Policy Targeting under Network Interference*

Davide Viviano †

First version: June, 2019
This Version: January, 2023

Abstract

This paper studies the problem of optimally allocating treatments in the presence of spillover effects, using information from a (quasi-)experiment. I introduce a method that maximizes the sample analog of average social welfare when spillovers occur. I construct semi-parametric welfare estimators with known and unknown propensity scores and cast the optimization problem into a mixed-integer linear program, which can be solved using off-the-shelf algorithms. I derive a strong set of guarantees on regret, i.e., the difference between the maximum attainable welfare and the welfare evaluated at the estimated policy. The proposed method presents attractive features for applications: (i) it does not require network information of the target population; (ii) it exploits heterogeneity in treatment effects for targeting individuals; (iii) it does not rely on the correct specification of a particular structural model; and (iv) it accommodates constraints on the policy function. An application for targeting information on social networks illustrates the advantages of the method.

Keywords: Causal Inference, Welfare Maximization, Spillovers, Social Interactions.
JEL Codes: C10, C14, C31, C54.

*This paper is a revised version of Chapter 2 of the author's dissertation. I am grateful to Graham Elliott, James Fowler, Paul Niehaus, Yixiao Sun, and Kaspar Wüthrich for advice and support, and Isaiah Andrews, Brendan Beare, Jelena Bradic, Guido Imbens, Toru Kitagawa, Michal Kolesar, Craig Mcintosh, Karthik Muralidharan, James Rauch, Fredrick Savje, Jesse Shapiro, Elie Tamer, Alex Tetenov, Ye Wang, the editor and anonymous referees for comments and discussion. I particularly thank Vikram Jambulapati for invaluable discussions at the beginning of this project. I also thank participants at the EGSC Conference at the University of Washington in St. Louis 2019, at the Causal Inference with Interactions conference at Cemmap, at the Young Economists' Symposium at UPenn 2020, at the Econometric Society World Congress 2020, at the ASSA meeting 2021, at the 6th Annual Conference of Network Science and Economics, at the North American Econometric Society summer meeting 2021, and at the EEA-ESEM 2021 conference. All mistakes are my own.

†Stanford Graduate School of Business, and Department of Economics, Harvard University. Correspondence: dviviano@fas.harvard.edu.

1 Introduction

Consider a policymaker who must use a quasi-experiment, such as an existing experiment or observational study, to design a decision rule (policy) that assigns treatments based on observable characteristics. The main challenge is that treating an individual may generate spillovers on her friends or neighbors. Spillover effects may, in turn, affect the design of the optimal policy. This paper studies the problem of allocating treatments in the presence of spillover effects to maximize welfare, using information from a quasi-experiment. Applications include welfare, cash-transfer programs, and information campaigns, among others.[1]

A (large) population of n individuals is connected in a *single* network. Treatments generate spillovers to neighbors in the network. Researchers randomly sample $n_e \ll n$ units in a (quasi)experiment and randomize treatments among sampled individuals and their neighbors (whereas the remaining units are not necessarily in the experiment).[2] They then collect sampled individuals' covariates, treatment assignments, outcomes, neighbors' covariates and assignments.[3] The population network is not necessarily observed. The goal is to estimate a treatment rule to deploy on the entire population. Consider the example of targeting information to increase insurance take-up in a region subject to environmental disasters (Cai et al., 2015). Using variation from experiment participants sampled from a random subset of villages in this region, we estimate whom to target in the entire region.

The first challenge for targeting is that the population network may be unobserved due to the cost associated with collecting network data on large populations. For instance, researchers may only observe neighbors' information about the experiment participants. Collecting network information from the individuals in the entire population, such as a region or country, is often costly or infeasible.[4] Motivated by this fact, I develop a method that does not require us observe the population network. I allow for arbitrary constraints on the policy space, such as informational constraints. A second challenge is treatment effects heterogeneity. I leverage the assumption that spillovers occur through the number of treated neighbors, as is often documented in applications, and allow for treatment effects heterogeneity in arbitrary individual characteristics (e.g., covariates and number of neighbors).[5]

[1] Some examples of relevant applications are Barrera-Osorio et al. (2011); Egger et al. (2019); Opper (2016); Zubcsek and Sarvary (2011); Bond et al. (2012). Spillover effects have been documented in development economics (Banerjee et al., 2013), social economics (Sobel, 2006), and medicine (Christakis and Fowler, 2010), among other settings.

[2] Namely, during the experimental intervention, the treatment status of the remaining units can be equal to the baseline intervention of no treatment with probability one.

[3] This is possible by sampling a random subset of individuals from the population, eliciting neighbors' information from such individuals, and collecting covariates and treatment assignments from their neighbors.

[4] See Breza et al. (2020) for a discussion of the cost associated with collecting network information.

[5] In particular, I assume potential outcomes are functions of individual and neighbors' treatment assign-

The proposed method, entitled Network Empirical Welfare Maximization (NEWM), estimates the welfare as a function of the policy using arbitrary estimators (e.g., based on machine-learning). It then solves an exact optimization procedure over the policy space. I interpret policy targeting as a treatment choice problem (Manski, 2004; Kitagawa and Tetenov, 2018; Athey and Wager, 2021), here studied in the context of network interference. I evaluate the method's performance based on its maximum regret, that is, the difference between the largest achievable welfare and the welfare from deploying the estimated policy.

From a theoretical perspective, this paper makes three contributions: (i) it derives the first set of guarantees on the regret for treatment rules with spillovers; (ii) it introduces an estimation procedure with fast convergence rates of regret[6] with machine-learning (non-parametric) estimators and networked units; and (iii) it shows that for a large class of policy functions, the optimization problem can be written as a mixed-integer linear program, solved using off-the-shelf optimization routines.

The analysis proceeds as follows. First, I discuss the identification of social welfare under interference. Identification relies on the unconfoundedness of treatment assignments, and of the sampling indicators. I then study semi-parametric estimators for the welfare and analyze the performance of the estimated policy. I show that under regularity conditions, the regret of the estimated policy scales at the rate $1/\sqrt{n_e}$, whenever the maximum degree of the network (i.e., the number of neighbors) is uniformly bounded.[7] If the maximum degree grows with the population size, the rate also depends on the degree. Finally, I derive maximin lower bounds that match the upper bound. Throughout the analysis, I do not impose assumptions on the (joint) distribution of covariates.

A condition for these results to hold is that the optimization procedure achieves the in-sample optimum. I guarantee it by casting the problem in a mixed-integer linear program. I show that a linear representation of spillover effects in the objective function can be achieved

ments (but not neighbors' identity), the number of neighbors, arbitrary individual characteristics that are observable in the experiment but may not be observed on the target sample (e.g., covariates, centrality measures, or summary statistics of neighbors' covariates), and exogenous unobservables. This reduced form restriction on the spillover mechanism assumes that interference is local and anonymous. Models consistent with this restriction are models of exogenous and anonymous interference; see, for example, Manski (2013). For instance, Cai et al. (2015) leverage a two-stage experimental design to show "the network effect is driven by the diffusion of insurance knowledge" (i.e., treatment) "rather than purchase decisions" (i.e., outcome) (Cai et al., 2015, abstract), consistently with the model proposed in this paper. Other examples of empirical applications using models consistent with anonymous and exogenous interference include Sinclair et al. (2012); Duflo et al. (2011); Muralidharan et al. (2017), where for the third reference, networks can be considered groups of classrooms with units within each classroom being fully connected. Athey et al. (2018) provide a framework for testing local and anonymous spillovers.

[6]Such rates depend on the *product* of the rate of the estimated propensity score and conditional mean function, extending previous results with *i.i.d.* data to network interference (e.g., Farrell, 2015).

[7]Examples of applications with a small degree include Cai et al. (2015), the Add Health Study, and Jackson et al. (2012) among others. For theoretical models with bounded degree see De Paula et al. (2018).

by introducing additional linear constraints and binary decision variables.

The derivations present several challenges: (i) individuals depend on neighbors' assignments that we control through contraction inequalities; (ii) statistical dependence invalidates standard symmetrization arguments (Wainwright, 2019); and (iii) in the presence of observational studies with networks, machine-learning estimators may present non-vanishing bias even when existing methods are employed (Chernozhukov et al., 2018). For (iii), I introduce a novel cross-fitting algorithm for networked observations and characterize its properties.

I study the numerical properties of the method using data from Cai et al. (2015) and design a policy that informs farmers about insurance benefits to increase insurance take-up. The NEWM method leads to (out-of-sample) improvements in insurance take-up up to thirty percentage points to methods that ignore network effects (Kitagawa and Tetenov, 2018; Athey and Wager, 2021). I obtain these improvements despite not using network information in the design of the policy. Finally, I present several extensions, including trimming when individuals present poor overlap due to a large maximum degree, different target and sampled populations, and spillovers over the non-compliance (in the Appendix).

This paper builds on the growing literature on statistical treatment choice (Kitagawa and Tetenov, 2018, 2019; Athey and Wager, 2021; Mbakop and Tabord-Meehan, 2016; Armstrong and Shen, 2015; Bhattacharya and Dupas, 2012; Hirano and Porter, 2009; Stoye, 2009, 2012; Tetenov, 2012; Zhou et al., 2018), and classification (Elliott and Lieli, 2013; Boucheron et al., 2005, among others). Different from previous references, here I estimate the policy when treatments generate spillovers. This paper is the first to study the properties of targeting on networks in the context of the empirical welfare maximization literature.

A conceptual difference from the *i.i.d.* setting with single and multi-valued treatments as in Kitagawa and Tetenov (2018), Zhou et al. (2018) is that here individuals depend on neighbors' assignments, whereas treatments are individual-specific. This structure permits the population network not to be observable, with the complexity of the function class bounded using the maximum degree. The second difference is that individuals exhibit dependence and arguments based on *i.i.d.* sampling such as symmetrization failure. Optimization differs because individuals depend on neighbors' treatments.

This paper connects the literature on statistical treatment choice with that on targeting on networks. I provide an overview below and a more extensive discussion in Section 2.5.

The influence-maximization literature mostly focuses on detecting the most influential "seeds" based on particular notions of centrality, motivated by a particular model. See Bloch et al. (2017) for a review. Recent advances include Jackson and Storms (2018), Akbarpour et al. (2018), Banerjee et al. (2019), Banerjee et al. (2014), Galeotti et al. (2020) in economics, and Kempe et al. (2003), Eckles et al. (2019), among others in computer science. This paper

differs in (i) its approach because I leverage experimental variation to construct policies that maximize the *empirical* welfare (instead of policies justified by game theoretic structures);[8] (ii) setup because I allow for constraints on the policy class and heterogeneity in treatment effects, within a local interference framework. Su et al. (2019) study first-best policies *without* constraints on the policy and for linear models. I do not impose such structural assumptions. The presence of constraints (and possible infeasibility of the first-best policy) justifies the regret analysis in the current paper. Laber et al. (2018) consider a Bayesian model whose estimation relies on intensive Monte Carlo methods and the correct model specification.

This paper also connects to the literature on social interaction (Manski, 2013; Manresa, 2013; Auerbach, 2019), and causal inference under interference (Liu et al., 2019; Li et al., 2019; Hudgens and Halloran, 2008; Goldsmith-Pinkham and Imbens, 2013; Sobel, 2006; Sävje et al., 2021; Aronow and Samii, 2017). The exogenous and anonymous interference condition is most closely related to Leung (2020). However, knowledge of treatment effects is not sufficient to construct welfare-optimal treatment rules in the presence of either (or both) constraints on the policy functions or treatment effects heterogeneity. Additional references include Bhattacharya et al. (2019) and Wager and Xu (2021), who study pricing with social interactions, through partial identification and sequential experiments, respectively. Here, instead, I study empirical welfare maximization for individualized treatment rules. See Kline and Tamer (2020) and Graham and De Paula (2020) for further references.[9]

Finally, more recent works that study targeting in new directions include Kitagawa and Wang (2020) in the context of a parametric model of disease diffusion, Ananth (2021) in settings with an observed network of the target population, and Viviano (2020) in the context of sequential experiments.

The paper is organized as follows. Section 2 presents the problem setup and main conditions. Estimation and theoretical analysis is contained in Section 3. Section 4 and online Appendix B present extensions. Section 5 contains an application. Section 6 concludes. Appendix A (at the end of the main text) presents a practical guide to implement the algorithm, online Appendix C a numerical study and online Appendix D theoretical derivations.

[8] Measures of centrality are typically justified by a particular game of strategic interactions (e.g., Galeotti et al., 2020), and validated in experiments against a given benchmark policy (e.g., Banerjee et al., 2014). Here I instead use experimental variation to directly learn the best policy from a large class.

[9] Further literature studying spillovers includes that on optimally allocating individuals across *independent* groups (Li et al., 2019; Graham et al., 2010; Bhattacharya, 2009). This problem differs from ours for several reasons: (i) policy functions denote group-assignment mechanisms instead of binary treatment allocations, inducing a different definition and identification of welfare; (ii) the allocation does not allow for constraints; and (iii) the authors assume many small independent clusters.

2 Problem description

In this section, I introduce the notation and problem setup. Practitioners may refer to Algorithm 1 in Appendix A for a user-friendly description of the steps of the procedure.

2.1 Setup and overview

Consider a population of n individuals connected under an adjacency matrix A. Each individual is associated with an arbitrary vector of characteristics $Z_i \in \mathcal{Z}$ and a binary indicator $D_i \in \{0,1\}$ indicating the treatment assignment in an experiment. Let

$$A \in \mathcal{A}_n \subseteq \{0,1\}^{n\times n}, \quad N_i = \Big\{ j \in \{1,\cdots,n\} \setminus \{i\} : A_{i,j} = 1 \Big\}, \quad Z = (Z_i)_{i=1}^n, \quad D = (D_i)_{i=1}^n,$$

where $\mathcal{A}_n$ denotes the set of symmetric and unweighted adjacency matrices, N_i denotes the friends of individual i, and $|N_i|$ denotes the degree of i. We impose no conditions on Z.

Following Abadie et al. (2020), I define $R_i \in \{0,1\}$ as a random variable indicating whether individual i's (and neighbors') relevant characteristics are sampled during the experiment, and $R_i^f = 1\Big\{ \sum_{k\neq i} A_{i,k} R_k > 0 \Big\}$ as the indicator of whether at least one neighbor is sampled. Researchers collect

$$\Big[R_i \Big(Y_i, Z_i, D_i, N_i, Z_{k\in N_i}, D_{k\in N_i} \Big), R_i \Big]_{i=1}^n, \quad R_i \Big| A, Z \sim_{i.i.d.} \text{Bern}(n_e/n), \tag{1}$$

where Y_i denotes the post-treatment outcome in the experiment, and n_e the expected number of sampled individuals.[10] Sampled units and their neighbors (but not necessarily the other units in the population) are assigned treatments in the experiment ($D_i = 1$) with positive probability. Section 2.2 presents a complete formalization.

Section 2.4 formalizes the policy-targeting exercise: once the experiment is completed, the researcher's goal is to design a treatment rule that a policymaker will deploy on the *entire* population. I consider settings where researchers only observe a (small) subset of individuals ($n_e \ll n$), and the adjacency matrix A may remain unobserved to the researchers.

Finally, in Section 3, I estimate a policy with guarantees valid for finite (possibly large) n and characterize convergence rates as $n, n_e \to \infty$. Convergence rates are with respect to a sequence of data-generating processes indexed by n, each with a *single* network $A \in \mathcal{A}_n$, where I explicitly condition on $A \in \mathcal{A}_n, Z \in \mathcal{Z}^n$ unless otherwise specified.[11]

[10] Similar approaches to measure uncertainty in the context of statistical inference have also been adopted by De Paula et al. (2018). This information can be obtained by sampling a random subset of individuals from the population and then collecting information from sampled units and their neighbors. See Kolaczyk (2009) for a discussion on sampling methods with networks.

[11] A *special* case of an asymptotic framework with a single network are settings where the network is

2.2 Data-generating process and experiment

With interference, unit i's outcome depends on its own and other units' treatment. In full generality, I can write $Y_i = \tilde{r}_n(i, D, A, Z, \varepsilon_i)$ for some unobserved random variables ε_i capturing uncertainty in potential outcomes, and unknown $\tilde{r}_n(\cdot)$.

Assumption 2.1 (Interference)**.** For $i \in \{1, \cdots, n\}$, let

$$Y_i = r\Big(D_i, T_i, Z_i, |N_i|, \varepsilon_i\Big), \quad T_i = g_n\Big(\sum_{k \in N_i} D_k, Z_i, |N_i|\Big), \tag{2}$$

for some function $r(\cdot)$ unknown to the researcher, and function $g_n(\cdot) : \mathbb{Z} \times \mathcal{Z} \times \mathbb{Z} \mapsto \mathcal{T}_n \subseteq \mathbb{Z}$, known to the researcher, with $g_n(0, Z_i, |N_i|) = 0$ almost surely, and unobservables ε_i.

Under Assumption 2.1, outcomes depend on (i) the number of first-degree neighbors ($|N_i|$), (ii) the number of first-degree treated neighbors (or a function of this, T_i), and (iii) individual's treatment status (D_i), observables (Z_i), and unobservables (ε_i). Assumption 2.1 states that interactions are anonymous (Manski, 2013), and spillovers occur within neighbors. Heterogeneity occurs through the dependence with Z_i and $|N_i|$. The model relates to Leung (2020), and Athey et al. (2018) provide methods to test anonymous and local interference.

Here, $r(\cdot)$ is unknown and $g_n(\cdot)$ is known and characterizes how individuals depend on neighbors' treatments – that is, the exposure mapping (Aronow and Samii, 2017); $g_n(0, \cdot) = 0$ is without loss of generality, because $r(\cdot)$ also depends on $(Z_i, |N_i|)$. The function g_n depends on n because its support $\mathcal{T}_n$ can vary with n. For example, g_n can be equal to the number of treated neighbors $T_i = \sum_{k \in N_i} D_k$, and the degree can grow with n. This scenario is the most agnostic one because r is unknown and therefore equivalent to $g_n(\cdot)$ being unknown. Alternatively, $g_n(\cdot)$ can be equal to a step function of the share of treated neighbors (Sinclair et al., 2012). The size of $\mathcal{T}_n$ affects treatments' overlap discussed below.

Assumption 2.2 ((Quasi)experiment)**.** For $i \in \{1, \cdots, n\}$, $R_i^f = 1\Big\{\sum_k A_{i,k} R_k > 0\Big\}$, the following holds:

(i) $D_i = f_D\Big(Z_i, R_i, (1 - R_i)R_i^f, \varepsilon_{D_i}\Big)$, for $\varepsilon_{D_i}|A, Z \sim_{i.i.d.} \mathcal{L}$, with $\varepsilon_{D_i} \perp \Big((\varepsilon_j)_{j=1}^n, (R_j)_{j=1}^n\Big)$, for some function $f_D(.)$ and distribution $\mathcal{L}$ (known in an experiment and to be estimated in a quasi-experiment);

(ii) $P(D_i = 1|Z_i, R_i = 1), P(D_i = 1|Z_i, R_i = 0, R_i^f = 1) \in (\gamma, 1 - \gamma)$ almost surely, for some $\gamma \in (0, 1)$, and for all $t \in \mathcal{T}_n$, $P\Big(T_i = t|Z_{k \in N_i}, |N_i|, R_{k \in N_i}, R_i = 1\Big) \geq \delta_n$ almost surely, for some $\delta_n \in (0, 1)$;

block diagonal and can be partitioned into independent components. Our framework does not require this assumption.

(iii) $R_i|A, Z \sim_{i.i.d.} \text{Bern}(n_e/n)$ with $n_e/n = \alpha \in (0, 1)$.

Condition (i) states the treatment is randomized in the experiment on observables Z_i, which may also contain network information, and possibly also on the indicator R_i. If individuals are not sampled in the experiment ($R_i = 0$), D_i can also depend on whether *at least one* friend is sampled (e.g., researchers collect neighbors' information and then randomize treatments across participants and their neighbors). Figure 1 presents an illustration.

Condition (ii) imposes positive overlap for sampled units and their friends, but not necessarily for the remaining units who are not sampled and are not friends of sampled units.[12] For example, the treatment of those units who do not participate in the experiment and whose friends do not participate in the experiment *can* be equal to the baseline value $D_i = 0$ almost surely, whereas it is randomized with positive probability for the experiment participants and their friends. Here, δ_n denotes the overlap constant of the neighbors' treatments of the sampled individuals. It depends on n, because the support of the exposure mapping T_i may vary with n. Section 2.3 imposes restrictions on δ_n.

Condition (iii) states that selection indicators R_i are exogenous. The expected number of sampled individuals n_e is proportional to n for expositional convenience only.[13]

Assumption 2.3 (Unobservables)**.** For all $i \in \{1, \cdots, n\}$,

(A) $\varepsilon_i \perp (R_j)_{j=1}^n \Big| A, Z$;

(B) $\varepsilon_i \Big| A, Z \sim \mathcal{U}_{Z_i,|N_i|}$ for unknown distributions $\mathcal{U}_{z,l}, z \in \mathcal{Z}, l \in \mathbb{Z}$;

(C) $\varepsilon_i \perp (\varepsilon_j)_{j \notin N_i \cup \{N_k, k \in N_i\}} \Big| A, Z$;

(D) $\mathbb{E}\Big[\sup_{d\in\{0,1\},t\in\mathbb{Z}} |r(d, t, Z_i, |N_i|, \varepsilon_i)|^3 \Big| A, Z\Big] \leq \Gamma^2$, almost surely, for some unknown $\Gamma < \infty$.

Condition (A) states that the sampling does not depend on unobservables. Condition (B) states that unobservables are identically distributed, conditional on the same individual covariates and number of friends, and conditionally independent of A and other units' characteristics. Condition (B) implies network exogeneity, attained if, for example, two individuals

[12] Positive overlap in (ii) implies that for sampled units or their neighbors, they receive treatments with positive probability. Positive overlap of individual treatments only needs to hold for those individuals who either are selected in the experiment ($R_i = 1$) or who have at least one friend selected in the experiment. Positive overlap of the neighbors' treatments ($P(T_i = t|\cdot) > \delta_n$) only needs to hold for sampled units ($R_i = 1$). Randomizing treatments among participants and their friends justifies the overlap restriction.

[13] All results hold if n_e is not proportional to n, and instead, $n_e = n^\rho$ for some $\rho < 1$. In this case, we would only need to replace the right-hand side $\mathcal{O}(n^{1/2-\xi})$ with $\mathcal{O}(n^{(1/2-\xi)\rho})$ in Assumption 2.4.

form a link based on observable characteristics and exogenous unobservables.[14] Condition (B) guarantees that the individual conditional mean function in Equation (3) is the same across units. Condition (C) states that unobservables are independent across individuals who do not share a common neighbor, similarly to Leung (2020). Condition (C) is consistent with a first-degree interference model as shown in Example 2.1. Finally, Condition (D) is a bounded moment assumption.

Our method can accommodate scenarios where (B) and (C) fail. I will *not* assume Condition (B) in settings where the individual treatment probabilities are either known or estimated parametrically.[15] In Section 4.2, I relax (C) and allow higher-order dependence.

Under Assumptions 2.2 and 2.3, let

$$\begin{aligned} m(d,t,z,l) &= \mathbb{E}\Big[r(d,t,z,l,\varepsilon_i)\Big|Z_i=z,|N_i|=l,T_i=t,D_i=d\Big] \\ e_n(d,t,\mathbf{x},\mathbf{u},z,l) &= P\Big(D_i=d,T_i=t\Big|Z_{k\in N_i}=\mathbf{x},R_{k\in N_i}=\mathbf{u},Z_i=z,R_i=1,|N_i|=l\Big) \end{aligned} \tag{3}$$

define the conditional mean and propensity score for sampled units ($R_i = 1$), respectively.[16] I will refer to $e_n(\cdot)$ as $e(\cdot)$. Finally, note that this paper does not impose *any* condition on the (joint) distribution of covariates.

Example 2.1 (Two-degree dependence)**.** Suppose that each individual is associated with *i.i.d.* unobservables η_i and $Y_i = \tilde{r}\Big(D_i, T_i, Z_i, |N_i|, \eta_i, \sum_{k\in N_i}\eta_k\Big)$ for some unknown function $\tilde{r}(\cdot)$. Then Assumption 2.1 and 2.3 hold with $\varepsilon_i = \Big(\eta_i, \sum_{k\in N_i}\eta_k\Big)$.

2.3 Network topology and overlap

The informativeness of the results in the next section requires restrictions on the network density and how this interacts with the overlap constant δ_n. I control the network's density through the maximum degree. Let $\mathcal{N}_n = \max_{i\in\{1,\cdots,n\}}|N_i| + 2$.

Assumption 2.4 (Maximum degree)**.** Assume $\mathcal{N}_n^{3/2}\log(\mathcal{N}_n)/\delta_n = \mathcal{O}\Big(n^{1/2-\xi}\Big)$, almost surely for some (unknown) $\xi \in (0, 1/2]$.

Assumption 2.4 bounds the ratio of the maximum degree and the overlap constant and trivially holds in networks with bounded degree.

[14] Network exogeneity is often explicitely stated in settings with random network formation. Examples include Leung (2020) (see its Appendix A.3, for strategic models of interactions), and Li and Wager (2022) for graphon models. See also Goldsmith-Pinkham and Imbens (2013) for a discussion.

[15] Identification in the absence of (B) relies on the correct specification of the propensity score, and on the exogeneity of the sampling indicators. These settings are discussed in Lemma 2.1, and Theorems 3.1, 4.2.

[16] Assumption 2.3 (B) guarantees $m(\cdot)$ is identical across units, and similarly, Assumption 2.2 for $e_n(\cdot)$. Here $e(\cdot)$ also depends on n because $g_n(\cdot)$ and its support might depend on n. $m(\cdot)$ does not depend on n because the *marginal* distribution of ε_i is the same for any n under Assumption 2.3 (B).

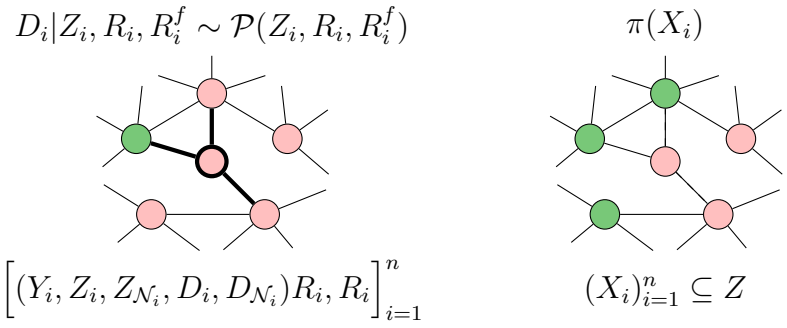

Figure 1: Example of the experiment (left-hand-side figure) and policy targeting exercise in Section 2.4 (right-hand-side figure). Green dots denote treated units, and pink dots denote untreated ones. In the first step, researchers run (or observe data from) an experiment on a (small) subset of individuals, here the black-tick unit. The treatment of such a unit and her friends is randomized with some positive probability, whereas the treatment of the other units can have arbitrary distributions (e.g., equal to the baseline value $D_i = 0$ almost surely if such units are not in the experiment). Researchers observe the vector of outcome, treatment, neighbors, treatments, and covariates of sampled units $((Y_i, Z_i, Z_{\mathcal{N}_i}, D_i, D_{\mathcal{N}_i})R_i)$, as well as the the identity of whom they sample (R_i). Researchers then design a treatment allocation $\pi(X_i)$ for the entire population using information X_i, a subset of Z_i.

Example 2.2 (Bounded degree)**.** Suppose that $\mathcal{N}_n \leq c_0$ almost surely for a constant c_0 independent of n. Then Assumption 2.4 holds with $\xi = 1/2$ almost surely.

Example 2.2 holds for many economic models, for instance, the ones considered in De Paula et al. (2018). In De Paula et al. (2018), the maximum degree is bounded by a finite constant independent of the network size. Economic applications with a bounded degree include Cai et al. (2015), the Add Health Study, and Jackson et al. (2012).[17]

Importantly, Assumption 2.4 allows for unbounded degree. In the presence of a growing degree, convergence rates in Section 3 will depend on the degree and δ_n.

Example 2.3 (Unbounded degree)**.** Suppose $\mathcal{N}_n = \mathcal{O}(n^{1/3})$, and for any n, $T_i = 1\left\{\sum_{k\in N_i} D_k/|N_i| > 1/2\right\}$, such that $P\Big(T_i = 1|Z_{k\in N_i}, R_{k\in N_i}, |N_i|, R_i = 1\Big) \in (\lambda, 1-\lambda)$, for some $\lambda \in (0, 1)$. Then Assumption 2.4 holds for $\xi < 1/2$.

Remark 1 (Assumption 2.1, overlap and trimming)**.** Additional restrictions on $g_n(\cdot)$ (and T_i) can improve overlap. For example, suppose that for some ordered τ_1, τ_2, τ_3,

$$r(d,t,z,l,e) = \begin{cases} \bar{r}_1(d,z,l,e) \text{ if } t/l \leq \tau_1 \\ \bar{r}_2(d,z,l,e) \text{ if } \tau_1 < t/l \leq \tau_2 \\ \bar{r}_3(d,z,l,e) \text{ if } \tau_2 < t/l \leq \tau_3 \end{cases} \tag{4}$$

[17] See https://addhealth.cpc.unc.edu/, Footnote 37, Page 1879.

for some possibly unknown functions $\bar{r}_1, \bar{r}_2, \bar{r}_3$. In this setting, the exposure mapping is a step-function in the share of treated neighbors (with finite support).

Although the finite-support assumption for T_i is not necessary, Assumption 2.4 requires that the overlap constant $\delta_n \to 0$ at a slower rate than $1/\sqrt{n}$. Section 4.1 presents theoretical results when Assumption 2.4 *fails* – that is, $\delta_n \to 0$ at a faster rate in n. □

2.4 Policy targeting

Once the experiment is concluded, a social planner will design a treatment mechanism that maximizes average social welfare in the *entire* population $i \in \{1, \cdots, n\}$, with adjacency matrix and covariates (A, Z), as described in Figure 1. Without loss of generality, partition $Z_j = \left[X_j, \tilde{X}_j\right]$, for two vectors $(X_j, \tilde{X}_j)$, $X_j \in \mathcal{X} \subseteq \mathcal{Z}$. The policymaker observes from the *entire* population

$$X = (X_j)_{j=1}^n, \quad X_j \in \mathcal{X},$$

denoting an arbitrary subset of individuals' characteristics. Examples include census or arbitrary network statistics *when* available to the policymaker. She designs a policy such that:

(1) Individuals may be treated differently, depending on observable characteristics;

(2) The assignment mechanism must be easy to implement without requiring knowledge of the population network A;

(3) The assignment mechanism can be subject to (economic or ethical) constraints.

I therefore consider an *individualized* treatment assignment $\pi : \mathcal{X} \mapsto \{0, 1\}, \pi \in \Pi_n(X) \subseteq \Pi$, where $\Pi_n(X)$ denotes the set of constraints on π, a subset of a given function class Π.[18] The map amounts to a partition of $\mathcal{X}$. The policy $\pi \in \Pi_n$ satisfies the conditions (1), (2), and (3). The policy can be implemented in an online fashion, and it does not require the network of the entire population if not available. Because I impose no restrictions on X_i, individual covariates can contain network statistics if available to the policymaker.

I define utilitarian welfare as the expected outcome once I assign treatments with policy $\pi(X_j)$ in the *entire* (finite) population. Under Assumption 2.1, welfare is defined as

$$W_{A,Z}(\pi) = \frac{1}{n}\sum_{i=1}^{n} \mathbb{E}\left[r\Big(\pi(X_i), T_i(\pi), Z_i, |N_i|, \varepsilon_i\Big)\Big|A, Z\right], \quad T_i(\pi) = g_n\Big(\sum_{k\in N_i} \pi(X_k), Z_i, |N_i|\Big). \quad (5)$$

[18] Here, $\Pi_n(X)$ may also depend on population characteristics X, whenever researchers observe X for the entire population (e.g., through census data). For example, in settings where X is observed, Π_n may require $\pi \in \Pi$, *and* the capacity constraint $\frac{1}{n}\sum_{i=1}^n \pi(X_i) \leq K$ holds for a constant K.

The definition of welfare implies no carryovers occur from the previous experimental intervention once we deploy policy π on the population.[19] I collect the assumptions below and defer their discussion and extensions in the remarks below.

Assumption 2.5 (Experiment and targeting)**.** The researcher observes $\left[R_i\left(Y_i, D_i, Z_i, D_{N_i}, Z_{N_i}\right), R_i\right]_{i=1}^n$ from an experiment as in Equation (1) and $X = (X_i)_{i=1}^n$ from the population, for arbitrary $X_i \in \mathcal{X} \subseteq \mathcal{Z}$. She then constructs a (data-dependent) policy $\hat{\pi}_n : \mathcal{X} \mapsto \{0,1\}, \hat{\pi}_n \in \Pi_n(X) \subseteq \Pi$, that a policymaker implements on the entire population $i \in \{1, \cdots, n\}$. Here, Π is a class of pointwise measurable functions[20] with finite VC dimension $\text{VC}(\Pi)$.[21] Each $\pi \in \Pi$, generates welfare $W_{A,Z}(\pi)$ in Equation (5).

I refer to $\Pi_n(X)$ as Π_n. Assumption 2.5 formalizes the discussion above and it also imposes restrictions on the complexity of the function class Π as in previous literature (e.g., Kitagawa and Tetenov, 2018).[22] Ideally, one would like to learn

$$\pi_n^* \in \arg\max_{\pi \in \Pi_n} W_{A,Z}(\pi). \tag{6}$$

However, π_n^* depends on $m(\cdot)$ and A, both unobserved. I replace the oracle problem in Equation (6) with its sample analog, and compare the estimated policy to π_n^*. I discuss identification below and defer estimation to the following section.[23]

Lemma 2.1 (Identification)**.** *Let Assumptions 2.1, 2.2, and (A) in 2.3 hold. For any* $\pi \in \Pi$

$$W_{A,Z}(\pi) = \frac{1}{n_e} \sum_{i=1}^{n} \mathbb{E}\left[R_i Y_i \frac{1\{T_i(\pi) = T_i, \pi(X_i) = D_i\}}{e(\pi(X_i), T_i(\pi), Z_{k\in N_i}, R_{k\in N_i}, Z_i, |N_i|)} \middle| A, Z\right]. \tag{7}$$

Proof of Proposition 2.1. The proof is in Appendix D.3.1. □

Lemma 2.1 illustrates how we can identify welfare using information from participants and is at the basis of our approach in Section 3. Lemma 2.1 leverages information from the

[19] In practice, carryovers do not occur if either the policy π is deployed sufficiently far in time from the experimental intervention or if the experiment run by researchers has a neglible effect on the entire population. See Athey and Imbens (2018) for a discussion on the no carryovers assumption.

[20] Pointwise measurability can be replaced by the measurability of each $\pi \in \Pi_n$. Under lack of pointwise measurability, the supremum over Π should be replaced by the lattice supremum as defined in Hajłasz and Malỳ (2002), corresponding to the supremum over a countable sub-family of Π.

[21] The VC dimension denotes the cardinality of the largest set of points that the function π can shatter. The VC dimension is a common measure of complexity (Devroye et al., 2013).

[22] Examples satisfying Assumption 2.5 include threshold-crossing rules or trees (Zhou et al., 2018).

[23] Identification here uses information from the propensity score. The propensity score defines the treatment exposure probabilities in the spirit of Imbens (2000), here taking into account individual and neighbors' assignments and covariates. I condition on neighbors' covariates because the number of treated neighbors $\sum_{k\in N_i} \pi(X_k)$ depends on the array of covariates $X_{k\in N_i}$, via the policy function π.

propensity score and exogeneity of the indicators R_i. It does not impose conditions on the outcomes' conditional mean functions (Assumption 2.3 (B)).

Remark 2 (Identificatiion of the propensity score)**.** Here, $e(\cdot)$ can be identify because

$$P\Big(D_i = d, \sum_{k\in N_i} D_k = t \Big| Z_{k\in N_i} = \mathbf{x}, R_{k\in N_i} = \mathbf{u}, Z_i = z, R_i = 1, |N_i| = l\Big)$$

$$= P\Big(D_i = d | Z_i = z, R_i = 1\Big) \sum_{w_1,\cdots,w_l : \sum_v w_v = t} \prod_{k=1}^{l} P\Big(D_{N_i^{(k)}} = w_k \Big| Z_{N_i^{(k)}} = \mathbf{x}^{(k)}, R_{N_i^{(k)}} = \mathbf{u}^{(k)}, R_{N_i^{(k)}} = 1\Big). \tag{8}$$

for $d \in \{0,1\}, s \in \mathbb{Z}, t \leq l$, where $\mathbf{x}^{(k)}$ indicates the k^{th} entry of $\mathbf{x}$, and similarly for $\mathbf{u}^{(k)}$. The expression only depends on marginal treatment probabilities, identified from the experiment.[24] $e(\cdot)$ can then be written as a function of marginal treatment probabilities.[25] □

Remark 3 (Non-reversible treatments)**.** Welfare here is defined conditional on the adjacency matrix and matrix of covariates, where the policy π can change the treatment of each unit in the population. Additional restrictions on the policy space may arise in this setting, if treatments are non-reversible (i.e., the policymaker must also treat those individuals treated in the experiment). In this case, we should encode such constraints in the policy function, choosing treatment rules of the form $\pi(X_i)(1 - D_i) + D_i$ (i.e., treatment is one if $D_i = 1$ and is $\pi(X_i)$ otherwise). Our results extend to this setting as discussed in Appendix B.1. □

Remark 4 (Different populations)**.** An interesting scenario is when individuals treated by the policymakers are drawn from a population *different* from the one eligible for the experiment (for example, we sample individuals from a country and we would like to implement the policy in a different country). Section 4.3 presents an extension when the target population's distribution is known, and Appendix B.4 when unknown. □

Remark 5 (Comparison with global treatment rules)**.** Whenever the network from the entire population A *is observed*, policymakers may consider a global policy $\tilde{\pi}_i(X_i, A)$ that also depends on $A \in \mathcal{A}_n$. Here, network statistics should be included in X_i if observable (e.g., measures of centrality as in Bloch et al., 2017), with policies $\pi(X_i)$. In either case optimization takes into account spillovers for the design of the best policy.

Although global assignments can be more flexible, I do not consider a global assignment rule for the following reasons: (i) it requires collecting network data from the entire population; and (ii) the complexity of the global function class can grow with the *population size*

[24] Note that if $P(D_i = 1|Z_i, R_i = 0, R_i^f = 1) \neq P(D_i = 1|Z_i, R_i = 1)$ (i.e., treatments of the neighbors of experiment participants is assigned differently than treatment to participants), $P(D_i = 1|Z_i, R_i = 0, R_i^f = 1)$ is identified because we observe the treatment assignments of the neighbors of sampled units.

[25] The reason is that $P(T_i = t|\cdot)$ is a sum of probabilities in Equation (8), for any $g_n(\cdot)$ in Assumption 2.1.

n, leading to overfitting.[26] The individualized assignment avoids (i) and (ii) and accommodates settings where the target population is (much) larger than the *sample* size, similarly to settings considered by Manski (2004). □

Remark 6 (Additional extensions)**.** One possible extension is to let R_i depend on Z_i. In this setting, identification follows similarly, after dividing each summand in Lemma 2.1 by $P(R_i = 1|Z_i)$. Our results follow similarly for $P(R_i = 1|Z_i) = \alpha(Z_i)n_e/n$, for $\alpha(z) \in (0, 1)$ bounded away from zero. A different extension includes spillovers over the individual compliance, discussed in Appendix B.3. Finally, higher-order interference follows similarly to what discussed here once we control for higher-order-degree neighbors. □

2.5 Spillovers in the related literature

I pause here to compare our framework and assumptions with existing models of spillovers.

The framework I present most closely connects to the literature on causal inference under interference, including, among others, Hudgens and Halloran (2008), Athey and Imbens (2018), Manski (1993), and the model in Leung (2020) in particular. The model in this paper allows for arbitrary heterogeneity in the number of friends, $|N_i|$, observables Z_i, and the exposure mapping T_i as a function of the number of treated friends. We can therefore achieve semi-parametric identification of policy effects in the spirit of the literature on (augmented) inverse probability weights (e.g., Tchetgen and VanderWeele, 2012; Aronow and Samii, 2017).

Interestingly, I do not require restrictions on observables Z_i, which can be arbitrarily dependent, and on the network A, other than restrictions on the maximum degree. This approach is possible once I explicitly incorporate sampling uncertainty as in Abadie et al. (2020) for policy learning. Similar restrictions on the degree are often imposed to obtain concentration of the estimated causal effects (e.g., Sävje et al., 2021). Here, the maximum degree restrictions together with the local interference assumption allow me also to control the complexity of the policy function class, characterized by the direct and spillover effects $\left(\pi(X_i), \sum_{k\in N_i} \pi(X_k)\right), \pi \in \Pi$.

I draw connections to the literature on information diffusion and optimal seeding. This literature mostly studies models where informed individuals transmit information to neigh-

[26] For instance, for a global function class obtained via unions and intersection of k_n half-planes, the VC dimension of the function class is of order $k_n \log(k_n)$ (Csikós et al., 2019). For a global policy, k_n (and the VC-complexity) can grow at a fast rate in n. As a result, guarantees with a global function class can be obtained only in settings with a small target population whose size does not grow with n_e as in settings studied by Ananth (2021). This differs from the large target population scenario considered here. In the absence of policy constraints (Π in our notation), an alternative approach is to impose modeling assumptions as in Kitagawa and Wang (2020), which, however, requires correct model specification. Here, we allow for policy constraints (e.g., A is not observed) and semi-parametric identification.

bors sequentially over multiple periods (Banerjee et al., 2013, 2014; Akbarpour et al., 2018; Kempe et al., 2003). These references do not take into account heterogeneity (Z_i in our case). They instead study network centrality measures that are motivated by the diffusion model considered. The current paper studies a static model with heterogeneity, with spillovers occurring through the number of treated friends.

In particular, as noted by Banerjee et al. (2013), models of information diffusion focus on either what Banerjee et al. (2013) defines as "information effects" (people become aware of certain opportunities or technologies) or "endorsement effects" (people's behavior may affect others' behavior), but not necessarily both (similar to what Manski 1993 defines exogenous and endogenous spillovers). Once we interpret the outcome Y_i as technology adoption, this paper mostly focuses on information effects through the dependence of the outcome on neighbors' treatments (information). It can accommodate endorsement effects in those settings where the function $r(\cdot)$ captures endorsement effects in a reduced form.[27]

Finally, a further distinction from the literature on seeding (Kempe et al., 2003; Kitagawa and Wang, 2020; Galeotti et al., 2020) is that the current paper focuses on constrained policies, motivated by the cost of collecting network data, instead of first-best (unconstrained) policies which would require information on the population network.

3 Network Empirical Welfare Maximization

Next, I introduce our procedure and its properties. I present results as non-asymptotic and valid in a finite sample.

3.1 Known propensity score

Suppose first researchers know the propensity score. Define

$$I_i(\pi) = 1\Big\{T_i(\pi) = T_i, \pi(X_i) = D_i\Big\},$$

[27] An example is having two periods $t \in \{1, 2\}$, where the treatment consists of providing information at time $t = 1$ to some individuals. At the time $t = 1$, individual outcomes only depend on individual treatments D_i, whereas at $t = 2$, diffusion occurs, and outcomes depend on the average number of friends who adopted the technology. Let $Y_{i,1} = D_i\tau + \varepsilon_{i,1}$ the outcome at time $t = 1$ with treatment effects τ and *i.i.d.* unobservables ε_i, and $Y_{i,2} = f(D_i, Y_{i,1}, \sum_{k\in N_i} Y_{k,1}, |N_i|, \varepsilon_{i,2})$, for some function $f(\cdot)$ and *i.i.d.* unobservables $\varepsilon_{i,2}$, the outcome at time $t = 2$. It follows that the model presented here encompasses this framework as a special case, where $\varepsilon_i = (\sum_{k\in N_i} \varepsilon_{k,1}, \varepsilon_{i,1}, \varepsilon_{i,2})$ in Assumption 2.3 and the outcome of interest is the end-line outcome $Y_{i,2}$.

with $T_i(\pi)$ as in Equation (5). Consider the following double robust estimator (AIPW) of welfare:

$$W_n(\pi, m^c, e) = \frac{1}{n_e} \sum_{i=1}^{n} R_i \left\{ \frac{I_i(\pi)}{e_i(\pi)} \Big(Y_i - m_i^c(\pi) \Big) + m_i^c(\pi) \right\}, \tag{9}$$

where

$$m_i^c(\pi) = m^c\Big(\pi(X_i), T_i(\pi), Z_i, |N_i|\Big), \quad e_i(\pi) = e\Big(\pi(X_i), T_i(\pi), Z_{k\in N_i}, R_{k\in N_i}, Z_i, |N_i|\Big).$$

The function m^c denotes an *arbitrary* regression adjustment, possibly different from the population conditional mean functions.[28]

The estimated welfare inherits double-robust properties in the spirit of Robins et al. (1994), and Tchetgen and VanderWeele (2012), Aronow and Samii (2017), Liu et al. (2019), who study inference with spillover effects. For known propensity scores, for any function m^c, the estimator is unbiased for $W_{A,Z}(\pi)$ (see Appendix D.3.1).

Assumption 3.1 (Regression adjustment: oracle setup)**.** For each $d \in \{0,1\}, t \in \mathcal{T}_n$, let $|m^c(d,t,Z_i,|N_i|)| < \Gamma$, almost surely, for a finite constant $\Gamma < \infty$, and for $z \in \mathcal{Z}, l \in \mathbb{Z}$, $m^c(d,t,z,l) \perp \Big(Y_i, R_i, D_i\Big)_{i=1}^n \Big| A, Z$.

Assumption 3.1 states that the regression adjustment is (i) uniformly bounded and (ii) independent of experiment participants. An example is $m^c = 0$, or m^c estimated on an independent population. Sections 3.2, and 4.2 study settings where (ii) fails. Let

$$\hat{\pi}_{m^c,e} \in \arg\max_{\pi\in\Pi} W_n(\pi, m^c, e).$$

Theorem 3.1 (Oracle Regret)**.** *Let Assumptions 2.1, 2.2, 2.5, 3.1, and (A), (C), (D) in 2.3 hold. For a universal constant $\bar{C} < \infty$, the following holds almost surely:*

$$\mathbb{E}\Big[\sup_{\pi\in\Pi_n} W_{A,Z}(\pi) - W_{A,Z}(\hat{\pi}_{m^c,e}) \Big| A, Z \Big] \leq \bar{C} \frac{\Gamma \mathcal{N}_n^{3/2}}{\gamma \delta_n} \sqrt{\frac{\log(\mathcal{N}_n) \mathrm{VC}(\Pi)}{n_e}}.$$

Proof of Theorem 3.1. The proof consists of three steps. First, I extend symmetrization arguments – widely studied for independent observations (e.g., Devroye et al., 2013; Kitagawa and Tetenov, 2018) – for network data studied here. To obtain symmetrization, I group units into groups of conditionally independent observations. Within each group, I provide bounds in terms of the Rademacher complexity[29] of the function class obtained from the composition

[28] Note that m^c can be arbitrary. Therefore, it does not require that the conditional mean functions are identical across units (Assumption 2.3 (B)).

[29] See Definition D.5 in the Appendix for the definition of Rademacher complexity.

of direct and spillover effects. As a second step, I bound the Rademacher complexity in each group (i) by deriving an extension of Ledoux and Talagrand (2011)'s contraction inequality (Lemma D.6), using (ii) Dudley's entropy integral bound (Wainwright, 2019, Theorem 5.22), and (iii) providing an upper bound on the covering number[30] of the product of the number of treated neighbors and individual treatment.[31] Finally, as the third step, I invoke Brooks (1941)'s theorem to control the number of groups containing conditionally independent units using the maximum degree.

Section 3.4 presents a proof sketch, and Appendix D.2 the complete proof. □

Theorem 3.1 provides a non-asymptotic upper bound on the regret, and it is the first result of this type under network interference.

The regret bound depends on the network topology through the maximum degree $\mathcal{N}_n$, the overlap constant δ_n, and the (expected) sample size n_e. The degree affects the regret bound through two channels: (i) dependence between outcomes conditional on the network and covariates and (ii) the complexity of the function class obtained by the composition of direct and spillover effects. For (i), I leverage Assumptions 2.1, 2.2 (i), and 2.3 (C), to show each individual observation is dependent with at most $2\mathcal{N}_n^2$ many other units. For (ii), I leverage instead Assumptions 2.1 and 2.5, to bound (ii) as a function of the VC dimension of Π and $\mathcal{N}_n$. The bound also depends on δ_n, which can vary with n. Intuitively, for larger networks (and larger degrees), the probability that individuals exhibit strict overlap may get smaller, depending on the exposure mapping considered. The bound is independent of α in Equation (1). Theorem 3.1 does not assume Assumption 2.3 (B).

The bound shrinks to zero as n_e increases, only if the maximum degree and the overlap constant grows at an appropriate slower rate than the sample size. We formalize this below.

Corollary 1 (Convergence rate with a possibly unbounded degree)**.** *Let the Assumptions in Theorem 3.1 hold. Suppose in addition that Assumption 2.4 holds. Then*

$$\mathbb{E}\Big[\sup_{\pi\in\Pi_n} W_{A,Z}(\pi) - W_{A,Z}(\hat{\pi}_{m^c,e})\Big| A, Z\Big] = \mathcal{O}\Big(n_e^{-\xi}\Big)$$

almost surely, for $\xi \in (0, 1/2]$ as defined in Assumption 2.4.

The corollary shows that the regret converges to zero at a rate that depends on the convergence rate of the maximum degree and the number of experiment participants. For bounded degree, the regret scales at rate $1/\sqrt{n_e}$.

[30] See Wainwright (2019) for a definition of covering numbers and Definition D.1 in the Appendix.

[31] Lemma D.7 presents the full argument of this second step. Lemma D.5 presents the bound on the covering number for (iii).

Corollary 2 (Example 2.2 cont'd)**.** *Let the Assumptions in Theorem 3.1 hold, and* $\mathcal{N}_n < c_0'$ *almost surely, for a constant* c_0' *independent of* n*. Then almost surely,*

$$\mathbb{E}\Big[\sup_{\pi\in\Pi_n} W_{A,Z}(\pi) - W_{A,Z}(\hat{\pi}_{m^c,e})\Big|A,Z\Big] = \mathcal{O}\Big(n_e^{-1/2}\Big).$$

In the following theorem, I show that a sequence of data-generating processes such that *any* data-dependent policy does not improve the convergence rate of $\hat{\pi}_{m^c,e}$ exists. Consistently with the regret guarantees in previous theorems, I provide the lower bound conditional on (A,Z).

Theorem 3.2 (Minimax lower bound)**.** *Let* Π *be the class of policies* $\pi : \mathcal{X} \mapsto \{0,1\}$*, with finite VC dimension* $\text{VC}(\Pi)$*,* $\mathcal{X} = \mathbb{R}^d \subseteq \mathcal{Z}$*, for some finite* $d < \infty$*. Let* $\mathcal{P}_n(A,Z)$ *the set of conditional distributions* $\mathcal{D}_n(A,Z)$ *of* $(Y_i,D_i,R_i)_{i=1}^n|A,Z$ *satisfying Assumptions 2.1, 2.2, 2.3. Then for any* $g_n(\cdot)$ *in Assumption 2.1, for any* $n_e \geq 16\text{VC}(\Pi)$*, and for any data-dependent* $\hat{\pi}_n \in \Pi$*, which depends on* $\Big[R_i(Y_i,Z_i,Z_{k\in N_i},D_i,D_{k\in N_i},N_i),R_i\Big]_{i=1}^n$*,*

$$\sup_{A\in\mathcal{A}_n^o, Z\in\mathcal{Z}^n}\sup_{\mathcal{D}_n(A,Z)\in\mathcal{P}_n(A,Z)} \frac{\delta_n}{\mathcal{N}_n^{3/2}\log^{1/2}(\mathcal{N}_n)}\mathbb{E}_{\mathcal{D}_n(A,Z)}\Big[\Big(\sup_{\pi\in\Pi} W_{A,Z}(\pi) - W_{A,Z}(\hat{\pi}_n)\Big)\Big|A,Z\Big] \geq \frac{\exp(-2\sqrt{2})}{2^{5/2}\log^{1/2}(2)}\sqrt{\frac{\text{VC}(\Pi)}{n_e}},$$

where $\mathcal{A}_n^o \subset \mathcal{A}_n$ *denotes the space of symmetric unweighted adjacency matrices satisfying Assumption 2.4, and* $\mathbb{E}_{\mathcal{D}_n}[\cdot]$ *denotes the expectation with respect to* $\mathcal{D}_n$*.*

Proof of 3.2. The proof follows similar steps of Devroye et al. (2013); Kitagawa and Tetenov (2018), once I construct a sufficiently sparse adjacency matrix for the worst-case lower bound, with two distinctions that, to my knowledge, are novel in the literature: I condition on covariates and consider random sampling indicators. See Appendix D.2 for details. □

Theorem 3.2 provides a worst-case lower bound to any data-dependent policy, holding uniformly for any $n_e \geq 16\text{VC}(\Pi)$. Theorem 3.2 establishes the minimax rate of convergence of $\hat{\pi}_{m^c,e}$ for the known propensity score, because I rescale the left-hand side by the additional term $\delta_n/(\mathcal{N}_n^{3/2}\log(\mathcal{N}_n))$, and because it matches Theorem 3.1.[32] Similar to lower bounds in the literature (Kitagawa and Tetenov, 2018), the bound is maximin over the data-generating process, including the adjacency matrix A satisfying Assumption 2.4.[33]

[32]The main intuition is to construct a sufficiently sparse adjacency matrix in the derivation of the lower bound.

[33]The lower bound also implies the same worst-case *expected* lower bounds when (A,Z) are drawn from some super-population. This follows from the fact that we can always select a degenerate distribution for (A,Z) once we look at the worst-case expected lower bound with respect to distributions of (A,Z).

3.2 Estimated nuisance functions

Next, I derive regret guarantees when estimating the conditional mean $m(\cdot)$ and/or propensity score $e(\cdot)$, as defined in Equation (3) under Assumptions 2.2, and 2.3. Define $\hat{m}$, and $\hat{e}$ the estimated conditional mean and propensity score as in Algorithm 2 (Appendix A), $W_n(\pi, \hat{m}, \hat{e})$ as the welfare with the estimated nuisance functions as in Equation (27), and

$$\hat{\pi}_{\hat{m},\hat{e}} \in \arg\max_{\pi \in \Pi} W_n(\pi, \hat{m}, \hat{e}). \tag{10}$$

I propose a modification of the *cross-fitting* algorithm (Chernozhukov et al., 2018) for interference, described in detail in Algorithm 2. I construct groups of sample units that are neither friends nor share a common friend. This information is available under the sampling mechanism in Section 2.2, because researchers observe the set of friends of each sampled individual. Within each group, I estimate the conditional mean function using standard cross-fitting. I repeat the same algorithm for the propensity score, where I first estimate the individual treatment probability and then aggregate such probabilities as in Remark 2. Algorithm 2 presents the details and consists of a sequence of mixed-integer linear programs.

To my knowledge, Algorithm 2 is novel to the literature on interference.[34] For settings where the network presents approximately independent components (e.g., regions), I also present a computational relaxation in Algorithm 3.[35] See Appendix A for details.

To study properties of the algorithm, I assume that the estimated nuisance functions satisfy the same bounded and overlap conditions as their population counterparts.[36]

Assumption 3.2 (Estimated nuisances)**.** Assume that for each $d \in \{0,1\}, t \in \mathcal{T}_n, i \in \{1,\dots,n\}$, and $\hat{m}^{(i)}(\cdot), \hat{e}^{(i)}(\cdot)$ as in Algorithm 2, $|\hat{m}^{(i)}(d,t,Z_i,|N_i|)| < \Gamma$ almost surely, for a finite constant Γ and $\hat{e}^{(i)}(d,t,Z_{k\in N_i},R_{k\in N_i},Z_i,R_i,|N_i|) \in (\gamma\delta_n, 1-\gamma\delta_n)$, almost surely, for γ, δ_n as defined in Assumption 2.2.

The rate of convergence here also depends on the product of the mean-squared error of the estimated conditional mean function and propensity score, averaged over the population

[34] In the context of clustering, Chiang et al. (2019) have proposed a different algorithmic procedure for inference with multi-way and clustered data. Their approach differs since they do not consider network interference (and a single network).

[35] Algorithm 3 constructs subgraphs of the network *recursively* to minimize the number of individuals with shared friends between different subgraphs. It estimates nuisance functions for unit i using information from units in the subgraphs different from the one of unit i.

[36] I can replace Assumption 3.2 with uniform consistency of $\hat{m}, \hat{e}$ as in Athey and Wager (2021).

covariates and number of neighbors:[37]

$$\mathcal{R}_n(A,Z) = \frac{1}{n}\sum_{i=1}^{n}\mathbb{E}\left[\sup_{d,t}\left(\hat{m}^{(i)}(d,t,Z_i,|N_i|) - m(d,t,Z_i,|N_i|)\right)^2 \Big| A, Z, R_i = 1\right]$$
$$\mathcal{B}_n(A,Z) = \frac{1}{n}\sum_{i=1}^{n}\mathbb{E}\left[\sup_{d,t}\left(\frac{1}{\hat{e}^{(i)}(d,t,Z_{k\in N_i},R_{k\in N_i},Z_i,|N_i|)} - \frac{1}{e(d,t,Z_{k\in N_i},R_{k\in N_i},Z_i,|N_i|)}\right)^2 \Big| A, Z, R_i = 1\right], \tag{11}$$

where $\hat{m}^{(i)}, \hat{e}^{(i)}$ are the estimated functions for unit i, as defined in Algorithm 2.

Theorem 3.3. *Let Assumptions 2.1, 2.2, 2.3, 2.4, 2.5, 3.2 hold. Suppose that $\hat{m}, \hat{e}$ are estimated as in Algorithm 2. Then*

$$\mathbb{E}\Big[\sup_{\pi\in\Pi_n} W_{A,Z}(\pi) - W_{A,Z}(\hat{\pi}_{\hat{m},\hat{e}})\Big| A, Z\Big] = \mathcal{O}\Big(n_e^{-\xi} + \sqrt{\mathcal{R}_n(A,Z)\times\mathcal{B}_n(A,Z)}\Big).$$

almost surely, for $\xi \in (0, \frac{1}{2}]$ as defined in Assumption 2.4.

Proof of Theorem 3.3. The proof leverages the network cross-fitting argument (Algorithm 2) combined with similar techniques used to derive Theorem 3.1. The rate $n_e^{-\xi}$ follows from Assumption 2.4. See Appendix D.2.3 for the complete derivation. □

Theorem 3.3 states that the regret bound depends on two components. The first component depends on the convergence rate of the maximum degree, overlap constant, and experiment size, similar to what was discussed in the presence of a known propensity score (e.g., Corollary 1). For a bounded degree as in Example 2.2, $\xi = 1/2$, and $\xi < 1/2$ otherwise. The second component depends on the estimation error of the nuisance functions, and in particular, it depends on the *product* of their convergence rates, in the same spirit of standard conditions in the *i.i.d.* setting (e.g., Farrell, 2015).

Remark 7 (Convergence rate of nuisance functions)**.** Appendix B.2 shows that using Algorithm 2, $\sqrt{\mathcal{R}_n(A,Z)\times\mathcal{B}_n(A,Z)} = \mathcal{O}(\mathcal{N}_n^2 n_e^{-(\zeta_m+\zeta_e)}/\delta_n)$, where $n_e^{-2\zeta_m}$, and $n_e^{-2\zeta_e}/\delta_n^2$ are the rate of convergence of the mean squared error of the conditional mean and propensity score, respectively, on a sample of *independent observations*.[38] As a result, whenever $\mathcal{N}_n^{1/2} n_e^{-(\zeta_m+\zeta_e)} = n_e^{-1/2}$ (e.g., $n_e^{-\zeta_m} = n_e^{-\zeta_e} = \mathcal{N}_n^{-1/4} n_e^{-1/4}$), it follows that $\sqrt{\mathcal{R}_n(A,Z)\times\mathcal{B}_n(A,Z)} = \mathcal{O}(n_e^{-\xi})$.[39] Convergence rates for the estimation error of order $\mathcal{N}_n^{1/2} n^{-(\zeta_m+\zeta_e)} = n_e^{-1/2}$ imply

[37] Note that here I condition on $R_i = 1$ indicating the estimation error had unit i been sampled, since $\hat{m}_i, \hat{e}_i$ is not defined for non-sampled units.

[38] For example, $n_e^{-\zeta_m} = \sqrt{\log(p)/n_e}$ for the lasso under conditions in Negahban et al. (2012) and fixed sparsity, where p is the number of regressors. For the propensity score, we rescale by $1/\delta_n^2$ since otherwise the mean-square error may not be uniformly bounded as $\delta_n \to 0$.

[39] This follows because under Assumption 2.4, ξ is defined such that $n_e^{-\xi} = \log^{1/2}(\mathcal{N}_n)\mathcal{N}_n^{3/2} n_e^{-1/2}/\delta_n$.

that the estimation error of the nuisance functions does *not* affect the rate of the regret bound in Theorem 3.1 obtained in the absence of estimation error. Appendix B.2 presents formal results. □

3.3 Optimization

Next, I discuss the optimization procedure. For simplicity, consider the most agnostic case where $T_i = \sum_{k \in N_i} D_k$ denotes the sum of treated neighbors. Similar reasoning applies to T_i being a known function of the sum of treated neighbors. Define the estimated effect of assigning to unit i treatment d, after treating t neighbors:

$$q_i(d,t) = \left\{ \frac{1\{\sum_{k \in N_i} D_k = t, D_i = d\}}{e\Big(d, t, Z_{k \in N_i}, R_{k \in N_i}, Z_i, |N_i|\Big)} \Big(Y_i - m^c\Big(d, t, Z_i, |N_i|\Big)\Big) + m^c\Big(d, t, Z_i, |N_i|\Big) \right\}, \tag{12}$$

where I omit the dependence of $q_i(\cdot)$ with m^c and e for the sake of brevity. Second, let $B_i(\pi, h) = 1\Big\{ \sum_{k \in N_i} \pi(X_k) = h \Big\}$ be the indicator of whether h neighbors of individual i have been treated under policy π. We have the following:

$$\sum_{h=0}^{|N_i|} \Big\{ \Big(q_i(1,h) - q_i(0,h)\Big)\pi(X_i)B_i(\pi,h) + B_i(\pi,h)q_i(0,h) \Big\} = q_i\Big(\pi(X_i), \sum_{k \in N_i} \pi(X_k)\Big). \tag{13}$$

Namely, each element in the sum is weighted by the indicator $B_i(\pi, h)$, and only one of these indicators is equal to one. I can then define variables $p_i, p_i = \pi(X_i), \pi \in \Pi_n$ that denote the treatment assignment of each unit i either sampled ($R_i = 1$) or friend of a sampled unit ($R_i^f = 1$). For example, for $\pi(X_i) = 1\{X_i^\top \beta \geq 0\}, \beta \in \mathcal{B}$, similar to Florios and Skouras (2008),

$$\frac{X_i^\top \beta}{|C_i|} < p_i \leq \frac{X_i^\top \beta}{|C_i|} + 1, \quad C_i > \sup_{\beta \in \mathcal{B}} |X_i^\top \beta|, \quad p_i \in \{0,1\},$$

where p_i is equal to one if $X_i^\top \beta$ is positive, and zero otherwise. The key intuition is to introduce additional variables to write $B_i(\pi, h)$ using mixed-integer linear constraints. Define

$$t_{i,h,1} = 1\left\{ \sum_{k \in N_i} p_k \geq h \right\}, \quad t_{i,h,2} = 1\left\{ \sum_{k \in N_i} p_k \leq h \right\}, \quad h \in \{0, \cdots, |N_i|\}.$$

It follows that $t_{i,h,1} + t_{i,h,2} - 1 = B_i(\pi, h)$, and that such variables admit a mixed-integer linear program characterization. Formally, the optimization program is[40]

$$\max_{\{u_{i,h}\},\{p_i\},\{t_{i,1,h},t_{i,2,h}\}} \sum_{i=1}^{n} \sum_{h=0}^{|N_i|} R_i \Big\{ \Big(q_i(1,h) - q_i(0,h)\Big)u_{i,h} + q_i(0,h)(t_{i,h,1} + t_{i,h,2} - 1) \Big\} \tag{14}$$

[40]Here, the constraint on $u_{i,h}$ guarantees that $u_{i,h} = p_i(t_{i,h,1} + t_{i,h,2} - 1) = p_i \times t_{i,h,1} \times t_{i,h,2}$ since $(t_{i,h,1} + t_{i,h,2} - 1)$ is equal to one if both variables are ones and zero if either of the two variables are ones and the other is zero. The case where both variables are zero never occurs by construction.

under the following constraints:

$$
\begin{aligned}
&(A) \quad p_i = \pi(X_i), \quad \pi \in \Pi_n, \quad \forall i : R_i = 1 \text{ or } R_i^f = 1 \\
&(B) \quad \frac{p_i + t_{i,h,1} + t_{i,h,2}}{3} - 1 < u_{i,h} \leq \frac{p_i + t_{i,h,1} + t_{i,h,2}}{3}, u_{i,h} \in \{0,1\} \quad \forall h \in \{0, \cdots, |N_i|\}, \forall i : R_i = 1 \\
&(C) \quad \frac{(\sum_k A_{i,k} p_k - h)}{|N_i| + 1} < t_{i,h,1} \leq \frac{(\sum_k A_{i,k} p_k - h)}{|N_i| + 1} + 1, t_{i,h,1} \in \{0,1\}, \ \forall h \in \{0, \cdots, |N_i|\}, \forall i : R_i = 1 \\
&(D) \quad \frac{(h - \sum_k A_{i,k} p_k)}{|N_i| + 1} < t_{i,h,2} \leq \frac{(h - \sum_k A_{i,k} p_k)}{|N_i| + 1} + 1, t_{i,h,2} \in \{0,1\}, \ \forall h \in \{0, \cdots, |N_i|\}, \forall i : R_i = 1.
\end{aligned} \tag{15}
$$

The first constraint can be replaced by methods discussed in previous literature, such as maximum scores (Florios and Skouras, 2008). By contrast, the additional constraints are due to interference.[41] Whenever units have no neighbors, the objective function is proportional to the one discussed in Kitagawa and Tetenov (2018) under no interference. Therefore, the formulation generalizes the MILP formulation to the case of interference.[42]

Theorem 3.4. *Let* $T_i = \sum_{k \in N_i} D_k$. *Then* $\hat{\pi} \in argmax_{\pi \in \Pi} W_n(\pi, m^c, e)$, *if and only if it maximizes Equation* (14) *with constraints in Equation* (15).

The proof of Theorem 3.4 follows directly from the argument in the current section.

3.4 Derivation of Theorem 3.1: main steps

This section includes a sketch of the proof of Theorem 3.1, whereas Appendix D.2 presents formal definitions and derivations. For the sake of brevity, in the argument below, I further assume $Y_i \in [-\Gamma', \Gamma']$ for a finite constant $\Gamma' < \infty$; that is, the outcome is uniformly bounded. Appendix D.2 presents derivations for unbounded outcomes. Because $\Pi_n \subseteq \Pi$, it follows that

$$
\begin{aligned}
\mathbb{E}\left[\sup_{\pi \in \Pi_n} W_{A,Z}(\pi) - W_{A,Z}(\hat{\pi}_{m^c,e}) \middle| A, Z\right] &\leq 2\mathbb{E}\left[\sup_{\pi \in \Pi_n} \left| W_n(\pi, m^c, e) - W_{A,Z}(\pi) \right| \middle| A, Z\right] \\
&\leq 2\mathbb{E}\left[\sup_{\pi \in \Pi} \left| W_n(\pi, m^c, e) - W_{A,Z}(\pi) \right| \middle| A, Z\right],
\end{aligned} \tag{16}
$$

our focus will be bounding the right-hand side of Equation (16). Define

$$
Q_i(\pi, A, Z) = R_i \left[\frac{I_i(\pi)}{e_i(\pi)} \Big(Y_i - m_i^c(\pi) \Big) + m_i^c(\pi) \right],
$$

where the dependence with e, m^c is suppressed for convenience. Define $\mathcal{Q}_n(\pi, A, Z)$ as the *joint* distribution, of Q_i, namely $\Big(Q_i(\pi, A, Z)\Big)_{i=1}^n \Big| A, Z \sim \mathcal{Q}_n(\pi, A, Z)$, for given π, A, Z.

[41] In practice, we observe that including additional (superfluous) constraints stabilizes the optimization problem. These are $\sum_h (t_{i,h,1} + t_{i,h,2} - 1) = 1$ for each i and $\sum_i \sum_h u_{i,h} = \sum_i p_i$.

[42] Also, observe that the formulation differs from those provided for allocation of an individual into small peer groups (Li et al., 2019) since the latter case does not account for the individualized treatment assignments encoded in the constraints (A)-(D), and in the variables $t_{i,h}$.

Define $(\sigma_i)_{i=1}^n$ *i.i.d.* Rademacher random variables independent of observables and unobservables,[43] and $\mathbb{E}_\sigma[\cdot]$ denotes the expectation only with respect to $(\sigma_i)_{i=1}^n$, conditional on observables and unobservables. By Lemma 2.1 $\mathbb{E}[W_n(\pi)|A,Z] = W_{A,Z}(\pi)$ for all $\pi \in \Pi$.

Symmetrization with network data Next, I extend the symmetrization argument (e.g., Lemma 6.4.2 in Vershynin, 2018) to the context of this paper. Define $\Big(Q_i'(\pi,A,Z)\Big)_{i=1}^n \Big| A, Z \sim \mathcal{Q}_n(\pi,A,Z)$, an independent copy of $\Big(Q_i(\pi,A,Z)\Big)_{i=1}^n$, conditional on (A,Z). It follows

$$(16) \leq \mathbb{E}\left[\sup_{\pi\in\Pi}\Big|\frac{1}{n_e}\sum_{i=1}^n\Big[Q_i(\pi,A,Z) - Q_i'(\pi,A,Z)\Big]\Big||A,Z\right] \quad (\because \text{Jensen's inequality}). \tag{17}$$

Ideally, using standard symmetrization arguments, I would like to bound the right-hand side in Equation (17). Unfortunately, this is not possible because of dependence. I instead partition observations into groups of conditionally independent random variables. I then obtain bounds that depend on the number of such groups. Let A^2 be the adjacency matrix obtained by connecting neighbors and two-degree neighbors under A. Let $\chi_n(A^2)$ be the smallest number of groups such that each group does not contain two units that either are neighbors or share a common neighbor under A, and $\mathcal{C}_n^2 = \{\mathcal{C}_n^2(g)\}_{g=1}^{\chi_n(A^2)}, \mathcal{C}_n^2(g) \subseteq \{1,\cdots,n\}$, the smallest set of such groups.[44] Then

$$\begin{aligned}
&\mathbb{E}\left[\sup_{\pi\in\Pi}\Big|\frac{1}{n_e}\sum_{i=1}^n\Big[Q_i(\pi,A,Z) - Q_i'(\pi,A,Z)\Big]\Big||A,Z\right] \quad (\because \text{ triangular inequality}) \\
&\leq \sum_{g\in\{1,\cdots,\chi_n(A^2)\}} \underbrace{\mathbb{E}\left[\sup_{\pi\in\Pi}\Big|\frac{1}{n_e}\sum_{i\in\mathcal{C}_n^2(g)}\Big[Q_i(\pi,A,Z) - Q_i'(\pi,A,Z)\Big]\Big||A,Z\right]}_{(II)}.
\end{aligned} \tag{18}$$

Note that Q_i equals zero if $R_i = 0$. Therefore, under Assumption 2.2 (i), it follows that Q_i can be written as a function of $\Big[R_i\Big(\varepsilon_i, R_i, \varepsilon_{D_i}, R_i^f, R_{j\in N_i}, R_{j\in N_i}^f, \varepsilon_{D_{j\in N_i}}, Z_i, |N_i|, Z_{k\in N_i}\Big)\Big]$, where $R_i^f = 1\{\sum_k A_{i,k}R_k > 0\}$. For each $j \in N_i$, R_j^f equals one almost surely conditional on $R_i = 1$. R_i^f is instead a deterministic function of $R_{j\in N_i}$. As a result, because $Q_i = 0$ if $R_i = 0$ almost surely, one can write Q_i only as a function of $\Big[R_i\Big(\varepsilon_i, R_i, \varepsilon_{D_i}, R_{j\in N_i}, \varepsilon_{D_{j\in N_i}}, Z_i, |N_i|, Z_{k\in N_i}\Big)\Big]$, its dependence with $R_{j\in N_i}^f$ can be dropped.

Under the distributional assumptions of each of these components, it follows that Q_i are jointly independent if they are not neighbors and do not share a common neighbor conditional

[43] Namely, $P(\sigma_i = 1) = P(\sigma_i = -1) = 1/2$.

[44] Such a set always exists. For example, in a fully connected network, $\mathcal{C}_n^2 = \{\{i\}\}, i \in \{1,\cdots,n\}, \chi_n(A^2) = n$, where each group only contains one unit, while in a network with no connection, $\mathcal{C}_n^2 = \{\{1,\cdots,n\}\}$, and $\chi_n(A^2) = 1$.

on A, Z.[45] Because $Q_i, Q_i'|A, Z$ have the same marginal distribution by construction,

$$(II) \leq 2\mathbb{E}\Big[\underbrace{\mathbb{E}_\sigma\Big[\sup_{\pi\in\Pi}\Big|\frac{1}{n_e}\sum_{i\in\mathcal{C}_n^2(g)}\sigma_i Q_i(\pi, A, Z)\Big|\Big]}_{(III)}\Big|A, Z\Big].$$

Bound on the function class complexity I control (III) with Lemma D.7. The idea of the lemma is the following. First, note that here $Q_i(\pi, \cdot)$ depends on π through $\Big(\pi(X_i), \sum_{k\in N_i}\pi(X_k)\Big)$. I show that $Q_i(\pi, A, Z)$ is Lipschitz in $\Big(\sum_{k\in N_i}\pi(X_k)\Big)$ with the Lipschitz contant proportional to $\frac{\Gamma'}{\gamma\delta_n}$. I then leverage extensions of the Ledoux-Talagrand contraction inequality (Lemma D.6, which extends Theorem 4.12 in Ledoux and Talagrand, 2011) to show

$$\mathbb{E}_\sigma\left[\sup_{\pi\in\Pi}\Big|\frac{1}{n_e}\sum_{i\in\mathcal{C}_n^2(g)}\sigma_i Q_i(\pi, A, Z)\Big|\right] \leq \frac{\bar{C}\Gamma'}{\gamma\delta_n}\mathbb{E}_\sigma\left[\sup_{\pi\in\Pi}\Big|\frac{1}{n_e}\sum_{i\in\mathcal{C}_n^2(g)}R_i\sigma_i\Big(\sum_{k\in N_i}\pi(X_k)\Big)\pi(X_i)\Big|\right] \tag{19}$$

for a universal constant $\bar{C} < \infty$. Using Theorem 5.22 in Wainwright (2019), I can bound the right-hand side in Equation (19), by an integral of the covering number of a function class obtained from $\Big(\sum_{k\in N_i}\pi(x_k)\Big)\pi(x_i), \pi \in \Pi$ – which we can bound by a function of the maximum degree and the VC dimension of Π (Lemma D.5) – and $\frac{\sqrt{\sum_{i=1}^n R_i 1\{i\in\mathcal{C}_n^2(g)\}}}{n_e}$.

Conclusions Collecting terms, for a universal constant $\bar{C} < \infty$, I show

$$\begin{aligned}(16) &\leq \bar{C} \times \sum_{g=1}^{\chi_n(A^2)} \times \frac{\Gamma'}{\gamma\delta_n} \times \sqrt{\log(\mathcal{N}_n)\mathcal{N}_n \mathrm{VC}(\Pi)} \times \mathbb{E}\left[\frac{\sqrt{\sum_{i=1}^n R_i 1\{i \in \mathcal{C}_n^2(g)\}}}{n_e}\Big|A, Z\right] \\ &\leq \bar{C} \times \sqrt{\chi_n(A^2)} \times \frac{\Gamma'}{\gamma\delta_n} \times \sqrt{\log(\mathcal{N}_n)\mathcal{N}_n \mathrm{VC}(\Pi)} \times \mathbb{E}\left[\frac{\sqrt{\sum_{i=1}^n R_i}}{n_e}\Big|A, Z\right] \quad (\because \text{concavity of } \sqrt{x}).\end{aligned}$$

The first term $\sqrt{\chi_n(A^2)}$ captures the dependence structure. By Brooks (1941)'s theorem, $\chi_n(A^2) \leq 2\mathcal{N}_n^2$ (see Lemma D.5). The second term captures Lipschitz-continuity of the objective function and depends on the overlap $1/\delta_n$. The third term captures the complexity of the function class of interest, increasing in the maximum degree. The last term captures concentration in the sample size. Using Jensen's inequality, $\mathbb{E}\Big[\frac{\sqrt{\sum_{i=1}^n R_i}}{n_e}\Big] \leq 1/n_e^{1/2}$. In Theorem 3.1, Γ replaces Γ' under bounded moments, instead of bounded outcomes.

Remark 8 (Independence of sampling indicators)**.** My results extend to settings where sampling indicators are locally dependent. For instance, if indicators are dependent between

[45] In particular, we leverage here Assumption 2.1 (interference is local); Assumption 2.2 (i) (treatments are conditionally independent); Assumption 2.3 (C) (unobservables are conditionally independent if two individuals do not share a common neighbor). I relax Assumption 2.3 (C) in Section 4.

two-degree neighbors, the proof above follows verbatim, because the sampling indicators in the set $\mathcal{C}_n^2(g), g \in \{1, \cdots, \chi(A_n^2)\}$ are independent. □

4 Main extensions

I discuss the main extensions here: trimming with poor overlap, higher-order dependence, and different target and sample units. Appendix B contains additional extensions.

4.1 Trimming to control overlap

In this subsection, I provide regret bounds whenever a few units may present a large degree. I consider the setting where $T_i = \sum_{k \in N_i} D_k$. To guarantee overlap, I introduce the following trimming estimator:

$$W_n^{tr}(\pi, m^c, e; \kappa_n) = \frac{1}{n} \sum_{i=1}^{n} R_i \left\{ \frac{I_i(\pi)}{e_i(\pi)} \Big(Y_i - m_i^c(\pi) \Big) 1\Big\{ |N_i| \leq \log_\gamma(\kappa_n) \Big\} + m_i^c(\pi) \right\}, \tag{20}$$

with $e_i(\pi), m_i(\pi), I_i(\pi)$ as in Equation (9). Here, $\log_\gamma(\kappa_n)$ defines the trimming constant, as the logarithm in scale γ of a user-specific κ_n (with γ in Assumption 2.2). The estimator excludes the direct effect on the largely connected nodes (with more than $\log_\gamma(\kappa_n)$ neighbors) but keeps information from the spillovers that such nodes generate. Define

$$\hat{\pi}_{\kappa_n}^{tr} \in \arg\max_{\pi \in \Pi_n} W_n^{tr}(\pi, m^c, e; \kappa_n), \quad P_n\Big(|N_i| \geq \log_\gamma(\kappa_n) \Big) = \frac{1}{n} \sum_{i=1}^{n} 1\Big\{ |N_i| \geq \log_\gamma(\kappa_n) \Big\}.$$

Theorem 4.1. *Suppose that* $P_n\Big(|N_i| \geq \log_\gamma(\kappa_n) \Big) < c$, *for a constant* $c < 1$. *Let* $T_i = \sum_{k \in N_i} D_k$, *and let Assumptions 2.1, 2.2, 2.3, 2.5, 3.1 hold. Then*

$$\mathbb{E}\Big[\sup_{\pi \in \Pi_n} W_{A,Z}(\pi) - W_{A,Z}(\hat{\pi}_{\kappa_n}^{tr}) \Big| A, Z \Big] = \mathcal{O}\left(\frac{\mathcal{N}_n^{3/2}}{\kappa_n} \sqrt{\frac{\log(\mathcal{N}_n) \mathrm{VC}(\Pi)}{n_e}} + P_n\Big(|N_i| \geq \log_\gamma(\kappa_n) \Big) \right).$$

Proof of Theorem 4.1. See Appendix D.2. □

Theorem 4.1 shows we can improve the regret bound for a suitable choice of κ_n under restrictions on the degree distribution. For instance, suppose $\sqrt{n}$-many individuals have a degree that can grow in n, whereas all other units have a degree bounded by at most $\log_\gamma(\kappa)$, for a constant κ independent of n. In this case, $P_n(|N_i| \geq \log_\gamma(\kappa)) = \mathcal{O}(\sqrt{\frac{\alpha}{n_e}})$, and

the regret is of order $\mathcal{O}\Big(\frac{\mathcal{N}_n^{3/2}}{\kappa}\sqrt{\frac{\log(\mathcal{N}_n)\mathrm{VC}(\Pi)}{n_e}}\Big)$, independent of δ_n. Theorem 4.1 illustrates how information can be leveraged from the *degree distribution* to improve convergence rates.

4.2 Regret with higher-order dependence

Next, I characterize regret bounds in settings where individuals can depend on friends up to the degree of order M, where M is a finite number and unknown. To simplify exposition, I assume the outcome is uniformly bounded.[46]

Assumption 4.1 (higher-order dependence and bounded outcome)**.** Suppose that for some unknown $M \geq 2$, (A) $\varepsilon_i \perp (\varepsilon_j)_{j \notin \cup_{k=1}^{M} N_{i,k}} \Big| A, Z$, where $N_{i,k}$ denotes the set of connection of i of degree k. Suppose in addition that (B) $Y_i \in [-\Gamma', \Gamma']$, for a positive constant $\Gamma' < \infty$.

Under Assumption 4.1, unobservables can depend on individuals of at most degree M. Suppose M is unknown and researchers do not have information from higher-order neighbors.[47] Define $m^c : \{0,1\} \times \mathbb{Z} \times \mathcal{Z} \times \mathbb{Z} \mapsto [-\Gamma', \Gamma']$ for some finite $\Gamma' < \infty$, $e^c(\cdot; |N_i|) : \mathcal{Z}^{|N_i|} \times \{0,1\}^{|N_i|} \times \mathcal{Z} \mapsto (\gamma\delta_n, 1-\gamma\delta_n)$, the *pseudo-true* conditional mean function and propensity score, and $\hat{m}, \hat{e}$ their corresponding estimators constructed arbitrarly (e.g., pooling information from all sampled units). Let[48]

$$\begin{aligned}
\tilde{\mathcal{R}}_n(A,Z) &= \frac{1}{n}\sum_{i=1}^{n} \mathbb{E}\left[\sup_{d,t}\Big(\hat{m}(d,t,Z_i,|N_i|) - m^c(d,t,Z_i,|N_i|)\Big)^2 | A, Z\right]. \\
\tilde{\mathcal{B}}_n(A,Z) &= \frac{1}{n}\sum_{i=1}^{n} \mathbb{E}\left[\sup_{d,t}\Big(\frac{1}{e^c(d,t,Z_{k\in N_i},R_{k\in N_i},Z_i)} - \frac{1}{\hat{e}(d,t,Z_{k\in N_i},R_{k\in N_i},Z_i)}\Big)^2 | A, Z\right]
\end{aligned} \tag{21}$$

denote the mean-squared errors of the estimators obtained from all sampled units, averaged over the population covariates and number of neighbors.

Theorem 4.2. *Let Assumptions 2.1, 2.2 hold, and Conditions (A), (D) in 2.3, Assumptions 2.4, 2.5, 3.1, 3.2, 4.1 hold. Assume either (or both) (i) $e^c(\cdot) = e(\cdot)$, or (ii) Assumption 2.3 (B) holds and $m^c = m$. Then, for $M \geq 2$, $\xi \in (0, 1/2]$ as in Assumption 2.4:*

$$\mathbb{E}\Big[\sup_{\pi\in\Pi_n} W_{A,Z}(\pi) - W_{A,Z}(\hat{\pi}_{\hat{m},\hat{e}})\Big| A, Z\Big] = \mathcal{O}\left(M\mathcal{N}_n^{M/2-1} n_e^{-\xi} + \frac{1}{\delta_n}\sqrt{\max\left\{\tilde{\mathcal{R}}_n(A,Z), \tilde{\mathcal{B}}_n(A,Z)\right\}}\right).$$

[46] A bounded outcome is not necessary, but it allows us to present easier-to-interpret conditions on the estimated nuisance functions. Without bounded outcome, we would require that the second equation in (21) is of the form $\frac{1}{n}\sum_{i=1}^{n}\mathbb{E}\Big[\sup_{d,t}\Big|(\frac{1}{e^c(d,t,Z_{k\in N_i},R_{k\in N_i},Z_i)} - \frac{1}{\hat{e}(d,t,Z_{k\in N_i},R_{k\in N_i},Z_i)})(Y_i - m^c(d,t,Z_i,|N_i|))\Big| | A, Z\Big]$.

[47] If M was known, researchers could run Algorithm 2, with appropriate modifications that requires us to also observe higher degree neighbors. In this case, results from Section 3 directly extend to this case, with convergence rates that depend on M similarly to what is described below.

[48] Different from Theorem 3.3, we do not need to condition on $R_i = 1$ in Equation (21) because no cross-fitting is used, and the estimated nuisance function is independent of i's index.

Proof of Theorem 4.2. See Appendix D.2.1 □

Theorem 4.2 provides a uniform bound on the regret, and it is double robust to correct specification of the conditional mean and the propensity score. The theorem's result depends on the convergence rate of $\hat{e}$ and $\hat{m}$ to their *pseudo*-true value. For parametric estimators of the conditional mean and the propensity score and bounded degree, the regret bounds scale at rate $1/\sqrt{n_e}$, divided by the overlap parameter.[49] For general machine-learning estimators, the rate can be slower than the parametric one, reflecting the "cost" of the lack of knowledge of the degree of dependence M. Here, $\mathcal{N}_n^{M/2-1}$ captures higher-order dependence. Theorem 4.2 does not require that Assumption 2.3 (B) holds in settings with a correctly specified propensity score, assuming $\hat{m}^c$ converges to *some* pseudo-true value m^c.

4.3 Different target and sample units

Next, I study the problem when experiment participants are not sampled from the target population. Consider a population with n individuals, connected under adjacency matrix A' and with covariates matrix Z' (I consider n target units for expositional convenience). Welfare on this new population is

$$W_{A',Z'}(\pi) = \frac{1}{n}\sum_{i=1}^{n} m\Big(\pi(X_i), \sum_k A'_{i,k}\pi(X'_k), Z'_i, \sum_k A'_{i,k}\Big), \quad X'_i \subseteq Z'_i. \tag{22}$$

Here, regret guarantees depend on assumptions on the support of (A', Z'). Define $\mathcal{S}_n(A, Z)$ as the empirical support of $Z_i, Z_{k\in N_i}, |N_i|$ for given adjacency matrix (A, Z), i.e., the set of unique values that $\left[Z_i, Z_{k\in N_i}, |N_i|\right]$ takes given (A, Z), and similarly $\mathcal{S}_n(A', Z')$ for A', Z'. Note $|\mathcal{S}_n(A, Z)| \leq n$ because each population has n individuals. Define

$$L(z, \mathbf{x}, l) = \frac{1}{n}\sum_{i=1}^{n} 1\Big\{Z_i = z, Z_{k\in N_i} = \mathbf{x}, \sum_k A_{i,k} = l\Big\},$$
$$L'(z, \mathbf{x}, l) = \frac{1}{n}\sum_{i=1}^{n} 1\Big\{Z'_i = z, Z'_{k\in N'_i} = \mathbf{x}, \sum_k A'_{i,k} = l\Big\},$$

the number of units in each population with individual covariates z, neighbors' observables $\mathbf{x}$, and number of friends l. Estimate the empirical welfare as follows:

$$\tilde{W}_n(\pi, m^c, e) = \frac{1}{n_e}\sum_{i=1}^{n} R_i \frac{L'\Big(Z_i, Z_{k\in N_i}, |N_i|\Big)}{L\Big(Z_i, Z_{k\in N_i}, |N_i|\Big)} \left\{\frac{I_i(\pi)}{e_i(\pi)}\Big(Y_i - m_i^c(\pi)\Big) + m_i^c(\pi)\right\}$$

[49] We can characterize convergence rates of nuisance functions using standard arguments under local or weak dependence (e.g. Chen and Shao, 2004).

with $I_i(\pi), e_i(\pi), m_i^c$ as in Equation (5). Here, the empirical welfare reweights observations by the ratio of the empirical distributions in the target population and the sampled units. Importantly, the functions $L(\cdot), L'(\cdot)$ must be observed from the populations, i.e., researchers observe the empirical distribution of the number of neighbors and neighbors' covariates from both populations (but not necessarily A, A').

Lemma 4.3. *Let Assumptions 2.1, 2.2, 2.3, and 3.1 hold conditional also on (A', Z'). Suppose $\mathcal{S}_n(A', Z') \subseteq \mathcal{S}_n(A, Z)$. Then*

$$\mathbb{E}\Big[\tilde{W}_n(\pi, m^c, e)\Big| A, Z, A', Z'\Big] = W_{A',Z'}(\pi).$$

Proof. See Appendix D.3.1. □

Lemma 4.3 shows that we can construct unbiased estimators of welfare, assuming knowledge the empirical distribution of the degree and individuals' and neighbors' covariates. One important assumption is a full-support assumption, that is the support of experiment participants must contain the support in the target sample.

Proposition 4.4. *Suppose the conditions in Theorem 3.1 hold conditional also on (A', Z'). Let $\hat{\pi}^t \in \arg\max_{\pi\in\Pi_n} \tilde{W}_n(\pi, m^c, e)$. Suppose $\mathcal{S}_n(A', Z') \subseteq \mathcal{S}_n(A, Z)$. Then for a universal constant $\bar{C} < \infty$*

$$\mathbb{E}\Big[\sup_{\pi\in\Pi_n} W_{A',Z'}(\pi) - W_{A',Z'}(\hat{\pi}^t)\Big| A, Z, A', Z'\Big] \leq \frac{\bar{C}\Gamma\bar{L}_{A,Z,n}\mathcal{N}_n^{3/2}}{\gamma\delta_n}\sqrt{\frac{\log(\mathcal{N}_n)\mathrm{VC}(\Pi)}{n_e}},$$

where $\bar{L}_{A,Z,n} = \max_{(Z_i, Z_{k\in N_i}, |N_i|)\in\mathcal{S}_n(A,Z)} L'\Big(Z_i, Z_{k\in N_i}, |N_i|\Big)\Big/ L\Big(Z_i, Z_{k\in N_i}, |N_i|\Big)$.

Proof. See Appendix D.2.5 □

Proposition 4.4 shows that we can achieve regret bounds which depend on the largest ratio between the empirical distribution on the target and sampled units over the empirical support of the individuals, and neighbors' covariates and of the number of neighbors.

Finally, note that in some settings the functions L, L' can be unknown. In this case, one might want to control the *expected* regret, assuming that $(A, Z), (A', Z')$ are independently drawn from a super-population. Appendix B.4 presents a discussion.

5 Empirical application

I now illustrate the proposed method using data originating from Cai et al. (2015). The authors study the effect of an information session on farmers' weather insurance adoption.

Individuals are grouped into approximately 180 addresses (villages) grouped into approximately 50 larger areas. According to the authors, "All rice-producing households were invited to one of the sessions, and almost 90% of them attended. Consequently, this provided us (the authors) with a census of the population of these 185 villages. In total, 5,335 households were surveyed" (Cai et al., 2015). Before conducting the experiment, researchers collected network data by asking each individual to indicate at most five friends (who can be in the same or different village).[50] In this application, I use information collected from those units for which information about their post-treatment outcome and their friend's identity is available; in total, 4511, a subset of the population. The experiment consists of two rounds of information sessions three days apart, each round containing two types of information sessions (simple and intensive). Households are randomized to each round and within each round to each type of information session. By using time variation over the two rounds, Cai et al. (2015) show the existence of significant neighbors' spillover effects of an intensive information session on second-round participants' outcomes and no endogenous spillover effects, consistently with the model presented in this paper.[51] I defer a discussion on how the model and assumptions of this paper connect to Cai et al. (2015) to Section 5.3.

5.1 Experimental setup and estimation

In the experiment, "the effect of social networks on insurance take-up is identified by looking at whether second round participants are more likely to buy insurance if they have more friends who were invited to first round intensive sessions" (Cai et al., 2015). Specifically, each round consists of two sessions held simultaneously. In the first round, households are assigned to either a 20-minute session during which researchers offer details about the insurance contract only (control arm, "simple" information session) or a 45-minute session that also provides details about the expected benefits of insurance (treatment arm, "intensive" information session). In the second round, farmers are assigned similarly to either intensive or simple information sessions. Although the main treatment arm consists of providing insurance information only, researchers also considered additional arms where they provided information about purchase decisions of other participants ("More info" in Figure 2). Here, I follow the main analysis in Cai et al. (2015) (Table 2), and focus on providing information on insurance benefits only, without additional information. Figure 2 illustrates the design.

I follow Cai et al. (2015) in the model specification. I estimate a model using all first-

[50] On average, 50% of the connections of sampled units have a different village. More than 90% of the connections are within the same area. This is a special case of the framework considered in this paper, with a block-diagonal network with a few independent blocks (areas).

[51] See Cai et al. (2015)'s abstract and Cai et al. (2015), Section C (Col 7, Table 5).

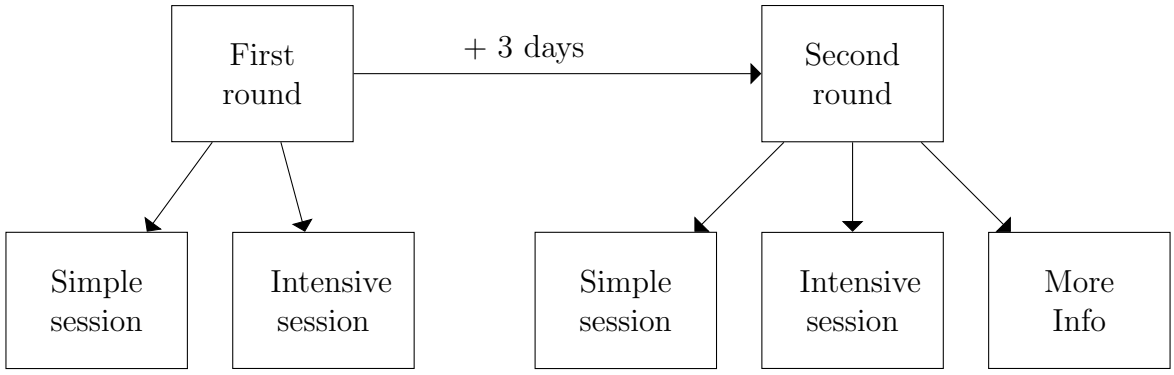

Figure 2: Design in Cai et al. (2015) with household-level treatment randomization. Participants are assigned at random to first and second rounds, and within each round, to different information sessions. Simple session denotes the control arm, where researchers provided information about the insurance contract only. Intensive session is the main treatment arm, where individuals are also provided with information about the benefits of insurance. "More info" contains additional arms with information about purchase decisions, omitted in our analysis and Cai et al. (2015)'s main analysis. Purchase decisions were made at the end of each information session.

round participants and those second-round participants either in the control arm or in the main (intensive) treatment arm.[52] I use the linear probability model as in Cai et al. (2015) (Table 2, Col (4)), controlling for area fixed effects, a large set of covariates, the average number of treated neighbors, individual treatment, and the interaction between individual and neighbors' treatments. The model in Cai et al. (2015) assumes homogenous treatment effects across covariates and villages. Here, I also allow for some heterogeneity in covariates and control for interaction terms of the rice area, a coefficient capturing risk aversion and education with individual and neighbors' treatments. Following Cai et al. (2015), I consider the "general network" as the main network, that is, the raw network data obtained from surveys where an individual generates spillover effects on i if she was indicated by i as a friend.[53] I then construct welfare using a *doubly-robust* estimator, with ten-fold cross-fitting

[52]Namely, I follow Column (2)-(5) in Table 2 in Cai et al. (2015). Therefore, I consider as focal units ($R_i = 1$) those units whose post-treatment outcome is observed and who are not assigned to the "More info" treatment arm in the second-round session. As discussed in Cai et al. (2015), I can drop observations in the "More info" treatment arms for estimating the conditional mean function because individuals in the second-round of information sessions do not generate spillover effects by design.

[53]For estimation, I follow Cai et al. (2015) and consider the general network matrix where spillovers only occur from individuals participating in the first information session to individuals in the second session (i.e., forcing the entries of the adjacency matrix to be zero for outgoing edges from second-round participants). When evaluating the out-of-sample performance of the policy, I use the original "general network" as an adjacency matrix because out-of-sample evaluations may not have the sequential structure of the experiment (i.e., some individuals may be treated and asked to make purchase decisions some time after treatment occurs, possibly generating spillovers also on the treated units participating in the same information session).

as in Algorithm 3.[54] The conditional mean is estimated via lasso with a small penalty (e^{-12}) to increase the stability of the estimator. The individual propensity score is estimated as in Remark 2 via a penalized logistic regression with a similar small penalty and 5% trimming.

5.2 Policy evaluation

I "simulate" the following environment: researchers collect information from villages in the first fifteen areas. They estimate the policy to treat individuals in the remaining villages. In the remaining villages, I assume the policymaker does not have access to the network information but only observes the farmer's education, risk aversion, and rice area. I then compute welfare effects *out-of-sample* on the villages outside the training set (first 15 areas). I repeat the same process via three-fold cross-fitting: I use the second fifteen areas as a training set and the remaining areas as a test set; similarly, I use the last group of areas as a training set and the first thirty areas as a test set. Finally, I compute the average out-of-sample improvements over the three out-of-sample evaluations. The out-of-sample evaluation uses the double-robust score, estimated out-of-sample. This exercise mimics settings where participants are sampled from a random subset of villages, and the treatment assigned to the experiment participants cannot be changed after the experiment (see Remark 3).[55]

I contrast to the empirical welfare-maximization method that ignores welfare effects in Athey and Wager (2021); Kitagawa and Tetenov (2018) and uses the *same* policy and models of the proposed procedure for both the propensity score and conditional mean function.[56]

As a first exercise, I consider *simple* policies that use information from transformations of two of the three covariates: education, rice area, and a coefficient capturing risk aversion. I compute simple classification trees obtained for all possible two-out-of-three combinations of such variables. The tree finds one optimal split over the first (continuous) variable. The split for the second variable is constrained to be at the population median value. This policy is simple to compute and communicate because it assigns treatments based on a few possible sub-groups. I study out-of-sample improvements while varying the treatment cost as $1\%, 3\%, 5\%$ of the insurance take-up benefit.[57] Table 1 provides welfare comparisons. We

[54] Algorithm 3 is a valid cross-fitting procedure in this setup. A few independent components (areas) exist that allows the discovery of 10 disconnected subgraphs.

[55] In this exercise, I sample areas instead of small villages to guarantee that the out-of-sample welfare estimates are independent of the training set, which is a desirable property for out-of-sample comparisons. This follows from the fact that individuals exhibit almost no connections between areas but many connections between small villages.

[56] I consider an AIPW estimator as in Athey and Wager (2021) that also controls for the *neighbors' treatments* when estimating the conditional mean function, and uses the individual propensity score.

[57] These costs are comparable to the direct treatment effect that we would estimate once observations from all villages as in Table 2, Col 2 in Cai et al. (2015) are pooled (approximately equal to 3%).

observe welfare improvements up to approximately thirty percentage points and positive effects uniformly across the specifications. These economically significant improvements are obtained despite the network not being observable in the target sample.

As a second exercise, I consider a more complex policy consisting of a maximum score that controls for education, rice area and risk aversion as follows:

$$\pi(X_i) = 1\Big\{\beta_0 + \text{Rice area} \times \beta_1 + \text{Risk aversion} \times \beta_2 + \text{Education} \times \beta_3 > 0\Big\}. \tag{23}$$

The parameters are estimated using the mixed-integer linear program in Section 3.3. Table 2 reports the average *out-of-sample* welfare improvement estimated via three-fold cross-fitting. It shows out-of-sample welfare improvements up to nine percentage points. This result illustrates the benefits of the procedure for more complex policy functions as well.

The cross-fitting procedure returns three policies estimated on independent samples. To investigate the properties of the estimated policy, Table 2 reports the coefficients of the estimated policy (NEWM) leading to the largest out-of-sample welfare.[58] The policy treats individuals who are more risk-averse, less educated, and with a smaller rice area. I contrast this policy with the one that ignores network effects (EWM). The two policies are substantially different when treating individuals with larger rice areas and risk aversion. This difference highlights the importance of taking into account spillover effects for policy targeting because different subgroups should be treated differently with spillover effects.

Table 1: *Out-of-sample* welfare improvement for a classification tree upon empirical welfare-maximization targeting rule in Athey and Wager (2021) that does not account for network effects in the design of the policy. Different columns denote different X variables considered for the design of the policy. Here C denotes the cost of the treatment. The policy is a classification tree that allows for the first covariate to be continuous and finds the best split over the first covariate, whereas the second covariate is whether such a variable is above or below its median value or missing.

	Educ & Rice-ar	Educ & Risk-av	Rice-ar & Risk-av
$C = 1\%$	0.146	0.084	0.289
$C = 3\%$	0.159	0.093	0.201
$C = 5\%$	0.093	0.111	0.143

[58] The policy with the largest out-of-sample welfare inherits the same rate of convergence of the regret as the one estimated on the entire sample. I report the policy with the largest out-of-sample welfare in the same spirit of standard cross-validation strategies.

Table 2: Estimated coefficients for $\pi(X) = 1\{X^\top\beta + \beta_0 > 0\}$, as a function of the rice area of the farmer, a coefficient capturing risk aversion and education. NEWM denotes the proposed method and EWM the double-robust empirical welfare-maximization procedure that ignores network effects. Coefficients are normalized by β_0, with estimated $\beta_0 = 1$ for both NEWM and EWM. The right-hand-side panel reports the average out-of-sample improvement of the NEWM method over policies that ignore network effects, estimated via three folds cross-fitting. C denotes the cost of treatment. The left-hand-side panel reports the estimated coefficients of the policy with the largest out-of-sample welfare for $C = 5\%$.

	Rice Area	Risk Aversion	Educ	Welfare Improvement		
				$C = 1\%$	3%	5%
NEWM	-0.068	0.395	-0.397	0.074	0.085	0.093
EWM	-0.003	-0.041	-0.473			

5.3 Assumptions and applicability of the method

This section concludes with a review of the assumptions required by the proposed procedure and their applicability in the context of the chosen application. Assumption 2.1 states that interference occurs through the neighbors' treatment assignments. In the context of our application, treatments denote (intensive) information sessions. This paper assumes potential outcomes are (possibly heterogeneous) functions of the number of informed neighbors. As a result, the model is best suited when information effects, as opposed to endorsement effects (i.e., effects driven by neighbors' purchase decisions), occur. This restriction is consistent with findings in Cai et al. (2015), who, by leveraging the sequential structure of the experiment, illustrate information effects and lack of endorsement effects. Quoting Cai et al. (2015)'s abstract: "*By varying the information available about peers' decisions and randomizing default options, we show that the network effect is driven by the diffusion of insurance knowledge rather than the purchase decisions.*" Insurance knowledge denotes the treatments, and purchase decisions are the outcomes of interest, consistent with our model.

A second restriction this paper imposes is that the maximum degree is sufficiently smaller than the sample size (Assumption 2.4). This restriction avoids overfitting and controls the complexity of the function class of interest. Following the specification in Cai et al. (2015), here individuals generate spillovers on those people indicated as friends, at most five of them. This feature is common in many (but not all) economic applications, such as the Add Health Study, Jackson et al. (2012) or De Paula et al. (2018).

The model specification of the conditional mean function in Cai et al. (2015) imposes a lack of heterogeneity in unobserved network statistics. However, because we augment the estimated conditional mean with the doubly robust score, the estimators also allow for

arbitrary network heterogeneity, even if such heterogeneity is not captured in the estimated conditional mean function. The reader may refer to Lemma 2.1 and Theorem 3.1 for details.

Finally, the sampling in Cai et al. (2015) guarantees that the welfare estimated using information from participants is an unbiased estimator of welfare once the policy is deployed *at scale* in rural China.[59] The main reason is that Cai et al. (2015) independently sample approximately 180 small villages in rural China, and, among such, they randomize treatments at the individual level.[60] This sampling induces local dependence within small villages, which is possible to accommodate in this paper's framework (see Remark 8).[61]

6 Conclusions

This paper introduced a method for estimating treatment rules under network interference. It considers constrained environments, and accommodates policy functions that do not necessarily depend on network information. The proposed methodology is valid for a large class of networks and does not impose restrictions on covariates. I cast the optimization problem into a mixed-integer linear program and derive guarantees on the policy regret.

The proposed method assumes anonymous and exogenous interactions. Future research can address the case of endogenous interactions by explicitly modeling the endogenous component, or considering weak dependence structures as in Leung (2022).

This paper estimates welfare-maximizing policies when the network information on the target sample is not observed by directly maximizing the empirical welfare. Extending our method by incorporating partial information on the population network is an interesting future direction. Combining the high-dimensional estimator of the network as in Alidaee et al. (2020) with the empirical welfare-maximization procedure is a possible approach.

Finally, the literature on influence maximization has often relied on structural models, whereas the literature on treatment choice has focused on semiparametric estimation. This paper opens new questions about the trade-off between structural assumptions and model-robust estimation of policy functions. Exploring this trade-off remains an open question.

[59] If instead, researchers were interested in the welfare effects of implementing the policy outside rural China (e.g., in a different *country*), we would need some reweighting as in Section 4.3.

[60] See, e.g., Figure I.2 in Cai et al. (2015).

[61] Similar sampling schemes can also be found in Alatas et al. (2012); Egger et al. (2019) among others, both with approximately 600 small villages independently drawn from a large region.

References

Abadie, A., S. Athey, G. W. Imbens, and J. M. Wooldridge (2020). Sampling-based versus design-based uncertainty in regression analysis. *Econometrica 88*(1), 265–296.

Akbarpour, M., S. Malladi, and A. Saberi (2018). Just a few seeds more: value of network information for diffusion. *Available at SSRN 3062830*.

Alatas, V., A. Banerjee, R. Hanna, B. A. Olken, and J. Tobias (2012). Targeting the poor: evidence from a field experiment in indonesia. *American Economic Review 102*(4), 1206–40.

Alidaee, H., E. Auerbach, and M. P. Leung (2020). Recovering network structure from aggregated relational data using penalized regression. *arXiv preprint arXiv:2001.06052*.

Ananth, A. (2021). Optimal treatment assignment rules on networked populations. *Working paper*.

Armstrong, T. and S. Shen (2015). Inference on optimal treatment assignments. *Available at SSRN 2592479*.

Aronow, P. M. and C. Samii (2017). Estimating average causal effects under general interference, with application to a social network experiment. *The Annals of Applied Statistics 11*(4), 1912–1947.

Athey, S., D. Eckles, and G. W. Imbens (2018). Exact p-values for network interference. *Journal of the American Statistical Association 113*(521), 230–240.

Athey, S. and G. W. Imbens (2018). Design-based analysis in difference-in-differences settings with staggered adoption. Technical report, National Bureau of Economic Research.

Athey, S. and S. Wager (2021). Policy learning with observational data. *Econometrica 89*(1), 133–161.

Auerbach, E. (2019). Identification and estimation of a partially linear regression model using network data. *arXiv preprint arXiv:1903.09679*.

Banerjee, A., A. G. Chandrasekhar, E. Duflo, and M. O. Jackson (2013). The diffusion of microfinance. *Science 341*(6144), 1236498.

Banerjee, A., A. G. Chandrasekhar, E. Duflo, and M. O. Jackson (2014). Gossip: Identifying central individuals in a social network. Technical report, National Bureau of Economic Research.

Banerjee, A., A. G. Chandrasekhar, E. Duflo, and M. O. Jackson (2019). Using gossips to spread information: Theory and evidence from two randomized controlled trials. *The Review of Economic Studies 86*(6), 2453–2490.

Barrera-Osorio, F., M. Bertrand, L. L. Linden, and F. Perez-Calle (2011). Improving the design of conditional transfer programs: Evidence from a randomized education experiment in colombia. *American Economic Journal: Applied Economics 3*(2), 167–95.

Bhattacharya, D. (2009). Inferring optimal peer assignment from experimental data. *Journal of the American Statistical Association 104*(486), 486–500.

Bhattacharya, D. and P. Dupas (2012). Inferring welfare maximizing treatment assignment under budget constraints. *Journal of Econometrics 167*(1), 168–196.

Bhattacharya, D., P. Dupas, and S. Kanaya (2019). Demand and welfare analysis in discrete choice models with social interactions. *Available at SSRN 3116716*.

Bloch, F., M. O. Jackson, and P. Tebaldi (2017). Centrality measures in networks. *Available at SSRN 2749124*.

Bond, R. M., C. J. Fariss, J. J. Jones, A. D. Kramer, C. Marlow, J. E. Settle, and J. H. Fowler (2012). A 61-million-person experiment in social influence and political mobilization. *Nature 489*(7415), 295.

Boucheron, S., O. Bousquet, and G. Lugosi (2005). Theory of classification: A survey of some recent advances. *ESAIM: probability and statistics 9*, 323–375.

Breza, E., A. G. Chandrasekhar, T. H. McCormick, and M. Pan (2020). Using aggregated relational data to feasibly identify network structure without network data. *American Economic Review 101*(8), 2454–84.

Brooks, R. L. (1941). On colouring the nodes of a network. In *Mathematical Proceedings of the Cambridge Philosophical Society*, Volume 37, pp. 194–197. Cambridge University Press.

Cai, J., A. De Janvry, and E. Sadoulet (2015). Social networks and the decision to insure. *American Economic Journal: Applied Economics 7*(2), 81–108.

Chen, L. H. and Q.-M. Shao (2004). Normal approximation under local dependence.

Chernozhukov, V., D. Chetverikov, M. Demirer, E. Duflo, C. Hansen, W. Newey, and J. Robins (2018). Double/debiased machine learning for treatment and structural parameters.

Chiang, H. D., K. Kato, Y. Ma, and Y. Sasaki (2019). Multiway cluster robust double/debiased machine learning. *arXiv preprint arXiv:1909.03489*.

Christakis, N. A. and J. H. Fowler (2010). Social network sensors for early detection of contagious outbreaks. *PloS one 5*(9).

Csikós, M., N. H. Mustafa, and A. Kupavskii (2019). Tight lower bounds on the vc-dimension of geometric set systems. *The Journal of Machine Learning Research 20*(1), 2991–2998.

De Paula, Á., S. Richards-Shubik, and E. Tamer (2018). Identifying preferences in networks with bounded degree. *Econometrica 86*(1), 263–288.

Devroye, L., L. Györfi, and G. Lugosi (2013). *A probabilistic theory of pattern recognition*, Volume 31. Springer Science & Business Media.

Duflo, E., P. Dupas, and M. Kremer (2011). Peer effects, teacher incentives, and the impact of tracking: Evidence from a randomized evaluation in kenya. *American Economic Review 101*(5), 1739–74.

Eckles, D., H. Esfandiari, E. Mossel, and M. A. Rahimian (2019). Seeding with costly network information. In *Proceedings of the 2019 ACM Conference on Economics and Computation*, pp. 421–422.

Egger, D., J. Haushofer, E. Miguel, P. Niehaus, and M. W. Walker (2019). General equilibrium effects of cash transfers: experimental evidence from kenya. Technical report, National Bureau of Economic Research.

Elliott, G. and R. P. Lieli (2013). Predicting binary outcomes. *Journal of Econometrics 174*(1), 15–26.

Farrell, M. H. (2015). Robust inference on average treatment effects with possibly more covariates than observations. *Journal of Econometrics 189*(1), 1–23.

Florios, K. and S. Skouras (2008). Exact computation of max weighted score estimators. *Journal of Econometrics 146*(1), 86–91.

Galeotti, A., B. Golub, and S. Goyal (2020). Targeting interventions in networks. *Econometrica 88*(6), 2445–2471.

Goldsmith-Pinkham, P. and G. W. Imbens (2013). Social networks and the identification of peer effects. *Journal of Business & Economic Statistics 31*(3), 253–264.

Graham, B. and A. De Paula (2020). *The Econometric Analysis of Network Data*. Academic Press.

Graham, B. S., G. W. Imbens, and G. Ridder (2010). Measuring the effects of segregation in the presence of social spillovers: A nonparametric approach. Technical report, National Bureau of Economic Research.

Hajłasz, P. and J. Malỳ (2002). Approximation in sobolev spaces of nonlinear expressions involving the gradient. *Arkiv för Matematik 40*(2), 245–274.

Hirano, K. and J. R. Porter (2009). Asymptotics for statistical treatment rules. *Econometrica 77*(5), 1683–1701.

Hudgens, M. G. and M. E. Halloran (2008). Toward causal inference with interference. *Journal of the American Statistical Association 103*(482), 832–842.

Imbens, G. W. (2000). The role of the propensity score in estimating dose-response functions. *Biometrika 87*(3), 706–710.

Jackson, M. O., T. Rodriguez-Barraquer, and X. Tan (2012). Social capital and social quilts: Network patterns of favor exchange. *American Economic Review 102*(5), 1857–97.

Jackson, M. O. and E. Storms (2018). Behavioral communities and the atomic structure of networks. *Available at SSRN 3049748*.

Kempe, D., J. Kleinberg, and É. Tardos (2003). Maximizing the spread of influence through a social network. In *Proceedings of the ninth ACM SIGKDD international conference on Knowledge discovery and data mining*, pp. 137–146. ACM.

Kitagawa, T. and A. Tetenov (2018). Who should be treated? Empirical welfare maximization methods for treatment choice. *Econometrica 86*(2), 591–616.

Kitagawa, T. and A. Tetenov (2019). Equality-minded treatment choice. *Journal of Business & Economic Statistics*, 1–14.

Kitagawa, T. and G. Wang (2020). Who should get vaccinated? individualized allocation of vaccines over sir network. *arXiv preprint arXiv:2012.04055*.

Kline, B. and E. Tamer (2020). Econometric analysis of models with social interactions. In *The Econometric Analysis of Network Data*, pp. 149–181. Elsevier.

Kolaczyk, E. (2009). Statistical analysis of network data.(springer series in statistics).

Laber, E. B., N. J. Meyer, B. J. Reich, K. Pacifici, J. A. Collazo, and J. M. Drake (2018). Optimal treatment allocations in space and time for on-line control of an emerging infectious disease. *Journal of the Royal Statistical Society: Series C (Applied Statistics) 67*(4), 743–789.

Ledoux, M. and M. Talagrand (2011). Probability in banach spaces. classics in mathematics.

Leung, M. P. (2020). Treatment and spillover effects under network interference. *Review of Economics and Statistics 102*(2), 368–380.

Leung, M. P. (2021). Network cluster-robust inference. *arXiv preprint arXiv:2103.01470*.

Leung, M. P. (2022). Causal inference under approximate neighborhood interference. *Econometrica 90*(1), 267–293.

Li, S. and S. Wager (2022). Random graph asymptotics for treatment effect estimation under network interference. *The Annals of Statistics 50*(4), 2334–2358.

Li, X., P. Ding, Q. Lin, D. Yang, and J. S. Liu (2019). Randomization inference for peer effects. *Journal of the American Statistical Association*, 1–31.

Liu, L., M. G. Hudgens, B. Saul, J. D. Clemens, M. Ali, and M. E. Emch (2019). Doubly robust estimation in observational studies with partial interference. *Stat 8*(1), e214.

Manresa, E. (2013). Estimating the structure of social interactions using panel data. *Unpublished Manuscript. CEMFI, Madrid*.

Manski (2004). Statistical treatment rules for heterogeneous populations. *Econometrica 72*(4), 1221–1246.

Manski, C. F. (1993). Identification of endogenous social effects: The reflection problem. *The review of economic studies 60*(3), 531–542.

Manski, C. F. (2013). Identification of treatment response with social interactions. *The Econometrics Journal 16*(1), S1–S23.

Mbakop, E. and M. Tabord-Meehan (2016). Model selection for treatment choice: Penalized welfare maximization. *arXiv preprint arXiv:1609.03167*.

Muralidharan, K., P. Niehaus, and S. Sukhtankar (2017). General equilibrium effects of (improving) public employment programs: Experimental evidence from india. Technical report, National Bureau of Economic Research.

Negahban, S. N., P. Ravikumar, M. J. Wainwright, and B. Yu (2012). A unified framework for high-dimensional analysis of m-estimators with decomposable regularizers. *Statistical science 27*(4), 538–557.

Opper, I. M. (2016). Does helping john help sue? evidence of spillovers in education. *American Economic Review 109*(3), 1080–1115.

Robins, J. M., A. Rotnitzky, and L. P. Zhao (1994). Estimation of regression coefficients when some regressors are not always observed. *Journal of the American statistical Association 89*(427), 846–866.

Sävje, F., P. Aronow, and M. Hudgens (2021). Average treatment effects in the presence of unknown interference. *Annals of statistics 49*(2), 673.

Sinclair, B., M. McConnell, and D. P. Green (2012). Detecting spillover effects: Design and analysis of multilevel experiments. *American Journal of Political Science 56*(4), 1055–1069.

Sobel, M. E. (2006). What do randomized studies of housing mobility demonstrate? causal inference in the face of interference. *Journal of the American Statistical Association 101*(476), 1398–1407.

Stoye, J. (2009). Minimax regret treatment choice with finite samples. *Journal of Econometrics 151*(1), 70–81.

Stoye, J. (2012). Minimax regret treatment choice with covariates or with limited validity of experiments. *Journal of Econometrics 166*(1), 138–156.

Su, L., W. Lu, and R. Song (2019). Modelling and estimation for optimal treatment decision with interference. *Stat 8*(1), e219.

Tchetgen, E. J. T. and T. J. VanderWeele (2012). On causal inference in the presence of interference. *Statistical methods in medical research 21*(1), 55–75.

Tetenov, A. (2012). Statistical treatment choice based on asymmetric minimax regret criteria. *Journal of Econometrics 166*(1), 157–165.

Vershynin, R. (2018). *High-dimensional probability: An introduction with applications in data science*, Volume 47. Cambridge university press.

Viviano, D. (2020). Policy choice in experiments with unknown interference. *arXiv preprint arXiv:2011.08174*.

Wager, S. and K. Xu (2021). Experimenting in equilibrium. *Management Science 67*(11), 6694–6715.

Wainwright, M. J. (2019). *High-dimensional statistics: A non-asymptotic viewpoint*, Volume 48. Cambridge University Press.

Zhou, Z., S. Athey, and S. Wager (2018). Offline multi-action policy learning: Generalization and optimization. *arXiv preprint arXiv:1810.04778*.

Zubcsek, P. P. and M. Sarvary (2011). Advertising to a social network. *Quantitative Marketing and Economics 9*(1), 71–107.

Appendix A Practical guide

This section provides details on the implementation. Algorithm 1 presents a summary.

Algorithm 1 Network Empirical Welfare Maximization

1: Sample individuals in a (quasi)experiment at random from the population of interest (see Remark 6 for stratified sampling).
2: For each sampled individual ($R_i = 1$) and their friends ($R_i^f = 1$) in the experiment randomize treatment assignments as in Assumption 2.2 (treatments do not need to be randomized among the remaining units in the population).
3: Collect information $\left[R_i\left(Y_i, D_i, T_i, N_i, Z_i, Z_{k\in N_i}\right), R_i\right]_{i=1}^n$, denoting sampling indicators ($R_i = 1$), post treatment outcome Y_i, treatment assignment D_i, neighbors' treatments T_i, *arbitrary* individual and neighbors' observable characteristics $Z_i, Z_{k\in N_i}$.
4: Run Algorithm 2 to estimate $\hat{m}, \hat{e}$ the conditional mean and propensity scores for sampled units ($R_i = 1$) as defined in Equation (3).
5: Run the optimization algorithm in Section 3.3 to estimate $\hat{\pi}$ using (arbitrary) individual level information $X_i \subseteq Z_i$.
6: Implement $\hat{\pi}$ on the population of interest by collecting individual-level information $(X_i)_{i=1}^n$ for all units in the population.

A.1 Cross-fitting: exact solution

The cross-fitting algorithm is described in Algorithm 2. It solves a *sequence* of mixed-integer linear programs of the form

$$(K^*, G^*) = \arg \min_{K\in\mathbb{Z}, G\in\{0,1\}^{n\times K}} \quad K \quad \text{such that} \quad \begin{array}{l} \sum_{k=1}^{K}\sum_{j=1}^{n} R_i R_j 1\{j \in \mathcal{I}_i\} G_{j,k} G_{i,k} = 0 \\ \sum_{k=1}^{K} G_{i,k} = 1, \quad \forall i \in \{1, \cdots, n\}, \end{array} \tag{24}$$

where $\mathcal{I}_i$ is defined in Equation (25) as the set of sampled units who are not friends or share a common friend with i. Each program consists of finding a feasible solution to the constraints in Equation (24) for given K. The program finds the smallest number of groups K^* and groups partition G^* such that two *sampled* individuals who are friends or share a common friend are not in the same group. Here, $G^*_{i,k} = 1$ if i is assigned to group k.

To estimate the conditional mean, the algorithm performs cross-fitting with J folds within each group, as in standard cross-fitting algorithms (Chernozhukov et al., 2018). If some of these groups are very small (with fewer than $J\check{P}$ units, for some small finite $\check{P}$), Algorithm 2 does not use information from such groups. Here, $\check{P}$ is a small constant and denotes the minimum number of observations such that the estimator is well-defined (e.g., the effective degrees of freedom for linear regression).[62] The propensity score is estimated using a similar approach. To estimate $\hat{e}^{(i)}$, researchers can also use information about the *treatments* of the neighbors of sampled units ($R_i = 1$) who have not been sampled, as described in Algorithm 2.[63]

A.2 (Approximate) network cross-fitting with subgraphs

Algorithm 3 presents a relaxation of network cross-fitting. It fixes K, and creates K groups *recursively*. Each iteration, it constructs two groups to *maximize* the number of individuals who are friends or share a common friend and are assigned to the *same* group. It then repeats the same optimization within each group until we obtain K groups in total. The algorithm constructs subgraphs by solving recursively max-cut optimization problems (see Algorithm 4). For each unit i, Algorithm 3 then estimates the conditional mean function using all groups *except* the group assigned to unit i. To estimate the propensity score, I construct subgraphs where I maximize the number of individuals who are neighbors (but not necessarily neighbors of neighbors) in each subgraph.[64] The slackness parameter s in Algorithm 4 guarantees subgraphs have approximately the same number of units up to s

[62] The presence of groups with a few units does not affect our results in Theorem 3.3, because these results are directly expressed in terms of average convergence rates of the nuisance functions (see Appendix D.2.3). It also does not affect the characterization of the convergence rate in Remark 7, and Appendix B.2. Intuitively, because $K^* \leq 2\mathcal{N}_n^2$ by Brooks (1941)'s theorem, the contribution of groups with few observations to the average estimation error is at most $\mathcal{O}(\mathcal{N}_n^2/n_e)$. See Appendix B.2 for details.

[63] This approach allows researchers to identify the propensity score if treatment probabilities for sampled units and their neighbors differ, but it is not necessary if these probabilities are the same. With the cross-fitting partition in Algorithm 2, due to the independence of treatments in Assumption 2.2 (i), I guarantee that the estimated propensity score is independent of unit i's outcome. The reason is that $\hat{e}^{(i)}$ is always estimated using information from treatments different from $(D_i, D_{k\in N_i})$.

[64] The reason is that, due to the independence of treatments in Assumption 2.2 (i), the estimated propensity score is independent of unit i's outcome if it is estimated using information from treatments different from $(D_i, D_{k\in N_i})$.

Algorithm 2 Network Cross-Fitting: Exact Optimization

Require: $\left[R_i\Big(Y_i, D_i, T_i, N_i, Z_i, Z_{k\in N_i}\Big), R_i\right]_{i=1}^n$, finite $\check{P}$, finite J.

1: For each $i \in \{1, \cdots, n\}$ construct

$$\mathcal{I}_i = \Big\{j \in \{1, \cdots, n\} \setminus \{i\} : R_j = 1 \text{ and } j \notin N_i, N_i \cap N_j = \emptyset\Big\}. \tag{25}$$

2: Solve Equation (24) and return K^*, G^*.

3: **for** $k \in \{1, \cdots, K^*\}$ **do**

a: Partition units $\{i : R_i G^*_{i,k} = 1\}$, to J folds $(F_k^j)_{j=1}^J$, equally sized up-to one element. Define $F_k^{j(i)}$ the fold containing unit i.

b: For i such that $G^*_{i,k}R_i = 1$ construct the estimator $\hat{m}^{(i)}(\cdot)$ of $m(\cdot)$, using $(Y_v, D_v, D_{k\in N_v}, Z_v, N_v)$ from units v in $(F_k^j)_{j=1}^J \setminus F_k^{j(i)}$. Let $\hat{m}^{(i)}(\cdot) = 0$ if $\sum_i G^*_{i,k}R_i \leq J\check{P}$.

4: **end for**

5: Repeat for the propensity score: for i such that $G^*_{i,k}R_i = 1$ estimate the *individual* conditional treatment probabilities using $(D_v, Z_v, R_v, (D_k(1-R_k), R_k, Z_k)_{k\in N_v})$ from units v in folds $(F_k^j)_{j=1}^J \setminus F_k^{j(i)}$. Aggregate such probabilities to construct and estimator of $e(\cdot)$ for unit i, $\hat{e}^{(i)}(\cdot)$ as in Remark 2. Let $1/\hat{e}^{(i)}(\cdot) = 0$ if $\sum_i G^*_{i,k}R_i \leq J\check{P}$.

6: Define

$$\hat{m}_i(\pi) = \hat{m}^{(i)}\Big(\pi(X_i), T_i(\pi), Z_i, |N_i|\Big), \quad \hat{e}_i(\pi) = \hat{e}^{(i)}\Big(\pi(X_i), T_i(\pi), Z_{k\in N_i}, R_{k\in N_i}, Z_i, R_i, |N_i|\Big) \tag{26}$$

and

$$W_n(\pi, \hat{m}, \hat{e}) = \frac{1}{n_e}\sum_{i=1}^n R_i\left\{\frac{I_i(\pi)}{\hat{e}_i(\pi)}\Big(Y_i - \hat{m}_i(\pi)\Big) - \hat{m}_i(\pi)\right\}. \tag{27}$$

return $W_n(\pi, \hat{m}, \hat{e})$.

units (e.g., five or ten).

The rationale is the following. If the network presents K completely independent and equally sized clusters, the algorithm will recover such clusters. In this case, unit i's prediction would use information from clusters except the one containing i; the predicted value for unit i would be independent of i's outcome, avoiding overfitting. The algorithm approximates this setup by constructing subgraphs that minimize the number of connections between such subgraphs.[65] I recommend choosing K by leveraging prior knowledge of the data, such as using the number of villages or regions.[66] Also, note that the effective sample size only shrinks by a factor $(K-1)/K = \mathcal{O}(1)$.

[65] Although optimization for clusterings with networks goes beyond the scope of this paper, we note that Leung (2021) presents an extensive discussion where clusters are not independent.

[66] For example, in the empirical application, units present almost all the connections within same *large areas* with 47 total areas; therefore, any $K \leq 47$ (e.g., $K = 10$) guarantees independent subgraphs.

Algorithm 3 Network Cross-Fitting: Approximate Optimization

Require: $\left[R_i\left(Y_i, D_i, T_i, N_i, Z_i, Z_{k\in N_i}\right), R_i\right]_{i=1}^{n}$, slackness parameter s, K folds.

1: Assign individuals into K folds by running Recursive Opt in Algorithm 4 with $\tilde{n} = n$, and slackness s.

2: For $i : R_i = 1$, construct $\hat{m}^{(i)}(\cdot)$, the estimator of $m(\cdot)$ for unit i, using data in all except i's fold.

3: Repeat for the propensity score: run Algorithm 4 with $\mathcal{H}_i = \{j \in \{1, \cdots, n\} : j \notin N_i, R_j + \sum_k A_{j,k} R_k > 0\}$ in lieu of $\mathcal{I}_i$. For each unit i, construct $\hat{e}^{(i)}(\cdot)$, the estimator of $e(\cdot)$ for unit i by: (i) estimating individual treatment probabilities with units in all folds except the one containing i; (ii) aggregating such probabilites as in Remark 2.

4: Construct $\hat{e}^{(i)}, \hat{m}^{(i)}$ and $W_n(\pi, \hat{m}, \hat{e})$ as in Equation (27). **return** $W_n(\pi, \hat{m}, \hat{e})$.

Algorithm 4 Recursive Opt

Require: input size $\tilde{n}$, $(R_i, \mathcal{I}_i)_{i=1}^{\tilde{n}}$, with $\mathcal{I}_i$ as in Equation (25), slackness parameter s, K

1: Solve

$$G^* \in \arg\min_{G\in\{0,1\}^{\tilde{n}\times\tilde{n}}} \sum_{i=1}^{\tilde{n}}\sum_{j\neq i}^{\tilde{n}} G_i(1-G_j)1\{j\in\mathcal{I}_i\}R_iR_j \quad G_i\in\{0,1\}, i\in\{1,\cdots,\tilde{n}\},$$

$$\frac{1}{n}\sum_{i=1}^{n} G_i \in \left[\frac{1}{2\tilde{n}}\sum_{i=1}^{\tilde{n}} R_i - s/\tilde{n}, \frac{1}{2\tilde{n}}\sum_{i=1}^{\tilde{n}} R_i + s/\tilde{n}\right].$$

2: **if** $K = 2$ **then**

3: **return** G^*.

4: **else**

5: **return**

$$\left[G^*, \text{Recursive Opt}\left(\sum_{i=1}^{\tilde{n}} G_i^*, (R_i, \mathcal{I}_i)_{G_i^*=1}, S', \frac{K}{2}\right), \text{Recursive Opt}\left(\tilde{n} - \sum_{i=1}^{\tilde{n}} G_i^*, (R_i, \mathcal{I}_i)_{G_i^*=0}, S', \frac{K}{2}\right)\right].$$

6: **end if**

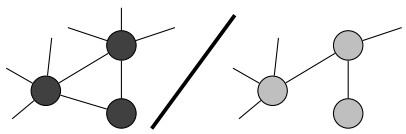

Figure 3: Illustration of Algorithm 3. The algorithm finds a maximum cut (black line) in the graph where two sampled individuals are connected if they are either friends or share a common friend. For each individual with a given color, they estimate the propensity score and nuisance functions using the units with the different color(s).