf{D} + \sum_{k=0}^{\infty} \beta_2^k \bar{\mathbf{A}}^k \mathbf{V}. \end{aligned}$$

The reduced form representation uses the row-normalized adjacency matrix  $\bar{\mathbf{A}}$  where each entry is divided by the total sum of its row. To ensure that the model has a unique solution, assume

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<sup>1</sup>This specification only features endogenous peer effects, as is commonly referred in the literature to the effect that outcome of individual  $j$  has on  $i$ , denoted by  $\beta_1$  and  $\beta_2$ . An extension with exogenous peer effects, stemming from  $\mathbf{D}$  and observed characteristics  $\mathbf{X}$ , is also possible with additional notation. An important challenge on estimating  $\beta_2$  in this linear-in-means sample selection model is that the selection equation presents multiple equilibria problems (Brock and Durlauf, 2001; Tamer, 2003; Boucher and Bramoullé, 2020).

that  $\mathbf{Y}^*$  and  $\mathbf{S}^*$  are continuously distributed and that the coefficients  $\beta_1$  and  $\beta_2$  are restricted to be less than one in absolute value. This representation shows that the latent outcomes and selection propensities depend not only of direct treatment status, but also on the treatment of others weighted by the endogenous peer effects  $\beta_1^k$  and  $\beta_2^k$  (Bramoullé et al., 2009). Powers of the adjacency matrix  $\bar{\mathbf{A}}$  represent the number of connections away from individual  $i$  that affect her outcomes and self-selection decision. In the example, wages and selection depend on friends, under  $\bar{\mathbf{A}}$ , and on indirect friendships through  $\bar{\mathbf{A}}^k$  with  $k > 1$ . However, this indirect effects are down-weighted since peer effects are  $|\beta| < 1$ .

In the next section, we restrict the selection equation to be correctly specified using the potential outcomes model framework. This restriction is fundamental to identify the proportion of individuals that are selected into the sample regardless of treatment exposure. Here, we analyze the implications of this assumption using the linear-in-means sample selection model. To simplify notation, assume that the dependence on treatment exposure vanishes after  $k = 0$  for both outcomes and selection. In addition, only the outcome equation features correlated effects, i.e.,  $\text{corr}(U_i, U_j) \neq 0$ . This leads to

$$Y_i^* = \frac{\alpha_1}{1 - \beta_1} + \gamma_1 D_i + \gamma_1 \beta_1 \sum_{j=1}^n \bar{A}_{ij} D_j + U_i + \beta_1 \sum_{j=1}^n \bar{A}_{ij} U_j,$$

$$S_i^* = \frac{\alpha_2}{1 - \beta_2} + \gamma_2 D_i + \gamma_2 \beta_2 \sum_{j=1}^n \bar{A}_{ij} D_j + V_i.$$

Under this simplified version of the model, without loss of generality, let the exposure mapping be  $T_i = (D_i, \mathbf{1}\{\sum \bar{A}_{ij} D_j > 0\})$  and  $t = (0, 1), t' = (0, 0)$ . The observed means of the latent outcome under each exposure are

$$E[Y_i^* | \mathbf{A}, T_i = t, S_i^* \geq 0] = \frac{\alpha_1}{1 - \beta_1} + \gamma_1 \beta_1 + E\left[U_i | \mathbf{A}, T_i = t, V_i \geq -\frac{\alpha_2}{1 - \beta_2} - \gamma_2 \beta_2\right]$$

$$+ \beta_1 \sum_{j=1}^n \bar{A}_{ij} E\left[U_j | \mathbf{A}, T_i = t, V_i \geq -\frac{\alpha_2}{1 - \beta_2} - \gamma_2 \beta_2\right],$$

$$E[Y_i^* | \mathbf{A}, T_i = t', S_i^* \geq 0] = \frac{\alpha_1}{1 - \beta_1} + E\left[U_i | \mathbf{A}, T_i = t', V_i \geq -\frac{\alpha_2}{1 - \beta_2}\right]$$

$$+ \beta_1 \sum_{j=1}^n \bar{A}_{ij} E\left[U_j | \mathbf{A}, T_i = t', V_i \geq -\frac{\alpha_2}{1 - \beta_2}\right].$$

This representation characterizes the bounds over treatment effects when SUTVA does not hold. When there is no interference in the selection and outcome equation ( $\beta_1 = \beta_2 = 0$ ), the means reduce to the conventional case where Lee bounds can be used. Furthermore, we can recover the spillover effect, which in this case is  $\gamma_1 \beta_1$ , by disentangling the proportion of inframarginal individuals ( $V_i \geq -\frac{\alpha_2}{1 - \beta_2}$ ) and marginal ones ( $-\frac{\alpha_2}{1 - \beta_2} - \gamma_2 \beta_2 \leq V_i < -\frac{\alpha_2}{1 - \beta_2}$ ). Under the approach of Zhang and Rubin (2003) and Lee (2009), trimming the outcome using the proportion  $p = \frac{\Pr(S_i^* \geq 0 | T_i = t')}{\Pr(S_i^* \geq 0 | T_i = t)}$  results in worst-case scenario bounds.

The main restriction that we impose on the sample selection model is that we can correctly predict when  $S_i^* \geq 0$  for all  $i$ . For instance, with our previous model, even on the presence of correlated effects on the selection equation (adding  $\beta_2 \sum_{j=1}^n \bar{A}_{ij} V_j$ ), we assume that we can still identify the proportion of inframarginal and marginal individuals. Incorrectly assuming that exposure does not vanish when  $k = 1$ , adds the term  $\gamma_2 \beta_2^2 \sum_{j=1}^n \bar{A}_{ij}^2 D_j$  to the selection equation. The elements  $\bar{A}_{ij}^2$  denote a weighted sum of all the paths of length two between  $i$  and  $j$ . If the chosen exposure mapping  $T_i$  does not capture this effect, and  $\gamma_2 \beta_2^2$  is strong enough to induce individuals to be selected into the sample, then the trimming proportion  $p$  will not be correctly identified.

Under the linear-in-means sample selection model, situations where the peer effects on the selection equation are small provide ideal conditions to correctly identify the proportion of marginal individuals. In these situations, these can be guaranteed even when the exposure mapping is misspecified. Additionally, a weak network dependence assumption where interference decays with distance can formalize this condition. In the next section, we provide a formal definition of the necessary assumptions to obtain sharp bounds for the spillover estimand in equation (1).

### 3 Partial Identification

In this section, we provide a formal definition of the necessary assumptions to obtain sharp bounds for the spillover estimand in equation (1). The method relies on an “exposure monotonicity” condition, which helps to define how exposure to treatment influences whether individuals are included in the sample. By trimming the outcomes based on worst-case scenarios, we can construct what are known as “spillover bounds.” When introducing covariates, a weaker version of this monotonicity assumption can be used to tighten the bounds. The following subsections discuss the assumptions and partial identification of the estimand for the case with and without covariates.

#### 3.1 Spillover Bounds

In general, unless the researcher is willing to impose strong assumptions on the sample selection mechanism, spillover effects are partially identified. This section discusses how to bound spillover effects using an exposure monotonicity condition. The *spillover bounds* are constructed using Lee’s approach to trim the outcome distribution under the worst-case scenario. Given the finite population model, random assignment of treatment guarantees that  $Y_i(d)$  and  $S_i(d)$  are independent of  $D_i$ . In addition, since the network is fixed, independence of  $\mathbf{A}$  and  $D_i$  rules out potential strategic interactions occurring because of the treatment assignment.

**Assumption 3.1** (Correct Specification).  $\tilde{S}_i(t) = \bar{S}_i(t)$

Assumption 3.1 is necessary to pin down the monotonicity of selection due to exposure. In practice, the exposure mapping selected by the researcher must provide enough information of the sample selection mechanism. That is, we can properly predict when individual  $i$  selects into the

sample even if the chosen exposure mapping is misspecified. In our sample selection model with network interference, this implies that the exposure mapping  $T_i$  correctly determines when  $S_i = 1$ <sup>2</sup>. Therefore, having a proper specification of the sample selection mechanism guarantees that this situation holds.

**Assumption 3.2** (Exposure Monotonicity).  $\bar{S}_i(t) \geq \bar{S}_i(t')$  for  $t \geq t'$  in the vector sense

This monotonicity condition generalizes Lee’s monotonicity for any exposure mapping. Similarly, exposure monotonicity implies that treatment exposure can only affect sample selection in “one direction”. Since the treatment exposure can be direct or social, inconsistencies of this exposure monotonicity can arise depending on the exposure of interest. Mogstad et al. (2021) and Goff (2023) discuss the implications of monotonicity with multiple instruments in the context of instrumental variables. Even though in this context monotonicity refers to how treatment affects sample selection, a “multiple treatment” analog can be argued in this situation. Hence, exposure monotonicity relates to the actual monotonicity assumption in Mogstad et al. (2021) and the vector monotonicity described by Goff (2023).

As an example, consider the two-dimensional exposure mapping  $T_i = (D_i, \mathbf{1}\{\sum A_{ij}D_j > 0\})$ , where the first element refers to the direct treatment and the second whether at least one connection received treatment. Under this exposure mapping, the monotonicity assumption implies that being exposed to the treatment either directly or indirectly (through a connection) weakly increases the likelihood of being selected into the sample. Under the previous assumptions, the following proposition shows how to construct the bounds for the spillovers estimand in equation (1).

**Proposition 1** (Spillover Bounds). *Under assumptions 3.1 and 3.2,  $\tau_0^L$  and  $\tau_0^U$  are sharp lower and upper bounds for the average spillover effect  $\tau(t, t')$ , where*

$$\begin{aligned} \tau_0^L &= E[Y_i | Y_i \leq q_{p_0}, T_i = t, S_i = 1] - E[Y_i | T_i = t', S_i = 1] \\ \tau_0^U &= E[Y_i | Y_i \geq q_{1-p_0}, T_i = t, S_i = 1] - E[Y_i | T_i = t', S_i = 1] \\ p_0 &= \frac{\Pr(S_i = 1 | T_i = t')}{\Pr(S_i = 1 | T_i = t)} \\ q_u &\text{ is the } u\text{-quantile of } Y \text{ given } T = t, S = 1 \end{aligned}$$

Proposition 1 generalizes Lee bounds where  $p_0$  is the proportion of individuals that are always selected regardless of treatment exposure. The proof in Appendix A shows that spillover effects  $\mu(t') = E[Y_i | T_i = t', S_i = 1]$  from the control group are point-identified (when  $p_0 > 0$ ). On the other hand, the spillover effects  $\mu(t)$  from the treated group are bounded by the worst case scenarios  $\mu^*(t) \in \{\mu^L, \mu^U\}$ . Under exposure monotonicity, the lowest value the spillover effects can take is when the proportion  $p_0$  of individuals with the highest  $Y$  are all compliers. Therefore, trimming  $\mu^*(t)$  from above at the  $p_0$  quantile obtains the worst-case of the lower bound. Likewise, the highest value is determined by trimming the  $1 - p_0$  quantile from below. Moreover, we can

<sup>2</sup>Alternatively, we can impose restrictions on the sample selection using a model of approximate network interference as in Leung (2022). The idea is that interference decreases with distance and can be bounded.

modify the assumption that every individual has the same probability of being selected relaxing the monotonicity condition with covariates.

### 3.2 Bounds with Covariates

Covariates can play an important role to tighten the bounds. If covariates explain individual's likelihood to be observed or their choices to engage in the outcome, incorporating them can tighten the bounds or even achieve almost point-identification. To create moment conditions that incorporate covariates, we rely on a weaker formulation of assumption 3.2. Define the network controls  $X_i = h(i, W, \mathbf{A})$  as a mapping of the potentially high-dimensional covariates  $W$  and network  $\mathbf{A}$ . Also define the conditional probability to be selected into the sample when treated as  $s(t, x) = \Pr(S_i = 1 \mid T_i = t, X_i = x)$  and the conditional share of selected individuals between the two exposure groups as  $p_0(x) = s(t', x)/s(t, x)$ .

**Assumption 3.3** (Conditional Exposure Monotonicity). *For the covariate set  $\mathcal{X} = \mathcal{X}_+ \cup \mathcal{X}_-$  and any  $t \geq t'$  in the vector sense. When  $X \in \mathcal{X}_+$ ,  $\bar{S}_i(t) \geq \bar{S}_i(t')$ . And if  $X \in \mathcal{X}_-$ ,  $\bar{S}_i(t) \leq \bar{S}_i(t')$ .*

Under assumption 3.3, we can partition the set of network controls on individuals that are induced by the treatment into be selected  $\mathcal{X}_+ := \{x : s(t, x) > s(t', x)\}$  and that are discouraged into be selected when treated  $\mathcal{X}_- := \{x : s(t, x) < s(t', x)\}$ . This conditional exposure monotonicity generalizes the weak monotonicity by Heiler (2023) and conditional monotonicity by Semenova (2023)<sup>3</sup> for general exposure mappings  $T_i$ .

Given the partition of the covariates, define the conditional  $u$ -quantiles of  $Y$  as  $q(u, x) = \inf \{q : u \leq P(Y_i \leq q \mid T_i = t, S_i = 1, X_i = x)\}$  and the nuisance parameters  $\eta_0(x) = \{s(t, x), s(t', x), q(u, x)\}$ . Semenova (2023) shows how to represent the lower and upper bound of Equation (1) using a semiparametric moment function. Under Assumption 3.3, the lower bound of Proposition 1 is

$$\begin{aligned} \tau_0^L &= \frac{E[\mathbf{1}\{p_0(X) \leq 1\} \cdot m_+^L(\eta_0) + \mathbf{1}\{p_0(X) > 1\} \cdot m_-^L(\eta_0)]}{E[\min(s(t', X), s(t, X))]}, \\ m_+^L(\eta) &= \frac{\mathbf{1}_i\{t\}}{\pi_i(t)} \cdot S_i \cdot Y_i \cdot \mathbf{1}\{Y_i \leq q(p(X), t, X)\} - \frac{\mathbf{1}_i\{t'\}}{\pi_i(t')} \cdot S_i \cdot Y_i, \\ m_-^L(\eta) &= \frac{\mathbf{1}_i\{t\}}{\pi_i(t)} \cdot S_i \cdot Y_i - \frac{\mathbf{1}_i\{t'\}}{\pi_i(t')} \cdot S_i \cdot Y_i \cdot \mathbf{1}\{Y_i \geq q(1 - 1/p(X), t', X)\}, \end{aligned}$$

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<sup>3</sup>We do not consider the case where there are individuals that are indifferent to be selected with either exposure  $\mathcal{X}_0 := \{x : s(t, x) = s(t', x)\}$ . This rules out the case where treatment exposure does not affect selection since this leads to point-identification. However, Semenova (2023) accounts for this in the identification results.

and the upper bound is

$$\begin{aligned}\tau_0^U &= \frac{E[\mathbf{1}\{p_0(X) \leq 1\} \cdot m_+^U(\eta_0) + \mathbf{1}\{p_0(X) > 1\} \cdot m_-^U(\eta_0)]}{E[\min(s(t', X), s(t, X))]}, \\ m_+^U(\eta) &= \frac{\mathbf{1}_i\{t\}}{\pi_i(t)} \cdot S_i \cdot Y_i \cdot \mathbf{1}\{Y_i \geq q(1 - p(X), t, X)\} - \frac{\mathbf{1}_i\{t'\}}{\pi_i(t')} \cdot S_i \cdot Y_i, \\ m_-^U(\eta) &= \frac{\mathbf{1}_i\{t\}}{\pi_i(t)} \cdot S_i \cdot Y_i - \frac{\mathbf{1}_i\{t'\}}{\pi_i(t')} \cdot S_i \cdot Y_i \cdot \mathbf{1}\{Y_i \leq q(1/p(X), t', X)\}.\end{aligned}$$

The bounds  $[\tau_0^L, \tau_0^U]$  are sharp bounds for the average spillover effect of the group that is always observed. They differ from Semenova's in that they incorporate the generalized propensity score  $\pi_i(t)$ , and the general vectors  $\{t, t'\}$  can also represent multiple treatments.

These bounds do not involve the covariate density function  $f_X(x \mid \bar{S}(t) = \bar{S}(t') = 1)$  and as long as we can accurately predict the nuisance parameter  $\eta(x)$ , the bounds will be tighter. This is related to our discussion on misspecification of the sample selection mechanism. A precise prediction of  $\eta(x)$  correctly determines where  $p_0(x)$  lies, and consequently which individual outcomes to trim. Even if every individual belongs to the group that is encouraged ( $\mathcal{X}_+$ ) or discouraged ( $\mathcal{X}_-$ ), using a flexible semiparametric estimation of the trimming quantile can potentially help tighten the bounds. Section 4 indicates how to estimate the bounds and conduct inference to account for the network dependence of the potential outcomes.

## 4 Estimation and Inference

This section constructs a Hajek-based estimator for the bounds described in proposition 1. The estimator is based on weighted least squares (WLS) and takes advantage of the generalized propensity score. First, we describe the estimation procedure that resembles Lee bounds using WLS. When the weighting matrix of the WLS contains the inverse of the propensity scores, this is numerically equivalent to the Hajek estimator. Then, the estimation procedure is extended to cover multiple treatments and covariate adjustment. If covariates are included, the procedure is divided in two stages to allow for flexible estimation of nuisance parameters. Finally, we show asymptotic results of the estimators accounting for network dependence.

### 4.1 Estimation

The Hajek representation is motivated by Gao and Ding (2023) who show that Hajek estimators have an inherent connection to the weighted least square (WLS) formulation. There are two advantages to using this representation: (1) Hajek estimators ensure location invariance of the outcome and has been shown to be more stable and efficient; and (2) the WLS formulation allows to cast the estimator into a generalized methods of moments (GMM) framework, which is useful for inference.<sup>4</sup>

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<sup>4</sup>Using a Horvitz-Thompson representation is also possible and Semenova (2023) uses a similar formulation when introducing high-dimensional covariates. Appendix A shows the equivalent estimators using this representation.

The Hajek-based estimators for the upper and lower bound feature the generalized propensity scores including the possibility of sample selection (Imbens, 2000). The bounds  $\hat{\tau}^L$  and  $\hat{\tau}^U$ , trimming proportion  $\hat{p}$ , and quantile  $\hat{y}_u$  are:

$$\begin{aligned}\hat{\tau}^L &= \mathbf{G} \left[ \mathbf{Z}_L^\top \mathbf{W} \mathbf{Z}_L \right]^{-1} \mathbf{Z}_L^\top \mathbf{W} \mathbf{Y} \\ \hat{\tau}^U &= \mathbf{G} \left[ \mathbf{Z}_U^\top \mathbf{W} \mathbf{Z}_U \right]^{-1} \mathbf{Z}_U^\top \mathbf{W} \mathbf{Y} \\ \hat{p} &= \frac{\sum w_i(t') \cdot S_i}{\sum w_i(t')} \bigg/ \frac{\sum w_i(t) \cdot S_i}{\sum w_i(t)} \\ \hat{q}_u &= \min \left\{ q : \frac{\sum w_i(t) \cdot S_i \cdot \mathbf{1}\{Y_i \leq q\}}{\sum w_i(t) \cdot S_i} \geq u \right\}\end{aligned}\tag{2}$$

where  $\mathbf{Z}_L$  and  $\mathbf{Z}_U$  are  $n \times 2$  matrices with rows  $Z_{L,i} = [\mathbf{1}_i\{t\} \mathbf{1}\{Y_i \leq \hat{q}_{\hat{p}}\}, \mathbf{1}_i\{t'\}]$  and  $Z_{U,i} = [\mathbf{1}_i\{t\} \mathbf{1}\{Y_i \geq \hat{q}_{1-\hat{p}}\}, \mathbf{1}_i\{t'\}]$ , respectively.  $\mathbf{W}$  is a diagonal matrix with elements  $w_i = \frac{1}{\pi_i(T_i)}$ .  $\mathbf{G} \equiv [1 \ -1]$  is a row vector and  $\mathbf{Y}$  is the vector of observed outcomes  $Y_i S_i$ . The propensity score is defined as  $\pi_i(t) = \Pr(\mathbf{1}_i\{t\})$  under the randomization protocol, the treatment indicator  $\mathbf{1}_i\{t\} = \mathbf{1}\{T_i = t\}$ , and the weights  $w_i(t) = \frac{\mathbf{1}_i\{t\}}{\pi_i(t)}$ .

The estimation of  $[\hat{\tau}^L, \hat{\tau}^U]$  resembles the procedure to calculate the Lee bounds. First, calculate the proportion  $\hat{p}$  using the generalized propensity score. Second, obtain the quantiles  $\hat{q}_{\hat{p}}$  and  $\hat{q}_{1-\hat{p}}$  from the distribution of  $Y$ . Last, calculate the worst-case scenario bounds  $[\hat{\tau}^L, \hat{\tau}^U]$  using weighted least squares. Unlike conventional Lee bounds, the dependence of individuals' outcomes changes how to conduct inference, which is discussed in Subsection 4.4.

## 4.2 Multiple Treatment

The spillover bounds can be extended to cases with multiple treatments, which is useful when the researcher wants to account for both direct and spillover effects. With multiple treatments, the exposure mapping is defined as  $T_i = (D_i, \mathbf{1}\{\sum A_{ij} D_j > 0\})$ , allowing for four possible values: individuals who are directly treated and have at least one treated friend (1, 1), individuals who are neither directly treated nor have treated friends (0, 0), individuals who are only directly treated (1, 0), and individuals who only have a treated friend (0, 1).

To accommodate multiple treatments under the mapping  $T_i = (D_i, \mathbf{1}\{\sum A_{ij} D_j > 0\})$ , we adjust equation (2). The treatment indicator  $\mathbf{1}_i\{t\}$  can be modified to the vector  $[\mathbf{1}_i\{(1, 1)\}, \mathbf{1}_i\{(0, 1)\}]$  for the treated group, and  $[\mathbf{1}_i\{(1, 0)\}, \mathbf{1}_i\{(0, 0)\}]$  for the control group. The row vector  $\mathbf{G}$  becomes  $\frac{1}{2}[1, 1, -1, -1]$  to contrast exposure effects due to spillovers. However, this contrast of exposures is not allowed under Assumption 3.2 because while it is possible to assume  $\bar{S}_i(1, 1) \geq \bar{S}_i(1, 0)$  and  $\bar{S}_i(1, 1) \geq \bar{S}_i(0, 0)$ , the assumption  $\bar{S}_i(1, 0) \geq \bar{S}_i(0, 1)$  is not defined.

A valid estimand for the overall effects, using the exposure mapping  $T_i = (D_i, \mathbf{1}\{\sum A_{ij} D_j > 0\})$ , can be defined as follows. The group exposed to treatment is represented by the three-dimensional treatment indicator  $[\mathbf{1}_i\{(1, 1)\}, \mathbf{1}_i\{(1, 0)\}, \mathbf{1}_i\{(0, 1)\}]$ . The control group is represented by  $\mathbf{1}_i\{(0, 0)\}$ , which includes individuals who are neither directly treated nor have any treated connections. By

using the row vector  $\mathbf{G} \equiv [\frac{1}{3}, \frac{1}{3}, \frac{1}{3}, -1]$ , this estimand captures the effects of any type of exposure, whether direct or social, to the treatment.

### 4.3 Covariate Adjustment

Estimating the bounds with covariate adjustment involves first estimating a vector of nuisance parameters  $\hat{\eta}$ , which includes selection probabilities and conditional quantiles. The estimation process is divided into two stages. In the first stage, selection probabilities and outcome quantiles are obtained using semiparametric estimation, regularization, or non-parametric methods with cross-fitting and cross-validation. In the second stage, the semiparametric moment functions are estimated and sorted. When using regularized first-stage estimators, orthogonalization of the moment conditions is necessary.

#### 4.3.1 First Stage

We focus on post-lasso methods to explain the first stage, although any semiparametric or machine learning estimation method can be employed. The first step is to estimate the probability of being selected into the sample  $s_0(t, x)$  and the trimming threshold  $p_0(x)$ . We utilize  $\ell_1$ -penalized logistic regression. The logistic function for selection is

$$s(t, x) = \Lambda(x' \alpha_s) + r_s(x) \quad \text{for } t \in \mathcal{T},$$

where  $\Lambda(\cdot)$  is the logistic CDF,  $\alpha_s$  is the parameter vector, and  $r_s(x)$  represents approximation error. To estimate  $\alpha_s$ , we maximize the penalized log-likelihood function using the optimal penalty parameter  $\lambda_s$  proposed by Belloni et al. (2017), Equation (6.5), or through cross-validation. The selection probabilities are then  $\hat{s}(t, x) = \Lambda(x' \hat{\alpha}_s)$  for  $t \in \mathcal{T}$ , and the trimming threshold is  $\hat{p}(x) = \hat{s}(t', x) / \hat{s}(t, x)$ . If  $\hat{p}_i(x) < 1$ , individual  $i$  belongs to the group  $\mathcal{X}_+$  because they are induced to be selected when exposed to the treatment. Conversely, if  $\hat{p}_i(x) > 1$ , the individual is discouraged from participating when exposed to the treatment and belongs to group  $\mathcal{X}_-$ . Flexible machine learning methods, such as tree-based methods, can also be used to obtain high-quality estimates of the nuisance functions.

The  $u$ -th conditional quantile can be approximated as

$$q(u, t, x) = x' \alpha_q(u) + r_q(u, x) \quad \text{for } t \in \mathcal{T},$$

where  $\alpha_q(u)$  is the parameter vector for the  $u$ -th quantile, and  $r_q(u, x)$  represents approximation error. We minimize the penalized loss function with the penalty parameter  $\lambda_q$  according to Belloni and Chernozhukov (2013) or through cross-validation. The  $u$ -th quantile is then estimated as  $\hat{q}(u, x) = x' \hat{\alpha}_q$ . Although we emphasize  $\ell_1$ -penalized logistic and quantile regression, any machine learning method can be used. Alternative quantile prediction methods include random forest quantile regressions and gradient boosting quantile regressions. The theoretical results hold under the

respective convergence rates.

Assumption 3.1 highlights an important aspect of this step. The correct specification of spillovers in the selection mechanism ensures that individuals can be accurately classified into the groups  $\mathcal{X}_+$  and  $\mathcal{X}_-$ . Semenova (2023) discusses similar misclassification issues when predicting  $s_0(t, x)$  and  $s_0(t', x)$ . She suggests that a sufficient condition is to have the support of  $p_0(x)$  bounded away from both zero and one. Future research should consider the impact of misspecification of the exposure mapping on the selection mechanism.

### 4.3.2 Second Stage

Neyman orthogonality and cross-fitting provide high-quality estimation and inference in settings requiring regularized estimators. Semenova (2023) provides correction terms that prevent carrying over first-stage regularization bias. The goal is to orthogonalize the moment conditions so that first-stage estimation errors only have second-order effects, which do not affect the asymptotic variance of the bounds.

To incorporate the distinction between the groups  $\mathcal{X}_+$  and  $\mathcal{X}_-$ , we generalize the estimator  $\hat{\tau}^\Delta = \mathbf{G} [\mathbf{Z}^\top \mathbf{W} \mathbf{Z}]^{-1} \mathbf{Z}^\top \mathbf{W} \tilde{\mathbf{Y}}^\Delta$ , where  $\Delta \in \{L, U\}$ . The row vector  $\mathbf{G} \equiv [1 \ -1]$  contrasts exposures  $t$  and  $t'$ .  $\mathbf{Z}$  contains the treatment exposures  $\mathbf{1}_i\{t\}$  and  $\mathbf{1}_i\{t'\}$ , and the diagonal weighting matrix  $\mathbf{W}$  has elements  $w_i = \frac{1}{\pi_i(T_i)}$ . The outcome  $\tilde{\mathbf{Y}}^\Delta$  is transformed using correction terms to ensure Neyman orthogonality of the estimation process. The correction terms, which are detailed in Appendix A, ensure that first-stage regularization bias is not introduced into the asymptotic variance of the bounds. The estimand is obtained by dividing  $\hat{\tau}^\Delta$  by  $\bar{s} = \frac{1}{n} \sum \min\{\hat{s}_i(t, x), \hat{s}_i(t', x)\}$ .

The second important ingredient is cross-fitting, which controls the potential bias from overfitting when using modern machine learning methods. Cross-fitting is a method to prevent overfitting in the first stage by splitting the sample into  $K$  folds. The first stage is estimated  $K$  times, each time using  $K - 1$  folds to estimate the nuisance function  $\hat{\eta}(\cdot)$  and the remaining fold to predict the nuisance parameters  $\hat{s}_i(\cdot)$  and  $\hat{q}_i(\cdot)$ . The second stage is estimated using the predicted values of the nuisance parameters. A formal definition of  $K$ -fold cross-fitting is provided by Chernozhukov et al. (2018).

## 4.4 Inference

We assume the outcomes exhibit approximate neighborhood interference (ANI) in order to determine the asymptotic properties of the bounds. Leung (2022) defines ANI as a restriction on the effect of treatment from distant individuals  $j$  (in the network space) on the outcome of  $i$ . ANI restricts this effect to be small, but potentially non-zero. Under this assumption, he shows that we can apply asymptotic results provided by Kojevnikov et al. (2021) on  $\psi$ -dependence. Here, we provide a general overview of the assumptions from Leung (2022), and also discussed by Gao and Ding (2023), that are necessary to show consistency and asymptotic normality of the bounds  $\hat{\tau}^L$  and  $\hat{\tau}^U$ .

Let  $\mathcal{A}_n$  denote the set of all possible networks with  $n$  units and  $\mathcal{N}_n = \{1, \dots, n\}$  denote the set of units. Define a  $K$ -neighborhood as  $\mathcal{N}(i, K; A) = \{j \in \mathcal{N}_n : \ell_A(i, j) \leq K\}$ , where  $\ell_A(i, j)$  is the length of the shortest path between  $i$  and  $j$ . When  $K = 2$  and  $\mathbf{A}$  describes friendships,  $\mathcal{N}(i, 2; A)$  includes all friends and friends-of-friends of  $i$ . Denote subvectors of  $d$  and subnetworks of  $\mathbf{A}$  belonging to  $\mathcal{N}(i, K; A)$  as  $d_{\mathcal{N}(i, K; A)} = (d_j : j \in \mathcal{N}(i, K; A))$  and  $A_{\mathcal{N}(i, K; A)} = (A_{kl} : k, l \in \mathcal{N}(i, K; A))$ . Finally, let  $D'$  be an independent copy of  $D$ , and  $D^{(i, s)} = (D_{\mathcal{N}_A(i, s; A)}, D'_{-\mathcal{N}_A(i, s; A)})$  fixes the realized treatment for units in  $\mathcal{N}(i, K; A)$  but allows the treatment for units outside  $\mathcal{N}(i, K; A)$  to be different from  $D$ .

**Assumption 4.1** (Regularity Conditions). (*KNE*) *K-Neighborhood Exposure*: There exists a  $K \in \mathbb{N}$  such that, for any  $n \in \mathbb{N}$  and  $i \in \mathcal{N}_n$ , if  $\mathcal{N}(i, K; A) = \mathcal{N}(i, K; A')$ ,  $A_{\mathcal{N}(i, K; A)} = A'_{\mathcal{N}(i, K; A')}$ , and  $d_{\mathcal{N}(i, K; A)} = d'_{\mathcal{N}(i, K; A')}$ , then  $T(i, d, A) = T(i, d', A')$  for all  $d, d' \in \{0, 1\}^n$  and  $A, A' \in \mathcal{A}_n$ . (*OV*) *Overlap*:  $\pi_i(t)$  is uniformly bounded away from 0 and 1. (*BO*) *Bounded Outcomes*:  $|Y_i(d)| < \bar{Y} < \infty$ .

Assumption 4.1 outline standard regularity conditions. The first part (KNE) restricts the exposure mapping  $T(\cdot)$  only to  $K$ -Neighborhoods. This is common on applied work where the research is interested on the network effects of units that are connected up to  $K$ -steps apart. Assumption (OV) restricts the proportion of always-observed  $p_0$ , in addition to restrictions on the sequence of networks. Since the propensity score is calculated using the structure of the network, there are types of networks in  $\mathcal{A}_n$  that are limited. A network that is very dense induces everyone to be exposed to the treatment which changes the composition of always-observed and compliers in the sample. Third, we assume in (BO) that potential outcomes are bounded.

**Assumption 4.2** (Weak Network Dependence). (*ANI*) *Approximate Neighborhood Interference*:  $\sup_n \theta_{n, s} \rightarrow 0$  as  $s \rightarrow \infty$ . (*WD*) *Weak Dependence for CLT*: There exist  $\epsilon > 0$  and a positive sequence  $\{m_n\}_{n \in \mathbb{N}}$  such that as  $n \rightarrow \infty$ ,  $m_n \rightarrow \infty$  and

$$\begin{aligned} \Sigma^{-2} n^{-2} \sum_{s=0}^n |\mathcal{H}_n(s, m_n)| \tilde{\theta}_{n, s}^{1-\epsilon} &\rightarrow 0, \\ \Sigma^{-3/2} n^{-1/2} M_n(m_n, 2) &\rightarrow 0, \\ \Sigma^{-1/2} n^{3/2} \tilde{\theta}_{n, m_n}^{1-\epsilon} &\rightarrow 0. \end{aligned}$$

Assumption 4.2 is critical to restrict network interference. Approximate Neighborhood Interference (ANI) restricts the level of interference from distant individuals, where interference from individuals at distance  $s$  is defined as  $\theta_{n, s} \equiv \max_i \mathbf{E} [|Y_i(\mathbf{D}) - Y_i(\mathbf{D}^{(i, s)})|]$ . Leung (2022) shows that the linear-in-means model and the complex contagion model features ANI. Under assumptions 3.1 - 3.2 and 4.1 - 4.2 (ANI), we can show the data is  $\psi$ -dependent. This is straightforward from Leung's (2022) weak dependence theorem 1.

The second part of assumption 4.2 (WD) limits the dependence across individuals by imposing that  $\tilde{\theta}_{n, s} = \theta_{n, \lfloor s/2 \rfloor} \mathbf{1}\{s > 2 \max\{K, 1\}\} + \mathbf{1}\{s \leq 2 \max\{K, 1\}\}$  decays fast enough counterbalancing the growth of the  $s$ -neighborhoods.  $M_n^\partial(s) = n^{-1} \sum_{i=1}^n |\mathcal{N}_A^\partial(i, s)|$  is the average size of the set

of units exactly distance  $s$  from  $i$  which is  $\mathcal{N}_A^\partial(i, s)$ . Define the asymptotic variance of the Hajek estimator with known trimming proportion and quantile as  $\Sigma = \text{Var} \left( n^{-1/2} \sum_{i=1}^n \frac{1_i(t)}{\pi_i(t)} (Y_i - \mu^*(t)) : t \in \mathcal{T} \right)$ . Let  $M_n(s, k) = n^{-1} \sum_{i=1}^n |\mathcal{N}(i, s; A)|^k$ , the  $k$ th moment of the  $s$ -neighborhood size within network  $A$ .  $\mathcal{H}_n(s, m)$  denotes the set of paired couples  $(i, k)$  and  $(j, l)$  such that the units within each couple are at most path distance  $m$  apart from each other, and the two pairs are exactly path distance  $s$  apart. The three conditions on assumption (WD) restrict the type of networks and the extent of interference among individuals.

Fisher's (1935) use of additive regressions and Lin's (2013) fully-interacted regressions motivate covariate adjustment under complete randomization. The assumptions and results presented here do not explicitly account for covariate adjustment but can be extended using Gao and Ding's (2023) results. The next theorem shows that the bounds are asymptotically normal and the asymptotic variance accounts for the estimation of the trimming proportion and quantile.

**Theorem 1** (Asymptotic Normality). *Under assumptions 3.1 - 3.2 and 4.1 - 4.2, we have*

$$\begin{aligned} \sqrt{n} (\hat{\tau}^L - \tau_0^L) &\xrightarrow{d} N(0, \mathbf{V}_L) \\ \sqrt{n} (\hat{\tau}^U - \tau_0^U) &\xrightarrow{d} N(0, \mathbf{V}_U) \end{aligned}$$

Appendix A contains the proof of Theorem 1 and the explicit expression for the variance-covariance matrices  $\mathbf{V}_L$  and  $\mathbf{V}_U$ . It uses the WLS representation of the estimator to create similar moment conditions to Lee (2009) and obtain asymptotic normality for GMM estimators with non-smooth moment functions. The variance of the bounds is decomposed in three terms: the variance when quantile threshold  $q_{p_0}$  and trimming proportion  $p_0$  are known, the variance of the quantile  $q_{p_0}$ , and the variance of the trimming proportion  $p_0$ .

For estimation, we use the network HAC variance estimator with adjusted kernel by Gao and Ding (2023). The different components of the estimator are

$$\begin{aligned} \hat{\mathbf{V}}_\Delta^\beta &= \left( \mathbf{Z}_\Delta^\top \mathbf{W} \mathbf{Z}_\Delta \right)^{-1} \left( \mathbf{Z}_\Delta^\top \mathbf{W} \mathbf{E}_\Delta \mathbf{K}^+ \mathbf{E}_\Delta \mathbf{W} \mathbf{Z}_\Delta \right) \left( \mathbf{Z}_\Delta^\top \mathbf{W} \mathbf{Z}_\Delta \right)^{-1}, \\ \hat{V}_\Delta^q &= \frac{\left( \hat{q}_* - \hat{\beta}_\Delta \right)^2}{\sum S_i w_i(t)} \left( \frac{1 - \hat{p}}{\hat{p}} \right), \\ \hat{V}_\Delta^p &= \left( \hat{q}_* - \hat{\beta}_\Delta \right)^2 \left( \frac{\hat{p} - \hat{\alpha}}{\hat{\alpha} \sum w_i(t)} + \frac{1 - \hat{\alpha}}{\hat{\alpha} \sum w_i(t')} \right), \end{aligned} \tag{3}$$

where  $\Delta \in \{L, U\}$  for the lower and upper bound,  $\mathbf{E}_\Delta$  is a diagonal matrix with residuals from the WLS estimation, and  $\mathbf{K}^+$  is an adjusted kernel matrix. For the second component,  $\hat{q}_*$  is the estimated quantile with  $*$   $\in \{\hat{p}, 1 - \hat{p}\}$  for the lower and upper bound, and  $\hat{\beta}_\Delta$  is the WLS coefficient for the group that was trimmed. The last component  $\hat{V}_\Delta^p$  features  $\hat{\alpha} = \frac{\sum w_i(t') \cdot S_i}{\sum w_i(t')}$ .

Gao and Ding (2023) define the elements of the kernel matrix  $\mathbf{K}$  as  $K_{ij} = 1(\ell_A(i, j) \leq b)$  so that the kernel places nonzero weight between units  $i$  and  $j$  when they are at most  $b$  steps apart in the network space. The adjustment they propose to the kernel matrix guarantees that

the variance covariance matrix  $\widehat{\mathbf{V}}_{\Delta}^{\beta}$  is positive definite and asymptotically conservative. Using the eigendecomposition of  $\mathbf{K}$ , the adjusted kernel matrix  $\mathbf{K}^+$  is defined as  $\mathbf{K}^+ = \mathbf{Q} \max\{\Lambda, 0\} \mathbf{Q}^{\top}$ , where  $\Lambda$  is a diagonal matrix with eigenvalues,  $\mathbf{Q}$  is the matrix of eigenvectors, and the maximum is taken element-wise. Finally, we use adjusted confidence intervals proposed by [Imbens and Manski \(2004\)](#) to capture uncertainty on the spillover effect and not the region of all rationalizable spillover effects.

When we are using smooth or sparse designs of the covariate distribution, we need to extend the regularity conditions of [Assumption 4.1](#). In addition to these regularity conditions, we need to introduce selection and quantile rates to ensure that the first stage nuisance parameters are estimated at a sufficiently fast rate. The new regularity assumptions and the first stage rates follow the work of [Semenova \(2023\)](#) and [Heiler \(2023\)](#).

**Assumption 4.3** (Regularity Conditions with Covariates). *(KNE)  $K$ -Neighborhood Exposure: There exists a  $K \in \mathbb{N}$  such that, for any  $n \in \mathbb{N}$  and  $i \in \mathcal{N}_n$ , if  $\mathcal{N}(i, K; A) = \mathcal{N}(i, K; A')$ ,  $A_{\mathcal{N}(i, K; A)} = A'_{\mathcal{N}(i, K; A')}$ , and  $d_{\mathcal{N}(i, K; A)} = d'_{\mathcal{N}(i, K; A')}$ , then  $T(i, d, A) = T(i, d', A')$  for all  $d, d' \in \{0, 1\}^n$  and  $A, A' \in \mathcal{A}_n$ . (MOV) Multiple Overlap:  $\pi_i(t)$  and  $s(t, x)$  are uniformly bounded away from 0 and 1. (RO) Regular Outcomes: the conditional density  $f(y | S = 1, T = t, X = x)$  is continuously differentiable, and with its derivative they are uniformly bounded from above and away from zero. (SEP) Separability: There is a constant  $\varepsilon > 0$  and a set  $\bar{\mathcal{X}} \subset \mathcal{X}$  with  $P(\mathcal{X} \setminus \bar{\mathcal{X}}) = 0$  such that  $\inf_{x \in \bar{\mathcal{X}}} |s_0(t', x) - s_0(t, x)| > \varepsilon$*

[Assumption 4.3](#) keeps (KNE) from [Assumption 4.1](#), but extends the conditions on overlap and regular outcomes. Specifically, it requires to have multiple overlap (MOV) not only on the propensity score, but also on the conditional probability of selection. It also strengthens the regularity condition on the outcomes (RO) expecting that they are continuously distributed without point masses. In addition, it imposes separability (SEP) on the conditional probabilities  $s_0(t', x)$  and  $s_0(t, x)$ . Thus, we can correctly predict if individuals belong to the group that is encouraged by the treatment exposure,  $\mathcal{X}_+$ , or discouraged by it,  $\mathcal{X}_-$ .

Define the  $L_p$  selection rate  $s_n^p = \sup_{t \in T} \sup_{s \in S_n^t} [\mathbb{E}(s(t, X) - s_0(t, X))^p]^{1/p}$ , the worst case selection rate  $s_n^\infty = \sup_{t \in T} \sup_{x \in \mathcal{X}} \sup_{s \in S_n^t} |s(t, x) - s_0(t, x)|$ , and the  $L_p$  quantile rate  $q_n = \sup_{t \in T} \sup_{q \in Q_n^t} \sup_{u \in U} [\mathbb{E}(q(u, t, X) - q_0(u, t, X))^p]^{1/p}$ , where  $\{S_n^t\}_{n \geq 1}$  is a sequence of sets, such that the first-stage estimates  $\widehat{s}(t, x)$  of the true function  $s_0(d, x)$  belong to  $S_n^t$  with probability at least  $1 - o(1)$ . Similarly, let  $\{Q_n^t\}_{n \geq 1}$  be a sequence of sets with the same property for quantiles.

**Assumption 4.4** (First Stage Rates). *The selection and quantile rates obey the following bounds*

$$s_n^2 + q_n^2 = o\left(n^{-1/4}\right), \quad s_n^1 = o(1), \quad q_n^1 = o(1), \quad s_n^\infty = o(1).$$

Using the Horvitz-Thompson estimand and orthogonalized moment conditions, [Semenova \(2023\)](#) shows that the first stage estimation error is negligible. The difference is that the moment conditions are not independent and identically distributed, but  $\psi$ -dependent. [Theorem 2](#) shows the

asymptotic normality of the estimator using the previous assumptions, while we leave the details of the explicit form of the variance covariance matrix to Appendix A.

**Theorem 2** (Asymptotic Normality with Nuisance Parameters). *Under assumptions 3.1 - 3.2 and 4.2 - 4.4, we have*

$$\sqrt{n} \begin{pmatrix} \hat{\tau}_{\bar{s}}^L - \tau_0^L \\ \hat{\tau}_{\bar{s}}^U - \tau_0^U \end{pmatrix} \xrightarrow{d} N(0, \mathbf{V})$$

## 5 Monte Carlo Simulations

To evaluate the performance of the spillover bounds, a Monte Carlo simulation study is conducted. The aim is to assess the finite sample properties of these bounds under various scenarios, with parameters calibrated according to the empirical application. Data is generated from a finite population model incorporating network interference, with 10,000 simulation draws. The Monte Carlo experiments include designs with correctly specified and misspecified selection models. In both designs, spillover effects are evaluated using the full population and the spillover bounds with the selected sample.

In alignment with the empirical application detailed in Section 6, three population samples are considered:  $n = 829$  for the three largest treated schools,  $n = 1811$  for the top eight, and  $n = 2814$  encompassing all 14 intervention schools. In these samples, each individual is, on average, connected to 2.5 friends. The network is constructed using a random geometric graph model, which assigns positions  $\rho_i \sim \text{Uniform}([0, 1]^2)$  and an average degree  $\bar{d} = 2.5$ . Here, two individuals are connected if their Euclidean distance is less than  $\sqrt{\bar{d}/(\pi n)}$ . The adjacency matrix  $\mathbf{A}$  is derived from this network structure.

The outcome and selection processes are generated in accordance with the sample selection model that incorporates social interactions, as introduced in Subsection 2.2. Two designs are proposed to demonstrate the performance of the bounds under both correct specification and misspecification of the sample selection mechanism. The first design contemplates a selection model that accurately reflects the exposure mapping at which the spillovers are evaluated. Conversely, the second design considers a selection equation that specifies the spillovers differently from the chosen exposure mapping, albeit satisfying approximate neighborhood interference. In both designs, the scenario where the true spillover parameter  $\tau_0 = 0$  is examined, and the bounds are compared with the scenario where it is incorrectly assumed that outcomes are missing at random.

The outcome and selection equations for the first design are generated from the following model<sup>5</sup>:

$$\begin{aligned} Y_i^* &= \alpha_1 + \beta_1 \frac{\sum_{j=1}^n A_{ij} Y_j^*}{\sum_{j=1}^n A_{ij}} + \gamma_1 D_i + U_i, \\ S_i^* &= \alpha_2 + \delta_2 T_i + V_i, \\ Y_i &= \mathbf{1}\{S_i^* > 0\} \cdot Y_i^*, \end{aligned}$$

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<sup>5</sup>In practice, we solve for the reduced form of the outcome model to obtain  $Y_i^*$ .

where  $U_i = 0.5U_i^* + 0.5(\rho_{i1} - 0.5)$  and  $V_i = 0.5V_i^* + 0.5(\rho_{i1} - 0.5)$ . Both error terms,  $U_i$  and  $V_i$ , account for unobserved homophily due to the first component of individual  $i$ 's location  $\rho_i$ , while the first component is generated by a multivariate normal distribution with mean zero,  $\sigma_U = 0.25$ ,  $\sigma_V = 0.5$ , and  $\sigma_{UV} = 0.125$ <sup>6</sup>. The treatment assignment  $D_i$  is generated from a Bernoulli distribution with probability 0.25, aligning with the average propensity score of the empirical application. The exposure mapping  $T_i$  is defined as  $T_i = \mathbf{1}\sum A_{ij}D_j > 0$ . The propensity score  $\pi_i(t')$  is generated from the Binomial distribution of having no friends treated.

For the second design, the model is the same as the first design, but the selection equation is misspecified. It is defined as:

$$\begin{aligned} Y_i^* &= \alpha_1 + \beta_1 \frac{\sum_{j=1}^n A_{ij} Y_j^*}{\sum_{j=1}^n A_{ij}} + \gamma_1 D_i + U_i, \\ S_i^* &= \alpha_2 + \beta_2 \frac{\sum_{j=1}^n A_{ij} S_j^*}{\sum_{j=1}^n A_{ij}} + \delta_2 \frac{\sum_{j=1}^n A_{ij} D_j}{\sum_{j=1}^n A_{ij}} + \gamma_2 D_i + V_i, \\ Y_i &= \mathbf{1}\{S_i^* > 0\} \cdot Y_i^*. \end{aligned}$$

The parameters from the outcome and selection equations are set so that  $p_0$ , the proportion of excess individuals that are always observed, is close to one. Under this condition, sample selection is expected to be less of an issue and the bounds should be narrower. For the outcome equation the vector parameter is  $(\alpha_1, \beta_1, \gamma_1) = (0, 0.8, 0)$ , which denotes strong network dependence on potential outcomes due to the large  $\beta_1$  coefficient and no direct and spillover effect. The selection equation on the first design has parameters  $(\alpha_2, \delta_2) = (0.4, 0.2)$ , while the second design has  $(\alpha_2, \beta_2, \gamma_2) = (0.1, 0.8, 0.2, 0.2)$ . These Monte Carlo experiments correspond to a case where the intervention has significant direct and spillover effects at the extensive margin, but no effects at the intensive margin.

Table 1 presents the average spillover effect  $\hat{\tau}(1, 0)$ , the oracle and empirical coverage, and the fraction  $\hat{p}$  of units that are always-observed for each sample size. The average spillover effect is the mean estimated spillover across the 10,000 simulation draws. The oracle coverage is the proportion of times the true parameter is included in the confidence interval using the standard deviation of the estimated spillover over the simulation draws. Two empirical coverages are calculated. The network coverage uses the network HAC variance estimator while the naive coverage assumes there is no network dependence and uses heteroskedastic-robust standard errors. The results are presented for both designs under correct and misspecified selection models. When there is no sample selection, which means that we have access to the full sample, using the WLS estimator by [Gao and Ding \(2023\)](#) gives a null spillover effect on average. Across all sample sizes, oracle and network coverage are close to 95 percent, which is the nominal level. This is true for both designs given that sample selection is not an issue.

When using the selected sample and incorrectly assuming that outcomes are missing at random,

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<sup>6</sup>[Heckman and Vytlacil \(2005\)](#) and [Heiler \(2023\)](#) discuss designs of a Generalized Roy model that shares a similar error structure.

Table 1. Simulation Results

	Design 1 Correct Specification			Design 2 Misspecification		
	Full	Selected	Bounds	Full	Selected	Bounds
<i>n</i> = 829						
$\hat{\tau}(1, 0)$	0.00	-0.06	[-0.18, 0.04]	0.00	-0.19	[-0.42, 0.03]
Oracle Coverage	0.950	0.888	0.979	0.952	0.399	0.975
Network Coverage	0.954	0.895	0.970	0.950	0.435	0.949
Naive Coverage	0.803	0.717	0.922	0.788	0.207	0.903
$\hat{p}$	0.93			0.83		
<i>n</i> = 1811						
$\hat{\tau}(1, 0)$	0.00	-0.07	[-0.16, 0.03]	0.00	-0.19	[-0.43, 0.02]
Oracle Coverage	0.950	0.801	0.983	0.949	0.055	0.975
Network Coverage	0.953	0.811	0.976	0.956	0.073	0.958
Naive Coverage	0.796	0.579	0.924	0.809	0.019	0.922
$\hat{p}$	0.94			0.83		
<i>n</i> = 2814						
$\hat{\tau}(1, 0)$	0.00	-0.07	[-0.17, 0.03]	0.00	-0.16	[-0.35, 0.03]
Oracle Coverage	0.949	0.690	0.984	0.953	0.064	0.983
Network Coverage	0.954	0.713	0.979	0.956	0.079	0.965
Naive Coverage	0.791	0.435	0.936	0.782	0.016	0.926
$\hat{p}$	0.93			0.85		

Note: Monte Carlo simulation results for the spillover bounds. The table shows the average spillover effect  $\hat{\tau}(1, 0)$ , the coverage of the oracle and weighted least squares (WLS) confidence intervals with network HAC and naive standard errors, and the fraction  $\hat{p}$  of units that are always-observed for different sample sizes. The results are presented for designs with correctly specified and misspecified selection equations. The column “Full” refers to the spillover effect using the full sample, “Selected” to the selected sample when incorrectly assuming that outcomes are missing at random, and “Bounds” to the spillover bounds that account for sample selection in the outcome. The naive coverage utilizes heteroskedastic-robust standard errors assuming i.i.d data, while network the network coverage uses network HAC standard errors with adjusted kernel and optimal bandwidth  $b = 3$ , and [Imbens and Manski’s \(2004\)](#) confidence interval with  $\bar{c} = 1.645$ .

the spillover effect is biased. This is because we lose point-identification since both treatment status and social exposure affect sample selection on the outcome. For the design with correct specification, the estimated spillover effect is about -0.06 with oracle coverages from 70 to 89 percent. Even though the simulations feature high shares of always-observed units (close to 0.95), the oracle coverage never reaches more than 90 percent. As expected, network coverage mimics the oracle coverage, while the naive coverage is lower when assuming outcomes missing at random with sample selection. When using the spillover bounds, the estimates are  $[-0.18, 0.04]$  for the smallest sample size and  $[-0.17, 0.03]$  for the largest one. The empirical coverage is close to the oracle coverage, improving with the sample size. It is important to notice that using naive standard errors can lead to anti-conservative estimates, as the empirical coverage is always lower than the oracle coverage, even when the sample selection is correctly specified.

With misspecification, the spillover effect is estimated at about -0.19, with oracle coverage ranging from 5 to 7 percent if we incorrectly assume missing outcomes at random. The network coverage is slightly higher, but the naive coverage is substantially lower. This indicates that the interplay between the misspecification of the sample selection mechanism and reduced proportions of always-observed units can result in significantly biased estimates. The spillover bounds, on the other hand, successfully recover the true spillover effect. The bounds are  $[-0.42, 0.03]$  for the smallest sample size and  $[-0.35, 0.03]$  for the largest. The coverage in this design is slightly lower than in the properly specified model, and the empirical coverage is smaller than the oracle coverage. This indicates that the bounds can recover the true spillover effect even when the selection model is misspecified, though coverage may be mildly anti-conservative due to the misspecification.

## 6 Field Experiment on Computer Use

To illustrate an application of the spillover bounds, we utilize data from a field experiment that randomized the provision of laptops to students in public schools in Peru. [Beuermann et al. \(2015\)](#) studied the short-term impacts of the “One Laptop per Child” program, which aims to promote self-empowered learning by providing personal laptops to children in developing countries. The authors implemented a randomized controlled trial, with randomization occurring at both the school and individual levels. Fourteen schools were randomly selected for treatment, and within each school, four students per classroom were chosen via a public lottery to receive a laptop. Due to the high compliance rate, the analysis focused on comparing lottery winners to nonwinners within the treatment schools.

[Beuermann et al. \(2015\)](#) found that the program successfully increased exposure to computers at home. On the extensive margin, the program increased the likelihood of using a computer at home by 33 percentage points, and on the intensive margin, it increased computer usage by approximately 18 minutes per day. The authors also investigated potential spillover effects among students using data on their close friends but found no evidence of such effects on computer usage. This section revisits the analysis of spillover effects of winning the laptop lottery, focusing on the intensive margin.

The estimand of interest is the average spillover effect for students who always use computers regardless of treatment exposure. This selected group of computer users is defined as students with positive minutes of usage during the previous day. The outcome of interest  $Y_i$  is the number of minutes of computer utilization the day before. The sample selection indicator  $S_i$  is defined as 1 if student  $i$  used a computer yesterday and 0 otherwise. We want to assess, the intensive margin, whether the intervention increased time spent on computers for students that would have used computers anyway. At the intensive margin, spillover and direct effects are only partially identified because the randomized experiment only guarantees that treated and control students are comparable at the baseline.

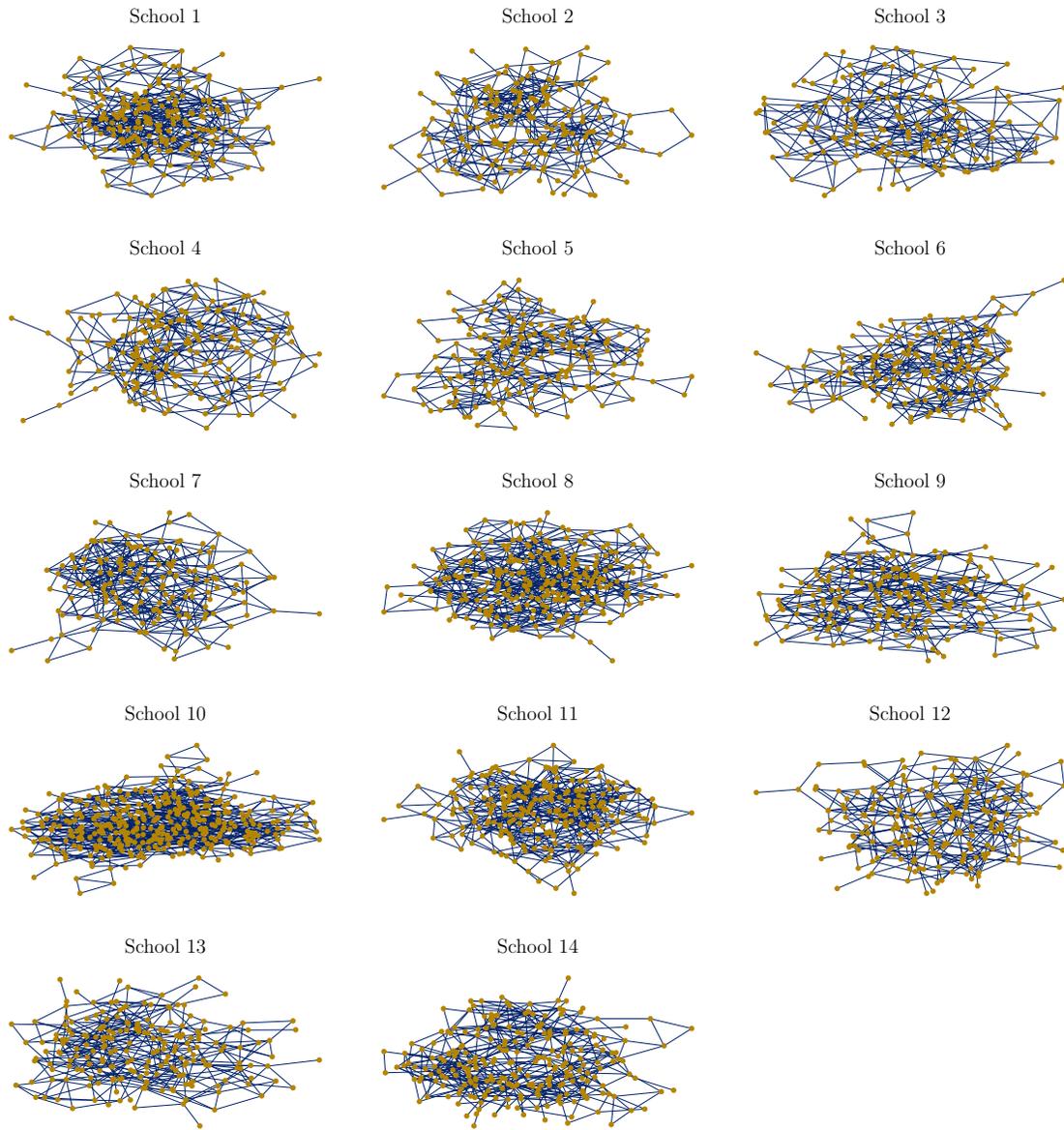
The primary estimand is the average spillover effect for students who always use computers regardless of treatment exposure. This group is defined as students with positive minutes of computer usage on the previous day. The outcome of interest,  $Y_i$ , is the number of minutes of computer usage the previous day. The sample selection indicator,  $S_i$ , is 1 if the student used a computer yesterday and 0 otherwise. We aim to assess whether the intervention increased computer usage time for students who would have used computers anyway. At the intensive margin, both spillover and direct effects are only partially identified because the randomized experiment ensures comparability of treated and control students only at baseline.

Students were asked to nominate up to four friends in their school. The intervention was randomly assigned to 28 schools, so the analysis focuses on these treatment schools to ensure students had a non-zero probability of being treated. The element  $A_{ij} \in \{1, 0\}$  of the adjacency matrix  $\mathbf{A}$  indicates whether student  $i$  nominated student  $j$  as a friend. Figure 1 displays the friendship networks across the 14 schools that were treated. The treatment indicator  $D_i$  is 1 if student  $i$  was assigned to the intervention and 0 otherwise. Thus, the exposure mapping  $T_i = \mathbf{1}\{\sum A_{ij}D_j > 0\}$  defines spillovers as having at least one treated friend. The propensity score  $\pi_i(t)$  is calculated using the hypergeometric distribution under the block randomization scheme. For direct treatment, the propensity score equals  $4/n_c$ , where  $n_c$  is the number of students in the classroom. For spillovers, the propensity score is calculated based on the randomization protocol and network structure.

Table 2 provides summary statistics for groups defined by the exposure mapping  $T_i = (D_i, \mathbf{1}\{\sum A_{ij}D_j > 0\})$ . The first element of  $T_i$  indicates direct treatment status, and the second indicates whether at least one friend was treated. About 45 percent of the winner and nonwinner students had at least one friend who won the laptop lottery. The total sample consists of 3,085 students, with 75 percent using a computer the previous day.

Without sample selection, the average number of minutes of computer use is about 120 minutes. The selection rate represents the proportion of students using a computer, i.e.,  $\Pr(S_i = 1)$ . Selection rates vary by direct treatment exposure but are similar across social exposure. The last column shows the mean log of computer utilization, conditional on using a computer ( $Y_i > 0$ ). Computer use is highest for students who are lottery winners and have at least one winner friend. Conversely, among students with no winner friends, lottery winners have the lowest computer use. In the

Figure 1. Friendship Networks across Schools



Note: This figure displays the friendship networks across the 14 schools that were treated. The nodes represent students, and the edges indicate friendship connections.

Table 2. Computer Utilization: Summary Statistics

Exposure	Observations	Mean Use	Selection Rate	Mean (log)
(0,0)	1399	119	0.726	4.80
(0,1)	1019	115	0.727	4.78
(1,0)	390	125	0.797	4.74
(1,1)	277	129	0.827	4.81
Overall	3085	119	0.745	4.78

Note: Summary statistics by groups defined by the exposure mapping  $T_i = (D_i, \mathbf{1}\{\sum A_{ij}D_j > 0\})$ . The first element of the exposure mapping  $T_i$  refers to the direct treatment status, and the second indicates whether at least one friend received treatment. Mean computer use is the average number of minutes of computer utilization the day before, including zeros. The selection rate is the proportion of students that used a computer. The last column presents the mean of the log of computer utilization, conditional on using a computer ( $Y_i > 0$ ).

following analysis, I will use spillover bounds to assess the presence of network interference on the intensive margin of computer utilization.

### 6.1 Spillover Bounds without Covariates

Under the current exposure mapping, the sample can be divided into four groups to estimate direct and spillover effects by comparing direct and social exposure differences. Direct effects are assessed by contrasting students who won the lottery with those who did not, considering whether they have at least one friend who won (winner friend) or none (nonwinner friend). Similarly, spillover effects are evaluated by comparing winner and nonwinner students. Table 3 presents the direct, spillover, and overall effects of the intervention on computer use, with bounds calculated using the trimming procedure described in section 4.

The key assumption in partially identifying the effects of the intervention is that winning or having a friend win the lottery increases students' likelihood of computer use. Under this assumption,  $1 - \hat{p}$  is calculated to identify the excess proportion of students induced to use computers due to treatment. Direct treatment effects are estimated after trimming the lowest and highest outcome values of 10 to 12 percent of the sample. With similar selection rates for spillovers, trimming is substantially smaller (1 to 3 percent). However, 8 percent of the sample is trimmed for overall effects.

Approximate neighborhood interference assumes that interference weakens with distance in the friendship network. The network comprises 20 components, with the largest having 100 students. Across all components, the average student distance is 2.5, and the longest path is 6. The network is sparse, with a density of 0.03, and has a low clustering coefficient of 0.1. This is consistent aligned with the assumption of approximate neighborhood interference.

Table 3 showcases the spillover bounds for computer utilization, offering insights into the direct

Table 3. Spillover Bounds on Computer Use

Sample	Direct Effect		Spillover Effect		Overall Effect
	Winner Friend (1)	Nonwinner Friend (2)	Winners (3)	Nonwinners (4)	Full (5)
Estimate					
$\hat{\tau}$	0.03	-0.04	0.11	0.00	0.00
CI	(-0.12, 0.17)	(-0.17, 0.09)	(-0.06, 0.27)	(-0.10, 0.09)	(-0.08, 0.08)
Bounds					
$\hat{\tau}$	[-0.13, 0.22]	[-0.22, 0.13]	[0.07, 0.15]	[-0.02, 0.02]	[-0.09, 0.08]
CI	(-0.25, 0.33)	(-0.34, 0.25)	(-0.09, 0.32)	(-0.13, 0.11)	(-0.17, 0.17)
$\hat{p}$	0.87	0.90	0.97	0.99	0.95

Note: This table presents direct and spillover effects under the exposure mapping  $T_i = (D_i, \mathbf{1}\{\sum A_{ij}D_j > 0\})$ . First element of the exposure mapping  $T_i$  refers to the direct treatment status and the second whether at least one friend received treatment. Columns (1) and (2) display direct effects of winning the lottery for students with at least one treated friend and with none, respectively. Columns (3) and (4) show spillover effects of having a treated friend for students that won the lottery and did not, respectively. Last column displays overall effects comparing any exposure to the intervention to none. Spillover estimates assume that outcomes are missing at random. Instead, spillover bounds are shown in brackets. Imbens and Manski's (2004) confidence interval with  $\bar{c} = 1.645$  are shown in parentheses below the bounds. For the confidence intervals, we use standard errors with network HAC variance (optimal bandwidth  $b = 2$ ). The fraction  $\hat{p}$  is the proportion of students who select into the sample.

and spillover effects of winning the lottery. Interestingly, the bounds for the direct effect of winning the lottery are quite broad and encompass zero. For students with a friend who won the lottery, the bounds range from a potential 13 percent decrease to a 22 percent increase in computer use, illustrating considerable variability. Similarly, for students without friends who won the lottery, the spillover bounds are wide, indicating a possible 22 percent decrease or a 13 percent increase in computer use due to winning the lottery. These findings echo in the overall effect estimates, where the bounds suggest a potential 9 percent decrease to an 8 percent increase in computer use attributed to the intervention.

Analyzing spillover effects reveals interesting dynamics. When assuming outcomes are missing at random, all the point-identified estimates are not statistically significant. In general, among students who won the lottery, having a friend who also won appears to positively influence computer use, with bounds indicating an increase of 7 to 15 percent. However, the confidence interval do not rule out a zero effect. Conversely, for nonwinner students, the bounds are notably tighter due to minimal trimming and encompass zero, indicating no apparent evidence of spillovers. These results are derived using confidence intervals with standard errors accounting for network interference and include the variance from the trimming procedure. While these findings contribute valuable insights, there remains scope for refinement and deeper exploration using information from covariates. Incorporating relevant covariates into the analysis holds promise for enhancing the precision of estimates, particularly in addressing variation inherent in the sample selection process.

## 6.2 Including Covariates on the Selection Process

Integrating covariates into the selection process offers a potential avenue to refine the spillover bounds by accounting for relevant observed characteristics. The covariates include demographics, family attributes, home environment, and past computer engagement. Additionally, we consider the average characteristics of friends, such as the proportion of friends with past computer use. This broader set of covariates enables a more nuanced understanding of the selection process. To model the selection probability, we employ parametric logistic regressions,  $\ell_1$ -penalized logistic regressions, and automatic search and aggregation machine learning techniques, such as Auto ML. Similarly, we leverage parametric quantile regressions,  $\ell_1$ -penalized quantile regressions, and non-parametric gradient boosting quantile regressions to estimate conditional quantiles.

In the parametric approach, our model formulation involves  $\widehat{s}(t, x) = \Lambda(x'\widehat{\alpha}_s)$ , where  $\Lambda(r) = \frac{\exp(r)}{1+\exp(r)}$  denotes the logistic function,  $\widehat{\alpha}_s$  represents the regularized coefficient vector, and  $x$  encompasses baseline covariates. Subsequently, the probability of being always-observed,  $\widehat{p}(x)$ , is derived as  $\frac{\widehat{s}(t', x)}{\widehat{s}(t, x)}$ . Post-lasso logistic regression ensures the treatment exposures  $\{t, t'\}$  to always be included. The estimation of  $u$  conditional quantiles ( $\widehat{q}(u, x)$ ) is performed over quantiles  $u \in \{0.01, 0.02, \dots, 0.99\}$ .

We extend our analysis with non-parametric methods, leveraging automated machine learning algorithms for selection prediction and gradient boosting quantile regression for estimating conditional quantiles. The selection process involves an exhaustive search among various algorithms, including logistic regression and tree-based methods, facilitated by the FLAML library in Python. Following the selection process, we employ gradient boosting quantile regression for non-parametric estimation of conditional quantiles.

In the first stage, 17 covariates<sup>7</sup> are incorporated to explain both the outcome and selection processes, detailed in Table B1. These covariates are further enriched by their interaction with the row-normalized adjacency matrix  $\mathbf{A}$ , capturing the average attributes of friends. We add the network degree of each student, which is the total number of friends, to the individual and friends attributes for a total of 35 covariates. These covariates are standardized to have zero mean and unit variance, except for the binary variables. The outcome variable of interest is the logarithm of the number of minutes of computer utilization from the previous day. Our aim is to estimate the direct, spillover, and overall effects of the intervention on computer use.

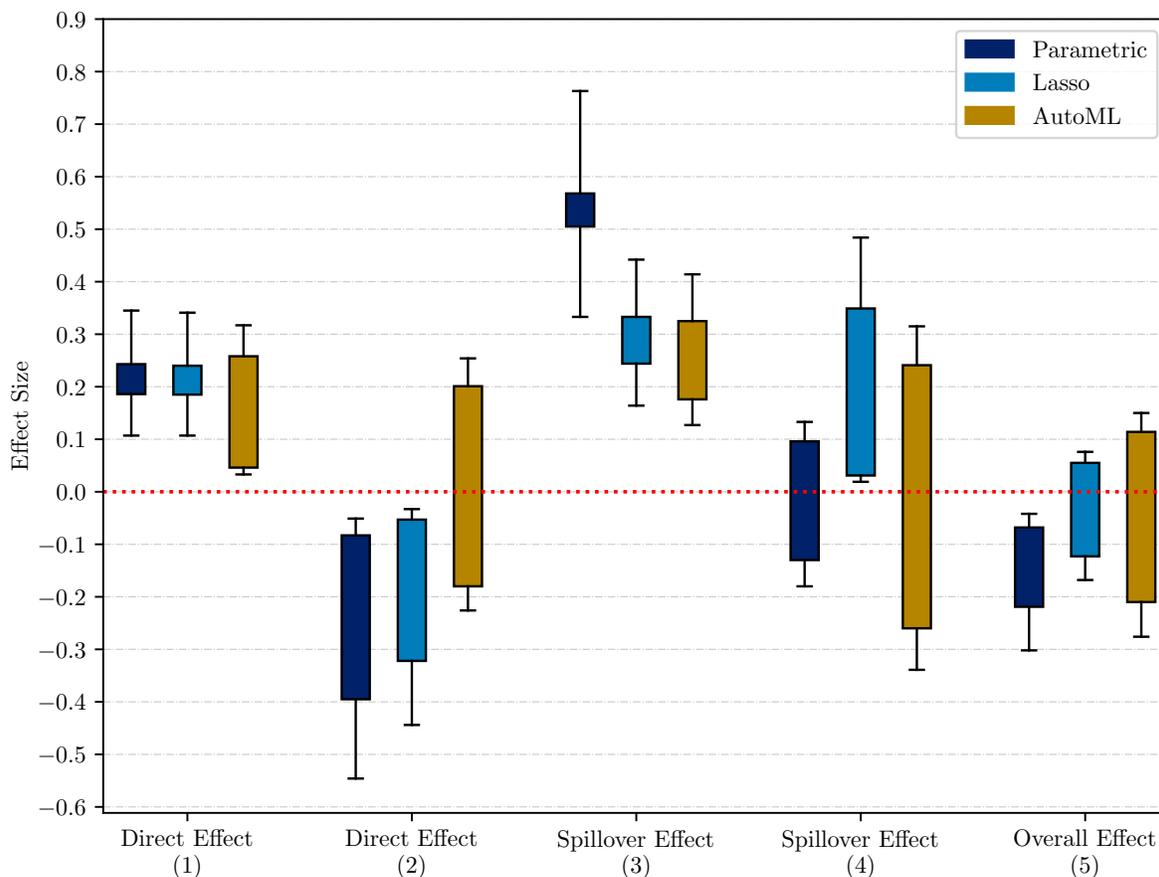
To estimate the spillover bounds, we implement cross-fitting and hyper-parameter tuning strategies. The sample is divided into 10 folds, with each iteration involving fitting of selection and outcome models on 9 folds, and prediction of  $\widehat{p}(x)$  and  $\widehat{q}(u, x)$  on the remaining fold. Hyper-parameter tuning is conducted via 10-fold cross-validation for each sample split. In the subsequent stage, bounds are computed using orthogonalized moment conditions, with individual outcomes trimmed based on thresholds derived from  $\widehat{q}(\widehat{p}, x)$ . Confidence intervals are computed using the network HAC variance estimator with bandwidth  $b = 2$ .

The spillover bounds for computer utilization employing different first stage estimation strate-

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<sup>7</sup>These covariates are part of [Beuermann et al.'s \(2015\)](#) specifications.

Figure 2. Spillover Bounds on Computer Use with Covariates



Note: This table presents direct and spillover effects under the exposure mapping  $T_i = (D_i, \mathbf{1}\{\sum A_{ij}D_j > 0\})$ . First element of the exposure mapping  $T_i$  refers to the direct treatment status and the second whether at least one friend received treatment. The first and second labels represent direct effects of winning the lottery for students with at least one treated friend and with none, respectively. The third and fourth labels show spillover effects of having a treated friend for students that won the lottery and did not, respectively. Last column displays overall effects comparing any exposure to the intervention to none. Spillover bounds are shown using boxplots. The bounds incorporate logistic and quantile regression under the parametric first stage estimation with navy blue color. It also uses post-lasso logistic and quantile regression on the first stage denoted by light blue color. The first stage estimation with automatic search of machine learning classifiers and gradient boosting quantile regression is denoted by gold color. [Imbens and Manski's \(2004\)](#) confidence interval with  $\bar{c} = 1.645$  are shown in parentheses below the bounds. For the confidence intervals, we use standard errors with network HAC variance (bandwidth  $b = 2$ ).

gies are displayed in Figure 2. In general, these bounds are more narrow compared to those without covariates. For students having at least one winner friend, the direct effect of winning the lottery is positive, while for those with nonwinner friends, it is negative but uninformative when using automated machine learning algorithms. The respective bounds are  $[0.19, 0.24]$  and  $[-0.32, -0.05]$  when using post-lasso methods on the first stage. The direct effect being positive for students with treated friends could be because having friends who also won the lottery creates a positive peer influence environment that encourages and motivates increased computer utilization. When friends have access to the same resources (in this case, the lottery winnings), they can engage in activities together, support each other, and reinforce behaviors like technology usage. However, students with no treated friends might lack that same peer environment which leads to a negative direct effect for students without treated friends. The post-lasso and machine learning methods yield similar results for the sample with winner friends, with direct effects ranging from 0.13 to 0.21 and 0.08 to 0.34, respectively.

Regarding the spillover effect of having a treated friend, it exhibits a positive impact for lottery winners, suggesting that their peers' lottery winnings influence their computer utilization positively. The bounds for this effect are  $[0.24, 0.33]$  with post-lasso methods. Similar results are obtained using a parametric specification and machine learning methods, with spillover effects ranging from 0.51 to 0.57 and 0.18 to 0.32, respectively. Surprisingly, for non-winners, the evidence also shows a positive spillover effect, with bounds of  $[0.03, 0.35]$  only for the post-lasso method. This suggests that the intervention has broader impacts on computer utilization amplified through friendships. Notably, incorporating a rich set of covariates refines our understanding of these dynamics. We find that only 30 percent of individuals are incentivized to increase computer usage due to having a friend who won the lottery, conditional on their own lottery win.

The overall intervention effect ranges from -12 to 6 percent across all methods. Evidence of overall effects remains inconclusive since we cannot entirely dismiss the possibility of null effects. However, the inclusion of relevant observed characteristics refines our understanding of the intervention's impact on computer utilization. The regularization procedure selects 20 to 30 variables across each sample split, with accuracies averaging around 80 percent. Among the selected covariates are past computer usage, whether the father works from home, and friend characteristics such as the average number of siblings and their past computer usage. These covariates are relevant for the selection process, contributing to the tightening of the bounds. Most of the classifiers selected were tree-based methods such as Extreme Gradient Boosting (XGBoost), Light Gradient-Boosting Machine (LGBM), and random forest. Similarly to post-lasso, accuracy levels oscillate around 80 percent.

## 7 Conclusion

In conclusion, this paper introduces a novel method to estimate spillover effects in the presence of nonrandom sample selection. The proposed spillover bounds extend the widely used Lee bounds to general exposures to treatments and rely on an exposure monotonicity assumption. This assumption

allows trimming the outcome distribution in a worst-case scenario to construct sharp bounds on the spillover effects for the always-observed group. The framework also accommodates the inclusion of covariates, which can help tighten the bounds by more flexibly modeling the selection process. Monte Carlo simulations demonstrate that the estimator performs well in finite samples and is robust to misspecification of the exposure mapping in the selection equation, as long as interference is sufficiently weak.

The empirical application revisits a randomized laptop provision program to students and analyzes spillover effects on computer utilization at the intensive margin. The estimated spillover bounds provides evidence of positive direct and spillover effects using different subgroups for the analysis. However, when analyzing the effects of the overall exposure to treatment, results suggest uninformative bounds. Including covariates in the selection process does not substantially tighten the bounds in that situation.

This paper makes several contributions. First and foremost, it proposes the first method to partially identify spillover effects under nonrandom sample selection. Second, it provides an alternative design-based inference for the popular Lee bounds in the absence of interference. Third, it extends Lee bounds to accommodate multiple treatments and arbitrary exposure mappings. As spillovers and sample selection are common issues in empirical work, the proposed method provides a useful tool for researchers to assess spillover effects in such settings. Future work could explore misspecification of the exposure mapping in the selection equation and alternative approaches that rely in exclusion restrictions.

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## A Proofs and Estimation Details

*Proof of Proposition 1.* Under Assumptions 3.1 and 3.2, individuals exposed to  $t'$  who are selected into the sample are also selected when exposed to  $t$ . Therefore, the expected potential outcome under exposure  $t'$  reduces to

$$\begin{aligned} E[\bar{Y}_i(t') \mid \bar{S}_i(t) = 1, \bar{S}_i(t') = 1] &= E[\bar{Y}_i(t') \mid \bar{S}_i(t') = 1] \\ &= E[Y_i \mid S_i = 1, T_i = t'], \end{aligned}$$

and the proportion of always-takers that are exposed to  $t$  is

$$\begin{aligned} p_0 &= \Pr(\bar{S}_i(t) = 1, \bar{S}_i(t') = 1 \mid \bar{S}_i(t) = 1) \\ &= \Pr(\bar{S}_i(t') = 1 \mid \bar{S}_i(t) = 1) \\ &= \frac{\Pr(\bar{S}_i(t) = 1 \mid \bar{S}_i(t') = 1) \Pr(\bar{S}_i(t') = 1)}{\Pr(\bar{S}_i(t) = 1)} \quad (\text{Bayes rule}) \\ &= \frac{\Pr(\bar{S}_i(t') = 1)}{\Pr(\bar{S}_i(t) = 1)} \quad (\text{Monotonicity}) \\ &= \frac{\Pr(S_i = 1 \mid T_i = t')}{\Pr(S_i = 1 \mid T_i = t)} \quad (\text{Independence}). \end{aligned}$$

Then, I show that  $\mu^U \equiv E[Y_i \mid Y_i \geq q_{1-p_0}, T_i = t, S_i = 1]$  is a sharp upper bound for  $E[\bar{Y}_i(t) \mid \bar{S}_i(t) = 1, \bar{S}_i(t') = 1]$ . Following Lee's proof of proposition 1, I define  $F(y)$  as the cumulative distribution function (CDF) of  $Y_i$  conditional on  $T_i = t$  and  $S_i = 1$ . Under Assumption 3.2, I can define a mixture of random variables so that  $F(y) = p_0 M(y) + (1 - p_0)N(y)$  with mixing proportion  $p_0$ .  $M(y)$  represents the CDF of  $\bar{Y}_i(t)$  given  $T_i = t, \bar{S}_i(t) = 1, \bar{S}_i(t') = 1$ , and  $N(y)$  the CDF of  $\bar{Y}_i(t) \mid T_i = t, \bar{S}_i(t) = 1, \bar{S}_i(t') = 0$ . Using Horowitz and Manski' (1995) Corollary 4.1, page 291,  $\mu^U \equiv \frac{1}{p_0} \int_{y_{1-p_0}}^{\infty} y dF(y) \geq \int_{-\infty}^{\infty} y dM(y) = E[\bar{Y}_i(t) \mid \bar{S}_i(t) = 1, \bar{S}_i(t') = 1]$  is a sharp upper bound, and  $p_0$  is uniquely determined by the population. Lastly, following a similar argument as Lee (2009), I can show that under these assumptions, any other bound contains  $[\tau_0^L, \tau_0^U]$ . ■

*Equivalent Spillover Bounds Estimators.* An equivalent estimator of the spillover bounds, for the sample of individuals that are selected ( $S_i = 1$ ), using the Horvitz-Thompson formulation is

$$\begin{aligned} \hat{\tau}^L &= \frac{1}{n} \sum_{i=1}^n \left[ \frac{\mathbf{1}_i\{t\}}{\pi_i(t)} \cdot \mathbf{1}\{Y_i \leq \hat{q}_{\hat{p}}\} \cdot S_i \cdot Y_i \right] - \frac{1}{n} \sum_{i=1}^n \left[ \frac{\mathbf{1}_i\{t'\}}{\pi_i(t')} \cdot S_i \cdot Y_i \right], \\ \hat{\tau}^U &= \frac{1}{n} \sum_{i=1}^n \left[ \frac{\mathbf{1}_i\{t\}}{\pi_i(t)} \cdot \mathbf{1}\{Y_i \geq \hat{q}_{1-\hat{p}}\} \cdot S_i \cdot Y_i \right] - \frac{1}{n} \sum_{i=1}^n \left[ \frac{\mathbf{1}_i\{t'\}}{\pi_i(t')} \cdot S_i \cdot Y_i \right]. \end{aligned}$$

While the Hajek representation for the spillover bounds in Section 4 is

$$\begin{aligned}\widehat{\tau}^L &= \frac{\sum_{i=1}^n \frac{\mathbf{1}_i\{t\}}{\pi_i(t)} \cdot \mathbf{1}\{Y_i \leq \widehat{q}_p\} \cdot S_i \cdot Y_i}{\sum_{i=1}^n \frac{\mathbf{1}_i\{t\}}{\pi_i(t)} \cdot \mathbf{1}\{Y_i \leq \widehat{q}_p\} \cdot S_i} - \frac{\sum_{i=1}^n \frac{\mathbf{1}_i\{t'\}}{\pi_i(t')} \cdot S_i \cdot Y_i}{\sum_{i=1}^n \frac{\mathbf{1}_i\{t'\}}{\pi_i(t')} \cdot S_i}, \\ \widehat{\tau}^U &= \frac{\sum_{i=1}^n \frac{\mathbf{1}_i\{t\}}{\pi_i(t)} \cdot \mathbf{1}\{Y_i \geq \widehat{q}_{1-p}\} \cdot S_i \cdot Y_i}{\sum_{i=1}^n \frac{\mathbf{1}_i\{t\}}{\pi_i(t)} \cdot \mathbf{1}\{Y_i \geq \widehat{q}_{1-p}\} \cdot S_i} - \frac{\sum_{i=1}^n \frac{\mathbf{1}_i\{t'\}}{\pi_i(t')} \cdot S_i \cdot Y_i}{\sum_{i=1}^n \frac{\mathbf{1}_i\{t'\}}{\pi_i(t')} \cdot S_i}.\end{aligned}$$

For ease of notation, denote  $\mathbf{1}_i\{t\}_q \equiv \mathbf{1}_i\{t\} \cdot \mathbf{1}\{Y_i \leq \widehat{q}_p\}$ . The previous estimator,  $\widehat{\tau}^L$ , can be represented via WLS as

$$\begin{aligned}\widehat{\tau}^L &= \begin{bmatrix} 1 & -1 \end{bmatrix} \begin{bmatrix} \frac{\sum \frac{\mathbf{1}_i\{t\}_p S_i Y_i}{\pi_i(t)}}{\sum \frac{\mathbf{1}_i\{t\}_p S_i}{\pi_i(t)}} \\ \frac{\sum \frac{\mathbf{1}_i\{t'\} S_i Y_i}{\pi_i(t')}}{\sum \frac{\mathbf{1}_i\{t'\} S_i}{\pi_i(t')}} \end{bmatrix} \\ &= \begin{bmatrix} 1 & -1 \end{bmatrix} \begin{bmatrix} 1/\sum \frac{\mathbf{1}_i\{t\}_p S_i}{\pi_i(t)} & 0 \\ 0 & 1/\sum \frac{\mathbf{1}_i\{t'\} S_i}{\pi_i(t')} \end{bmatrix} \begin{bmatrix} \sum \frac{\mathbf{1}_i\{t\}_p S_i Y_i}{\pi_i(t)} \\ \sum \frac{\mathbf{1}_i\{t'\} S_i Y_i}{\pi_i(t')} \end{bmatrix} \\ &= \begin{bmatrix} 1 & -1 \end{bmatrix} \begin{bmatrix} \sum w_i \mathbf{1}_i\{t\}_p S_i & 0 \\ 0 & \sum w_i \mathbf{1}_i\{t'\} S_i \end{bmatrix}^{-1} \begin{bmatrix} \sum w_i \mathbf{1}_i\{t\}_p S_i Y_i \\ \sum w_i \mathbf{1}_i\{t'\} S_i Y_i \end{bmatrix} \\ &= \begin{bmatrix} 1 & -1 \end{bmatrix} \begin{bmatrix} \sum w_i \mathbf{1}_i\{t\}_p^2 S_i^2 & \sum w_i \mathbf{1}_i\{t\}_p \mathbf{1}_i\{t'\} S_i^2 \\ \sum w_i \mathbf{1}_i\{t\}_p \mathbf{1}_i\{t'\} S_i^2 & \sum w_i \mathbf{1}_i\{t'\}^2 S_i^2 \end{bmatrix}^{-1} \begin{bmatrix} \sum w_i \mathbf{1}_i\{t\}_p S_i \\ \sum w_i \mathbf{1}_i\{t'\} S_i \end{bmatrix} \mathbf{Y} \\ &= \begin{bmatrix} 1 & -1 \end{bmatrix} \left( \begin{bmatrix} \mathbf{1}\{t\}_p^\top S_i \\ \mathbf{1}\{t'\}^\top S_i \end{bmatrix} \mathbf{W} \begin{bmatrix} \mathbf{1}\{t\}_p S_i & \mathbf{1}\{t'\} S_i \end{bmatrix} \right)^{-1} \begin{bmatrix} \mathbf{1}\{t\}_p^\top S_i \\ \mathbf{1}\{t'\}^\top S_i \end{bmatrix} \mathbf{W} \mathbf{Y} \\ &= \mathbf{G} \left[ \mathbf{Z}_L^\top \mathbf{W} \mathbf{Z}_L \right]^{-1} \mathbf{Z}_L^\top \mathbf{W} \mathbf{Y}.\end{aligned}$$

And the estimator  $\widehat{\tau}^U$  follows the same steps.

*Proof of Theorem 1.* It is sufficient to show that  $\widehat{\tau}^L$  is asymptotically normal. The moment conditions are

$$g(\theta) \equiv \begin{pmatrix} Z_{L,i}^\top (w_i Y_i - w_i Z_{L,i} \beta) \\ [\mathbf{1}\{Y_i > q_p\} - (1-p)] S_i w_i(t) \\ \left(S_i - \frac{\alpha}{p}\right) w_i(t) \\ (S_i - \alpha) w_i(t') \end{pmatrix}$$

where  $\theta^\top = (\beta, y_{1-p}, p, \alpha)^\top$ . Previously, I showed that  $\widehat{\beta}$  is numerically equivalent to the Hajek-based estimator. Therefore, I can write  $\widehat{\tau}^U = \mathbf{G} \widehat{\beta}$  as the difference in means. These moment conditions mimic the ones in Lee's (2009) proof of Proposition 2. The difference is on the first moment where I include the WLS representation of the moment condition. By Proposition 3 of Lee (2009), the estimator  $\widehat{\theta}$  is consistent and asymptotically normal using Theorem 7.2 of Newey

and McFadden (1994). However, under Assumptions 4.1 - 4.2 (ANI), we can show that the data is  $\psi$ -dependent. Therefore, it is necessary to change the CLT condition (iv) of Newey and McFadden's (1994) Theorem 7.2 by Theorem 3.2 of Kojevnikov et al. (2021). The latter holds due to Assumption 4.2 (See Gao and Ding, 2023). With  $\psi$ -dependent data, the asymptotic variance of the moment conditions is  $\mathbf{V} = \mathbf{D}^{-1}\Sigma(\mathbf{D}^{-1})^\top$ , where  $\mathbf{D} = E[\frac{\partial}{\partial\theta'}g(\theta)]$  partitioned as  $\begin{bmatrix} \mathbf{D}_\gamma & \mathbf{D}_\delta \\ 0 & \mathbf{M}_\delta \end{bmatrix}$  and  $\Sigma = E[g(\theta)g(\theta)^\top]$  partitioned as  $\begin{bmatrix} \Sigma_1 & 0 \\ 0 & \Sigma_2 \end{bmatrix}$ . The relevant part is the  $3 \times 3$  upper left block of  $\mathbf{V}$ , which is  $\mathbf{D}_\gamma^{-1}\Sigma_1(\mathbf{D}_\gamma^{-1})^\top + \mathbf{D}_\gamma^{-1}\mathbf{D}_\delta\mathbf{M}_\delta^{-1}\Sigma_2(\mathbf{M}_\delta^{-1})^\top\mathbf{D}_\delta^\top(\mathbf{D}_\gamma^{-1})^\top$ . The different matrices involved are

$$\begin{aligned} \mathbf{D}_\gamma &= E[w_i(t)S_i] \begin{bmatrix} -p_0 & 0 & (q_{p_0} - \beta_1) f(q_{p_0}) \\ 0 & -1 & 0 \\ 0 & 0 & -f(q_{p_0}) \end{bmatrix}, \\ \mathbf{D}_\delta &= E[w_i(t)S_i] \begin{bmatrix} 0 & 0 \\ 0 & 0 \\ -1 & 0 \end{bmatrix}, \\ \mathbf{M}_\delta &= \begin{bmatrix} -\frac{\alpha_0}{p_0} E[w_i(t)] & -\frac{1}{p_0} E[w_i(t)] \\ 0 & -E[w_i(t')] \end{bmatrix}, \\ \Sigma_1 &= \begin{bmatrix} \mathbf{V}_\beta & 0 \\ 0 & E[w_i(t)S_i] p_0 (1 - p_0) \end{bmatrix}, \\ \Sigma_2 &= \begin{bmatrix} \frac{\alpha_0}{p_0} \left(1 - \frac{\alpha_0}{p_0}\right) E[w_i(t)] & 0 \\ 0 & \alpha_0 (1 - \alpha_0) E[w_i(t')] \end{bmatrix}. \end{aligned}$$

After some algebra, the variance covariance matrix for the lower bound of the spillover effects results in

$$\mathbf{V}_L = \begin{bmatrix} V_{11}^\beta + V_L^q + V_L^p & V_{12}^\beta \\ V_{21}^\beta & V_{22}^\beta \end{bmatrix},$$

where  $V_{ij}^\beta$  are the elements  $(i, j)$  of the asymptotic covariance matrix  $\mathbf{V}_\beta$  of the WLS estimator of  $\beta$ , the variance from estimating the quantile is  $V_L^q = \frac{1}{E[w_i(t)S_i]} \frac{1-p_0}{p_0} (q_{p_0} - \beta_1)^2$ , and  $V_L^p = (q_{p_0} - \beta_1)^2 \left[ \frac{p_0 - \alpha_0}{\alpha_0 E[w_i(t)]} + \frac{1 - \alpha_0}{\alpha_0 E[w_i(t')]} \right]$ . ■

*Correction Terms for Orthogonality.* The correction terms to ensure Neyman orthogonality are

$$\begin{aligned}
\text{cor}_+^L(\eta) &= q(p(x), x) \left( \frac{\mathbf{1}_i\{t'\}}{\pi_i(t')} \cdot (S_i - s(t', x)) \right. \\
&\quad - \frac{\mathbf{1}_i\{t\}}{\pi_i(t)} \cdot p(x) \cdot (S_i - s(t, x)) \\
&\quad \left. + \frac{\mathbf{1}_i\{t\}}{\pi_i(t)} \cdot S_i \cdot (\mathbf{1}\{Y_i \leq q(p(x), x)\} - p(x)) \right), \\
\text{cor}_-^L(\eta) &= -q(1 - 1/p(x), x) \left( \frac{\mathbf{1}_i\{t'\}}{\pi_i(t')} \cdot \frac{1}{p(x)} \cdot (S_i - s(t', x)) \right. \\
&\quad - \frac{\mathbf{1}_i\{t\}}{\pi_i(t)} \cdot (S_i - s(t, x)) \\
&\quad \left. - \frac{\mathbf{1}_i\{t'\}}{\pi_i(t')} \cdot S_i \cdot \left( \mathbf{1}\{Y_i \leq q(1 - 1/p(x), x)\} - 1 + \frac{1}{p(x)} \right) \right), \\
\text{cor}_+^U(\eta) &= q(1 - p(x), x) \left( \frac{\mathbf{1}_i\{t'\}}{\pi_i(t')} \cdot (S_i - s(t', x)) \right. \\
&\quad - \frac{\mathbf{1}_i\{t\}}{\pi_i(t)} \cdot p(x) \cdot (S_i - s(t, x)) \\
&\quad \left. + \frac{\mathbf{1}_i\{t\}}{\pi_i(t)} \cdot S_i \cdot (\mathbf{1}\{Y_i \leq q(1 - p(x), x)\} - 1 + p(x)) \right), \\
\text{cor}_-^U(\eta) &= -q(1/p(x), x) \left( \frac{\mathbf{1}_i\{t'\}}{\pi_i(t')} \cdot \frac{1}{p(x)} \cdot (S_i - s(t', x)) \right. \\
&\quad - \frac{\mathbf{1}_i\{t\}}{\pi_i(t)} \cdot (S_i - s(t, x)) \\
&\quad \left. - \frac{\mathbf{1}_i\{t'\}}{\pi_i(t')} \cdot S_i \cdot \left( \mathbf{1}\{Y_i \leq q(1/p(x), x)\} - \frac{1}{p(x)} \right) \right).
\end{aligned}$$

Then, the bias-corrected moment functions are  $g^L = \mathbf{1}\{p(x) \leq 1\} \cdot g_+^L(\eta) + \mathbf{1}\{p(x) > 1\} \cdot g_-^L(\eta)$  and  $g^U = \mathbf{1}\{p(x) \leq 1\} \cdot g_+^U(\eta) + \mathbf{1}\{p(x) > 1\} \cdot g_-^U(\eta)$ , where  $g_-^L(\eta) \equiv m_-^L(\eta) + \text{cor}_-^L(\eta)$ ,  $g_+^L(\eta) \equiv m_+^L(\eta) + \text{cor}_+^L(\eta)$ ,  $g_-^U(\eta) \equiv m_-^U(\eta) + \text{cor}_-^U(\eta)$ , and  $g_+^U(\eta) \equiv m_+^U(\eta) + \text{cor}_+^U(\eta)$ . For the estimation process, we transform the outcome using the former corrections. The transformed outcome is

$$\begin{aligned}
\tilde{Y}_{+,i}^L &= \begin{cases} Y_i S_i \mathbf{1}\{Y_i \geq q_{\hat{p}}\} + q_{\hat{p}} [S_i (\mathbf{1}\{Y_i \leq q_{\hat{p}}\} - \hat{p}) - \hat{p} (S_i - \hat{s}_i(t, x))] & \text{if } T_i = t, \\ Y_i S_i - q_{\hat{p}} [S_i - \hat{s}_i(t', x)] & \text{if } T_i = t', \end{cases} \\
\tilde{Y}_{-,i}^L &= \begin{cases} Y_i S_i + q_{1-1/\hat{p}} [S_i - \hat{s}_i(t, x)] & \text{if } T_i = t, \\ Y_i S_i \mathbf{1}\{Y_i \leq q_{1-1/\hat{p}}\} + q_{1-1/\hat{p}} \left[ \frac{1}{\hat{p}} (S_i - \hat{s}_i(t', x)) + S_i \left( \mathbf{1}\{Y_i \leq q_{1-1/\hat{p}}\} - \left(1 - \frac{1}{\hat{p}}\right) \right) \right] & \text{if } T_i = t', \end{cases} \\
\tilde{Y}_{+,i}^U &= \begin{cases} Y_i S_i \mathbf{1}\{Y_i \geq \hat{q}_{1-\hat{p}}\} + \hat{q}_{1-\hat{p}} [S_i (\mathbf{1}\{Y_i \leq \hat{q}_{1-\hat{p}}\} - (1 - \hat{p})) - \hat{p} (S_i - \hat{s}_i(t, x))] & \text{if } T_i = t, \\ Y_i S_i - \hat{q}_{1-\hat{p}} [S_i - \hat{s}_i(t', x)] & \text{if } T_i = t', \end{cases} \\
\tilde{Y}_{-,i}^U &= \begin{cases} Y_i S_i + \hat{q}_{1/\hat{p}} [S_i - \hat{s}_i(t, x)] & \text{if } T_i = t, \\ Y_i S_i \mathbf{1}\{Y_i \leq \hat{q}_{1/\hat{p}}\} + \hat{q}_{1/\hat{p}} \left[ \frac{1}{\hat{p}} (S_i - \hat{s}_i(t', x)) + S_i \left( \mathbf{1}\{Y_i \leq \hat{q}_{1/\hat{p}}\} - \frac{1}{\hat{p}} \right) \right] & \text{if } T_i = t'. \end{cases}
\end{aligned}$$

*Proof of Theorem 2.* Let  $g_s = E[\min(s(t', X), s(t, X))]$ . Under Assumption 4.3 and 4.4,  $g_s$ ,  $g^L$ , and  $g^U$  converge in probability and the first and second moments are bounded by Lemma A.7 and A.2 in Semenova (2023). Using the Delta method for  $\mu \equiv \left[ \frac{g^L}{g_s}, \frac{g^U}{g_s} \right]^\top$ , then

$$\sqrt{n} \begin{pmatrix} \frac{\hat{\tau}_s^L}{\hat{s}} - \tau_0^L \\ \frac{\hat{\tau}_s^U}{\hat{s}} - \tau_0^U \end{pmatrix} \xrightarrow{d} N(0, \mathbf{V})$$

where  $\tau_0^L = \frac{g^L}{g_s}$  and  $\tau_0^U = \frac{g^U}{g_s}$ . The asymptotic variance is  $\mathbf{V} = \mathbf{D}\Sigma\mathbf{D}^{-1}$  and

$$\mathbf{D} = \begin{pmatrix} 1 & 0 & -g^L/g_s^2 \\ 0 & 1 & -g^U/g_s^2 \end{pmatrix}, \quad \Sigma = (g - \bar{g})\mathbf{K}^+(g - \bar{g})^\top,$$

where  $g \equiv [g^L, g^U, g_s]^\top$ . ■

## B Appendix Tables and Figures

Appendix Table B1. Covariates Descriptions

Variable	Description
Past use	Minutes of computer usage from baseline survey
Age	Age of respondent
# of siblings	Number of siblings
# of young siblings	Number of younger siblings
Sex	1 if male
Father lives home	1 if father lives at home
Father works home	1 if father works at home
Mother works home	1 if mother works at home
Home phone	1 if household has a phone
Home power	1 if household has electricity
Home car	1 if household has a car
Home moto	1 if household has a motorcycle
Past week home	1 if respondent used a computer at home last week
Past week school	1 if respondent used a computer at school last week
Past week cafe	1 if respondent used a computer at a cafe last week
Past week friend house	1 if respondent used a computer at a friend's house last week
Past week other	1 if respondent used a computer elsewhere last week

Note: This table describes the covariates used in the empirical application.

Appendix Table B2. Spillover Bounds on Computer Use with Covariates (Parametric)

	Direct Effect		Spillover Effect		Overall Effect
	(1)	(2)	(3)	(4)	
$\hat{\tau}$	[0.19, 0.24]	[-0.40, -0.08]	[0.51, 0.57]	[-0.13, 0.10]	[-0.22, -0.07]
CI	(0.11, 0.35)	(-0.55, -0.05)	(0.33, 0.76)	(-0.18, 0.13)	(-0.30, -0.04)
(0,0)		X		X	X
(0,1)	X			X	X
(1,0)		X	X		X
(1,1)	X		X		X

Note: This table presents direct and spillover effects under the exposure mapping  $T_i = (D_i, \mathbf{1}\{\sum A_{ij}D_j > 0\})$ . First element of the exposure mapping  $T_i$  refers to the direct treatment status and the second whether at least one friend received treatment. Columns (1) and (2) display direct effects of winning the lottery for students with at least one treated friend and with none, respectively. Columns (3) and (4) show spillover effects of having a treated friend for students that won the lottery and did not, respectively. Last column displays overall effects comparing any exposure to the intervention to none. Spillover bounds, denoted by  $\hat{\tau}$ , are shown in brackets. The bounds use logistic and quantile regression on the first stage. [Imbens and Manski's \(2004\)](#) confidence interval with  $\bar{c} = 1.645$  are shown in parentheses below the bounds. For the confidence intervals, we use standard errors with network HAC variance (optimal bandwidth  $b = 2$ ).

Appendix Table B3. Spillover Bounds on Computer Use with Covariates (Post-Lasso)

	Direct Effect		Spillover Effect		Overall Effect
	(1)	(2)	(3)	(4)	
$\hat{\tau}$	[0.19, 0.24]	[-0.32, -0.05]	[0.24, 0.33]	[0.03, 0.35]	[-0.12, 0.06]
CI	(0.11, 0.34)	(-0.44, -0.03)	(0.16, 0.44)	(0.02, 0.48)	(-0.17, 0.07)
(0,0)		X		X	X
(0,1)	X			X	X
(1,0)		X	X		X
(1,1)	X		X		X

Note: This table presents direct and spillover effects under the exposure mapping  $T_i = (D_i, \mathbf{1}\{\sum A_{ij}D_j > 0\})$ . First element of the exposure mapping  $T_i$  refers to the direct treatment status and the second whether at least one friend received treatment. Columns (1) and (2) display direct effects of winning the lottery for students with at least one treated friend and with none, respectively. Columns (3) and (4) show spillover effects of having a treated friend for students that won the lottery and did not, respectively. Last column displays overall effects comparing any exposure to the intervention to none. Spillover bounds, denoted by  $\hat{\tau}$ , are shown in brackets. The bounds incorporate **post-lasso logistic and quantile regressions** on the first stage. [Imbens and Manski's \(2004\)](#) confidence interval with  $\bar{c} = 1.645$  are shown in parentheses below the bounds. For the confidence intervals, we use standard errors with network HAC variance (optimal bandwidth  $b = 2$ ).

Appendix Table B4. Spillover Bounds on Computer Use with Covariates (Auto ML)

	Direct Effect		Spillover Effect		Overall Effect
	(1)	(2)	(3)	(4)	
$\hat{\tau}$	[0.05, 0.23]	[-0.13, 0.26]	[0.18, 0.32]	[-0.37, 0.24]	[-0.15, 0.25]
CI	(0.04, 0.28)	(-0.16, 0.32)	(0.13, 0.41)	(-0.48, 0.32)	(-0.20, 0.34)
(0,0)		X		X	X
(0,1)	X			X	X
(1,0)		X	X		X
(1,1)	X		X		X

Note: This table presents direct and spillover effects under the exposure mapping  $T_i = (D_i, \mathbf{1}\{\sum A_{ij}D_j > 0\})$ . First element of the exposure mapping  $T_i$  refers to the direct treatment status and the second whether at least one friend received treatment. Columns (1) and (2) display direct effects of winning the lottery for students with at least one treated friend and with none, respectively. Columns (3) and (4) show spillover effects of having a treated friend for students that won the lottery and did not, respectively. Last column displays overall effects comparing any exposure to the intervention to none. Spillover bounds, denoted by  $\hat{\tau}$ , are shown in brackets. The bounds incorporate **automatic search of machine learning classifiers and gradient boosting quantile regression** on the first stage. [Imbens and Manski's \(2004\)](#) confidence interval with  $\bar{c} = 1.645$  are shown in parentheses below the bounds. For the confidence intervals, we use standard errors with network HAC variance (optimal bandwidth  $b = 2$ ).