

Developing and Deploying an AI-Augmented Intervention for HIV prevention in Youth Experiencing Homelessness

Bryan Wilder¹ and Amulya Yadav²

¹ Machine Learning Department, Carnegie Mellon University

² College Of Information Sciences and Technology, Pennsylvania State University

Introduction

Each year, approximately 4.2 million youth in the United States experience some form of homelessness [Morton et al. 2018]. One of the key health challenges for this population is high HIV prevalence, with reported prevalence in the range of 2-11% [Young and Rice 2011], up to 10 times that for youth with stable housing [National HCH Council 2012].

One proposed mechanism for fostering positive behavior change in high-risk populations is the *peer change agent* model. The main idea is to recruit peer leaders from the population of youth experiencing homelessness (YEH) to serve as advocates for HIV awareness and prevention. Use of peer leaders has been suggested in the public health and social science literature due to the central role that peers play in risk behaviors for YEH, including behaviors related to HIV spread [Green Jr et al. 2013, Rice et al. 2010, 2012]. Indeed, peer change agent models have succeeded in past HIV prevention interventions in other contexts [Medley et al. 2009]. However, there have also been notable failures [Group et al. 2010], and it has been argued that such failures may be attributable to the strategy used for selecting peer leaders [Schneider et al. 2015]. The long-standing and most widely adopted method in the public health literature for selecting peer leaders is to identify the most popular individuals in the social network of the youth [Kelly et al. 1997] (formally, the highest degree nodes). This poses the question: are high-degree youth the best peer leaders to disseminate messages about HIV prevention? This question has relevance far beyond HIV prevention; analogous social network interventions are used widely across diverse domains, e.g., development, medicine, education, etc. [Banerjee et al. 2013, Kim et al. 2015, Paluck et al. 2016, Valente and Pumpuang 2007].

Similar problems (related to information dissemination on social networks) have also been extensively studied in computer science. In particular, the *influence maximization* problem, formalized by [Kempe et al. 2003], asks how a limited number of seed nodes can be selected from a social network to maximize information diffusion. The influence maximization problem has been the subject of extensive work by the theoretical computer science and artificial intelligence communities [Borgs et al. 2014, Chen et al. 2009, 2010, Goyal et al. 2011, Tang et al. 2014]. However, to our knowledge, no work prior to this project had connected the computational literature on influence maximization to the use of network-driven interventions in public health and related fields. Computational work in this field has mainly focused on developing highly efficient algorithms for use on large-scale social media networks (often motivated by advertising applications), while interventionists in health domains have not used explicitly algorithmic approaches to optimize the selection of peer leaders. This large gap between the theory of influence maximization and its practice may have been exacerbated by the fact that previous computational work on influence maximization assumes access to data (e.g., the full network structure and a stochastic model of information spread) which are simply not available in real-world public health contexts.

This chapter reports the results of a project which bridges the gap between computational work on influence maximization and corresponding health interventions in the real world. As a research team composed of computer scientists and social workers, we developed, implemented, and evaluated an intervention for HIV prevention in YEH where the peer leaders are algorithmically selected. This intervention was developed over the course of several years, alternating between algorithm design and smaller-scale pilot tests to evaluate feasibility. The final system, which we refer to as CHANGE (CompreHensive Adaptive Network samplinG for social influence), was evaluated in a large-scale clinical trial enrolling 713 youth across two years and three geographical sites. The trial compared interventions planned with CHANGE to those using the standard public health methodology of selecting the youth with highest degree centrality (DC), as well as an observation-only control group (OBS). *Results from this clinical trial demonstrate that CHANGE was substantially more effective than the standard DC method at increasing adoption of behaviors protective against HIV spread.* To our knowledge, this is the first empirically validated success of using AI methods to improve social network interventions for health. It is critically important for “AI for Social Good” work to result in deployed and rigorously evaluated interventions, and this chapter provides one such example.

The remainder of the chapter is organized as follows. First, we survey related work from both a computational and application perspective. Second, we introduce a formalization of the problem of selecting peer leaders from a computational perspective. Third, we briefly review the design of the CHANGE system to address this problem (deferring most details to earlier technical publications [Wilder 2018, Wilder et al. 2018a,b]). Fourth, we present the design of the clinical trial. Fifth, we present and analyze results from the trial. Sixth, we discuss lessons learned over the course of the project which may help inform future attempts to design and implement AI-augmented public health interventions.

Related Work

A great deal of research in computer science has been devoted to the influence maximization problem. The majority of this work has focused on computationally efficient algorithms for large social networks [Borgs et al. 2014, Chen et al. 2009, 2010, Goyal et al. 2011, Tang et al. 2014] and assumes that the underlying social network and model of information diffusion are perfectly known. There is also more recent literature on algorithms to learn or explore these properties. Predominantly though, such work requires many repeated interactions with the system. For example, algorithms to estimate the parameters of an unknown model of information diffusion [Du et al. 2014, He et al. 2016, Kalimeris et al. 2018, Narasimhan et al. 2015, Pouget-Abadie and Horel 2015] typically require the observation of hundreds of cascades on the same network. Collecting this amount of data is intractable for public health interventions, where a single round of the intervention takes months. Other work concerns the bandit setting, where the algorithm can repeatedly select sets of nodes and observe the

resulting cascade [Chen et al. 2013, Wang and Chen 2017, Wen et al. 2017]. Similarly, these algorithms accept poor performance in early rounds as the price for improvement over the long run, but waiting tens or hundreds of rounds for improved performance is not an option in our domain. Such techniques are a much better fit for problems concerning online social networks (for example, in advertising domains) where repeated experiments and large datasets are possible.

The most closely related computational work to ours concerns a robust version of the influence maximization problem [Chen et al. 2016, He and Kempe 2018, Lowalekar et al. 2016], building on the earlier work of [Krause et al. 2008] on general robust submodular maximization problems. Our algorithm for robust submodular optimization, for which an overview is provided below, differs from these approaches mainly in that it solves a fractional relaxation of the problem instead of repeatedly calling a greedy algorithm for discrete submodular optimization, which helps improve computational performance.

There is a large literature on social network interventions in public health [Kim et al. 2015, Valente and Pumpuang 2007], clinical medicine [Young et al. 2003], international development [Banerjee et al. 2013, Cai et al. 2015], education [Paluck et al. 2016], etc. Common strategies involve selecting high degree nodes (as compared to in our trial), selecting nodes at random, or asking members of the population to nominate others as influencers. The empirical evidence for the relative effectiveness of different strategies is mixed; [Kim et al. 2015] reports no or marginal improvement for nominations vs random selections (depending on the outcome measure), while [Banerjee et al. 2019] report statistically significant improvements for a nomination-based selection mechanism. [Chin et al. 2018] introduce improved statistical methods to compare the effectiveness of seeding strategies and conclude that nomination-based strategies do not measurably improve performance. Indeed, [Akbarpour et al. 2018] show that in some theoretical network models it may be preferable to recruit a slightly larger number of influencers at random rather than carefully map the network. We contribute to this literature by developing and empirically evaluating an algorithmic framework which combines both features reminiscent of the nomination-based strategies proposed by others (for gathering information about network structure) as well as robust optimization techniques for jointly optimizing the entire set of influencers who are selected (not part of previous empirically evaluated strategies). Our clinical trial demonstrates statistically significant improvements from this strategy compared to the baseline of selecting high-degree nodes, providing (to our knowledge) the first real-world evidence that systematic optimization leads to improved results.

Problem Description

The population of youth are the nodes of a graph $G = (V, E)$. We seek to recruit a set of youth S to be peer leaders, where $|S| \leq k$. In domain terms, this budget constraint reflects the fact that peer leaders are given a resource-intensive training and support process. The objective is to

maximize the total expected number of youth who receive information about HIV prevention, given by the function $f(S)$. Here, f encapsulates the dynamics of a probabilistic model of information diffusion across the network (discussed below). The optimization problem $\max_{|S| \leq k} f(S)$ is the subject of the well-known influence maximization problem. When the objective function f is instantiated using common models for information diffusion, the resulting optimization problem is submodular (i.e., there are diminishing returns to selecting additional peer leaders). While finding an optimal solution is NP-hard, a simple greedy algorithm obtains a $(1 - 1/e)$ -approximation [Kempe et al. 2003].

The most common choice for the model of information diffusion is the independent cascade model. In this model, each node who receives information transmits it to each of their neighbors with probability p . All such events are independent. The process proceeds in discrete time steps where each newly informed node attempts to inform each of their neighbors, and concludes when there are no new activations. $f(S)$ calculates the number of nodes who receive information when the nodes S are informed at the start of the process, in expectation over the random propagation.

The standard influence maximization problem concludes here. However, while developing an algorithmic framework applicable to public health contexts, we came across challenges which must be solved before, during, and after the setting imagined in standard influence maximization. These challenges opened up new algorithmic questions, addressed in a series of publications in the AI literature [Hu et al. 2018, Rice et al. 2018, Wilder 2018, Wilder et al. 2017, 2018a,b, Yadav et al. 2015, 2016a,b,c, 2017a,b,c, 2018a,b,c]. Here, we detail three steps for deploying an influence maximization intervention in the field.

First, information about the network structure G must be gathered. Previous work on influence maximization assumed that the network structure is known in advance. While this assumption may be reasonable for online social networks, we aim to disseminate information through the network consisting of real-world interactions between youth at a given center. Moreover, pilot studies revealed that information from an online social network (Facebook) was a poor proxy for actual connections at the center – not all youth used Facebook, and of those who did, many were not friends with their actual contacts at the drop-in center. Instead, network information must be gathered through in-person interviews where social workers ask youth to list those who they regularly interact with. Collecting data in this manner is time-consuming and expensive, often requiring a week or more of effort on the part of the social work team. Accordingly, the first stage of our algorithmic problem is to decide which nodes to query for network information. The algorithm is allowed to make M queries, where each query reveals the edges associated with the selected node. The queries can be adaptive, i.e., the choice of the i th node to be queried can depend on the answers given by nodes $1 \dots i - 1$.

Second, this network information is used to select an initial set of peer leaders. This stage more closely resembles the standard influence maximization problem. However, there is an additional complication that the propagation probability p is not known. Indeed, there is no

data source from which it could be inferred (as opposed to online platforms with abundant data; see related work). Instead, we formulate an uncertainty set \mathcal{U} containing a set of possible values for p which are consistent with prior knowledge (in CHANGE, we took \mathcal{U} to be a discretization of the interval $[0,1]$, reflecting limited prior knowledge). The aim is to find a set S which performs near-optimally for every scenario contained in \mathcal{U} . Formally, this corresponds to the robust optimization problem

$$\max_{|S| \leq k} \min_{p \in \mathcal{U}} \frac{f(S, p)}{OPT(p)}$$

where $OPT(p)$ denotes $\max_{|S| \leq k} f(S, p)$, i.e., the best achievable objective value if the propagation probability p were known. Normalizing by $OPT(p)$ encourages the algorithm to find a set S which simultaneously well-approximates the optimal value for each $p \in \mathcal{U}$ and avoids the trivial solution where solution to the inner min problem is always the smallest possible value of p . Note that since $OPT(p)$ is constant with respect to S , $\frac{f(S, p)}{OPT(p)}$ remains submodular with respect to S . Robust optimization of submodular functions is substantially more difficult than optimization of a single submodular function; in fact, it is provably inapproximable in general [Krause et al. 2008] and the aim is instead to approximate a tractable relaxation of the problem.

Third, after an initial set of peer leaders S is identified, recruitment proceeds in an adaptive manner. Not all youth invited to become peer leaders will actually attend the training session. A number of potential barriers exist, e.g., a given youth could have been arrested or not have had enough money for a bus ticket. Formally, we model that each youth who is invited will actually attend with probability q (based on experience in pilot studies, we took $q = 0.5$), where the attendance of each youth is independent of the others. For a given value of p , the resulting objective function is $f(S, p, q)$, which takes an expectation over both the randomness in which nodes are successfully influenced at the start of the process and in the subsequent diffusion. It is easy to show [Wilder et al. 2018b] that f remains submodular with this additional randomness. Because of this variation in attendance, as well as capacity limits for the initial training, peer leaders are recruited over multiple rounds, where the peer leaders selected in round t can depend on those who were successfully recruited in rounds $1 \dots t - 1$. In each round t , we select a set of peer leaders S_t with $|S_t| \leq k_t$ and observe which nodes are successfully recruited as peer leaders. The process continues for T rounds in total.

System Design

Our final proposed system for intervention planning is called CHANGE. CHANGE was originally introduced in [Wilder et al. 2018b]. The final version of CHANGE summarized here is nearly the same as the original, with the exception of the algorithm used for robust optimization, which was separately developed and published in [Wilder 2018]. We now provide an overview of CHANGE, mirroring the steps of the earlier problem formulation.

Network sampling

CHANGE uses a simple but well-motivated heuristic to select a subset of nodes to be queried for network information (in the discussion section, we briefly review our earlier work on a more theoretically sophisticated solution, and the rationale for choosing a simpler method). The chosen method splits the query budget M into two halves. Each query in the first half is made to a node selected uniformly at random from the network. Each query in the second half follows a query in the first half, and selects a uniformly random neighbor of the first node. This design is motivated by the friendship paradox, the observation that high-degree nodes are overrepresented when we sample random neighbors [Feld 1991]. Hence, the two stages of the query process balance between competing objectives: the first step encourages diversity, since random sampling ensures that we cover many different parts of the network, while the second step tends towards high-degree nodes who can reveal a great deal of network information.

Robust optimization

We now provide an overview of how CHANGE handles parameter uncertainty within a single stage of the planning process, before considering the multi-stage problem (with uncertain attendance) below. As mentioned above, max-min submodular optimization is NP-hard to approximate (within any nonzero factor) [Krause et al. 2008]. Accordingly, we need to somehow relax the problem to obtain meaningful guarantees. Let I denote the set of all feasible solutions (sets S where $|S| \leq k$) and $\Delta(I)$ be the set of all distributions over I (i.e., the $|I|$ -dimensional simplex). We developed an algorithm for the problem

$$\max_{D \in \Delta(I)} \min_{p \in \mathcal{U}S \sim D} \mathbb{E} \left[\frac{f(S, p)}{OPT(p)} \right] \quad (0.1)$$

which allows the algorithm to select a distribution over feasible sets and evaluates the worst case only in expectation over this distribution. In game theoretic terms, this allows the algorithm to select a mixed strategy instead of a pure strategy. At run-time, we sample from D ; the resulting set has guaranteed performance in expectation over the sampling, but strong guarantees cannot be obtained ex-post for the sampled set (as a result of the computational hardness of the original max-min problem). However, in practice we find that sampling several random sets and selecting the best one gives excellent empirical performance (i.e., closely matching or exceeding the expected value of the distribution).

Our algorithm for this problem, detailed in [Wilder 2018], uses a compact representation of the space of distributions (keeping track of only the marginal probability that each node is selected instead of each of the exponentially many potential subsets). It solves a fractional relaxation of the discrete max-min problem using this compact representation via a stochastic first-order method which is adapted to the particular properties of the objective. Then, we can use known rounding algorithms for submodular maximization to sample random sets from the distribution encoded by the solution to the fractional relaxation. This procedure guarantees a

$(1 - 1/e)^2$ -approximation for Problem 0.1, which can be improved to $(1 - 1/e)$ with some additional steps (which we did not find empirically necessary).

Multi-stage intervention with attendance uncertainty

We handle the multi-stage nature of the intervention by running the robust optimization problem at each stage, calculating the objective function in expectation over which peer leaders will attend and conditioning on the selection of those who have attended previous interventions. Formally, this means that at stage $t > 1$, we solve

$$\max_{D \in \Delta(I)} \min_{p \in \mathcal{U}} \mathbb{E}_{S_t \sim D} \left[\frac{f(S_t \cup S_1 \cup \dots \cup S_{t-1}, p, q)}{\max_{|S^*| \leq k} f(S^* \cup S_1 \cup \dots \cup S_{t-1}, p, q)} \right]$$

where $S_1 \dots S_{t-1}$ denote the sets of peer leaders who were successfully recruited in each previous stage. It is easy to show that the inner objective f remains submodular in S_t (see [Wilder et al. 2018b]), and so we retain the earlier guarantees on the quality of the solution obtained at each individual step. Moreover, in [Wilder et al. 2018b] we show that the multi-stage problem as a whole enjoys the property of *adaptive submodularity*, meaning that for any fixed parameter value p , solving

$$\max_{D \in \Delta(I)} \mathbb{E}_{S_t \sim D} \left[\frac{f(S_t \cup S_1 \cup \dots \cup S_{t-1}, p, q)}{\max_{|S^*| \leq k} f(S^* \cup S_1 \cup \dots \cup S_{t-1}, p, q)} \right]$$

at each step t and selecting the resulting set S_t enjoys an approximation guarantee relative to the optimal adaptive policy for selecting a sequence of sets $S_1 \dots S_t$ (again, with respect to a fixed p). More detailed discussion of the theoretical properties can be found in [Wilder et al. 2018b].

Study Design

We now move to the empirical portion of the project and provide an overview of the design of the clinical trial. All study procedures were approved by our institution’s Institutional Review Board. The study was designed to compare the efficacy of two different means of selecting peer leaders: the CHANGE system described above and the standard DC approach in public health (selecting the highest-degree youth). We additionally included an observation-only control group (OBS), for three arms in total. The study was conducted at three drop-in centers for YEH (My Friend’s Place¹, Safe Place for Youth², and Los Angeles LGBT Center³) in Los Angeles, USA. Drop-in centers provide basic services to YEH (e.g., food, clothing, case management, mobile HIV testing). Due to high transience in the YEH population, most clients at a given center leave within approximately six months. Accordingly, we tested each of the three methods at each of the three drop-in centers (giving nine deployments in total, each with a unique set of youth), ensuring that successive deployments at a given drop-in center

¹ <https://www.myfriendsplace.org/>

² <https://www.safeplaceforyouth.org/>

³ <https://lalgbtcenter.org/>

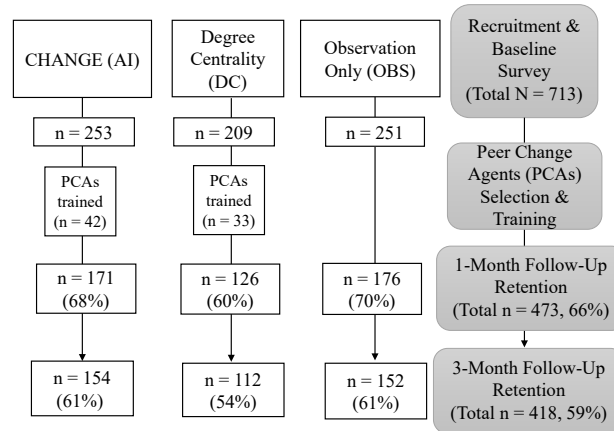


Figure 1: Number of participants recruited and retained in each arm of the study.

were separated by six months. Youth were only allowed to enroll in the study once, so even the small number of youth who were present at the center across multiple deployments were included only on the first time they attempted to enroll. Testing each method at each drop-in center helps account for differences in the demographic and other characteristics of youth who tend to access services at each center.

Each of the nine deployments used the following procedure. Figure 1 shows the number of youth recruited and retained for each phase of the study in each arm.

First, youth were recruited at the drop-in center over the course of a week to participate in the study. All participants gave informed consent. Each participant completed a baseline survey which assessed demographic characteristics, sexual behaviors, and HIV knowledge. Demographic characteristics included age, birth sex, gender identity, race/ethnicity, and sexual orientation. Youth were also surveyed about their living situation and relationship status.

Second, peer leaders were selected and trained (for the CHANGE and DC arms of the study). Each individual training consisted of approximately 4 youth and there were 3-4 trainings per deployment (depending on exact attendance). In total, approximately 15% of survey participants in each deployment were trained as peer leaders. In the CHANGE arm of the study, network information was queried from approximately 20% of the participants (sampled according to the mechanism described above). In the DC arm, we used a full survey of the network to find high-degree nodes, in order to give the strongest possible implementation to compare to.

Third, peer leaders had three months to disseminate HIV prevention messages. Peer leaders were supported via 7 weeks of 30-minute check-in sessions with study researchers, which focused on positive reinforcement of their successes as well as problem-solving strategies

and goals for the future. All peer leaders attended at least one check-in session, with modal attendance at five sessions. Peer leaders received \$60 in compensation for attending the initial training and \$20 for each check-in session.

Fourth, follow-up surveys were administered to the original study participants from the first step. Follow-up surveys assessed the same characteristics as the baseline survey. Differences in reported sexual behavior between baseline and follow-up were used as the primary metrics to evaluate the interventions. All such metrics were self-reported; we followed best practices in social science research to minimize bias in self-reported data (surveys were self-administered on a tablet and participants were guaranteed anonymity, each of which aim to reduce social desirability bias in reporting sensitive information). Additionally, any bias would be expected to influence each arm of the study equally, including the observation-only control group.

The training component of the peer change agent intervention was delivered by two or three facilitators from the social work research team. The training lasted approximately 4 hours (one half-day). Training was interactive and broken into six 45-minute modules on the mission of peer leaders (sexual health, HIV prevention, communication skills, leadership skills, and self-care). Peer leaders were asked to promote regular HIV testing and condom use through communication with their social ties at the drop-in center.

Study Results

We now present the results of the clinical trial, starting with an overview of the outcome variables and methodology for statistical analysis, and then giving the main results.

Outcome Variables

We compare two outcome variables across arms of the study. First, condomless anal sex (CAS), assessed via a survey question asking whether youth had anal sex without a condom at least once in the previous month. Second, condomless vaginal sex (CVS), assessed via a survey question asking whether youth had vaginal sex without a condom at least once in the previous month. CAS and CVS are both important behavioral risk factors for HIV transmission and so provide a direct assessment of the success of the intervention at producing a material health impact.

Statistical Methodology

We now discuss statistical methods for analyzing the result of an experiment like the one conducted. The goal of such methods is to analyze the *treatment effect*, or the difference in some outcome attributable to the intervention that individuals are assigned to. In our case, the treatment effects we would like to estimate are the expected reduction in the likelihood of engaging in condomless sex due to inclusion in either the CHANGE or the degree centrality arm of the study compared to no intervention, i.e., the control group.

To briefly review, there are two principal ways of analyzing the results of a field trial under “normal” circumstances (where the ways in which our setting is “abnormal” will be clarified later). The first method is to simply average the outcomes of participants in each arm of the trial and report confidence intervals or p -values based on simple formulas for the mean of IID random variables. The second common method is to specify a statistical model (often linear) for the outcome as a function of pre-treatment covariates (e.g., demographic variables) as well as the treatment assignment. This can help improve the precision of the estimated treatment effect (i.e., lower its variance) when the pre-treatment covariates are correlated with the outcome. Although the simple sample mean estimator is unbiased, randomization is expected to create differences in the pre-treatment covariates of individuals assigned to different arms, which creates variance. A model-based analysis helps reduce this variance by controlling for these random baseline differences (at the potential cost of introducing bias under some circumstances if the model is misspecified). See [Sheldon 2000] for a more detailed discussion. Approaches based on regression adjustments (typically with linear or logistic models) are very common in applied settings such as medicine and public health because the reduction in variance from controlling for covariates is sufficiently great that it is viewed as worthwhile to accept some potential bias from model misspecification.

Our setting deviates from the standard picture in that our measurements are not all IID. In fact, the IID assumption fails in two notable ways. First, the very premise of the study is that participants will be influenced by one another. This is a form of *interference*, where the outcomes of participants within the same group will be correlated via the spread of behaviors among them. This means that attempts to treat the responses as independent will produce overly optimistic confidence intervals. In the most pessimistic scenario, the effective number of independent samples we see could be as low as one sample per network, if the respondents within each network were perfectly correlated. Reality lies somewhere in the middle, where participants within the same network are imperfectly correlated, meaning that we have less information than if all of their responses were independent, but nevertheless more than if there if the entire network were completely correlated.

Second, we make multiple post-treatment measurements of the same individual (at one and three months after the intervention). These measurements are also correlated with one another, since we expect there to be (unobserved) characteristics of each individual person that influence their outcomes across time. Again, while these data points are not fully independent, we may still nevertheless be able to increase the precision of our estimates by jointly analyzing all of the responses instead of limiting ourselves to the smaller sample collected at a fixed time point.

A wide range of methods have been proposed in statistics, econometrics, and epidemiology to accommodate these structured forms of dependencies between observations. We do not give a complete treatment of these methods here, but will provide an overview of the main advantages and disadvantages of these methods as they pertain to the setting at hand.

One family of methods starts with one of the usual estimators discussed above but attempts to correct for interference (either within individuals or within networks) in the confidence intervals or p -values that are associated with the estimates. Effectively, we should think of our estimator as having higher variance due to the fact that some of our observations are correlated with one another, leading to wider confidence intervals. This idea is instantiated via a particular method for approximating the sampling variance of the treatment effect estimator. It is often referred to as “clustered standard errors” because it produces standard errors which account for the clustering of observations into groups within which correlations are possible. Clustered standard errors are an extension of the standard “sandwich estimator” of the variance of an estimand. Asymptotically, the sandwich estimator will produce consistent estimates of the standard errors of the estimator which, for an asymptotically normal estimator, can in turn be translated into confidence intervals or p -values. This asymptotic validity is a desirable property which does not require making distributional assumptions about the data (besides assumptions on the model or design which underlie the cluster structure). However, these methods are potentially problematic for our circumstances because we have only nine groups – too small for asymptotics to be meaningful – and simulation experiments have shown that the sandwich estimator may perform poorly in this few-clusters regime.

A second family of methods goes by a variety of names – random or mixed effects models, hierarchical models, multi-level models, etc [Gelman 2006]. These methods impose stronger distributional assumptions on the data. In particular, they model the data as being drawn from a statistical model (typically linear) which contains a shared, random error term across all observations within the same group, in contrast to the standard regression model where error terms are independent across observations. This shared error induces correlations in observations within the group. Consider an example where the groups correspond to the different nine different networks we intervene on. Intuitively, we can think of the shared error as modeling that, while the expected outcomes of individuals in a given network will depend on their covariates and treatment assignments through whatever regression equation is specified, the individuals in a given network will tend to all deviate from their expected outcomes in the same direction, depending on whether their shared diffusion process spread more or less widely than expected. The shared error term is typically modeled as drawn from a normal distribution and must be uncorrelated with the covariates of individuals in the group. If these assumptions are satisfied, we have more powerful statistical tools at our disposal with which to analyze the results. These can take the form of either frequentist hypothesis tests (after fitting the model with maximum likelihood) or Bayesian analyses which produce a full posterior over the parameters of interest.

Our analysis employs a Bayesian mixed-effects model, as this allows us to obtain a full posterior distribution over the treatment effect in a manner which accounts for the small number of clusters (i.e., avoids potentially inappropriate asymptotic approximations). We specified a linear model for each outcome variable which included terms for both the

improvement caused by participating in a given arm of the study (our estimand of interest) as well as terms for a range of control variables which account for differences in demographics and the baseline rate of risk behaviors in each arm of the study. The demographic control variables were age, birth sex, transgender identity, LGBQ identity, the combination of male sex and LGBQ identity, race, committed relationship, housing status, and drop-in center. We also included a “time” variable to account for changes in the entire population over time regardless of participation in a particular arm of the study. This combination of control variables helps separate the impact of the intervention from pre-existing differences between arms of the study and intervention-independent trends. Since the outcome of interest is binary, we used a logistic link function in the model.

We also incorporate random effects in the model to account for potential correlations between data points, as discussed above. We incorporate one such random effect for each participant and one for each intervention group, modeling the nested dependence structure of the data. Let x_i denote the covariates for individual i , $a_{\text{CHANGE},i}$ be an indicator variable for the assignment of individual i to the CHANGE arm, $a_{\text{DC},i}$ be an indicator variable for the assignment of individual i to the DC arm, $c(i)$ denote the intervention group of individual i , p_i be an indicator variable for the selection of individual i as a peer leader, and β be the model parameters. The end model is of the following form:

$$\text{logit}(y_{it}) = \beta_{\text{cov}} x_i + \beta_{\text{CHANGE}} \cdot t \cdot a_{\text{CHANGE},i} + \beta_{\text{DC}} \cdot t \cdot a_{\text{DC},i} + \beta_{\text{PL}} \cdot t \cdot p_i + \epsilon_i + \epsilon_{c(i)} + \epsilon_{it}.$$

In this model, log-odds of the outcome y_{it} are influenced by several sets of contributions. First, there is a contribution from the individual-level covariates, estimated as β_{cov} . Second, there is a contribution from assignment to a treatment arm, estimated as β_{CHANGE} and β_{DC} respectively. These terms are incorporated in the model as interactions between the treatment assignment and time, modeling improvement over time in individuals assigned to a given arm. Third, we control for improvement in individuals selected as peer leaders (regardless of which arm of the intervention they are in) via the inclusion of a time-peer leader interaction with coefficient β_{PL} . This helps us isolate improvement in the directly treated peer leaders from spillover into the group as a whole. Finally, we include the random effects ϵ_i and $\epsilon_{c(i)}$, which respectively capture correlations in multiple responses from the same individual and in responses from individuals in the same group. ϵ_{it} is an independent random term for each response. We also tested a Mundlak-Chamberlain style specification which guards against violations of the assumptions of random effects models by allowing the $\epsilon_{c(i)}$ to be correlated with the group means of the covariates [Chamberlain 1982, Mundlak 1978]. This model resulted in essentially identical estimates. We employ a Bayesian analysis with inference performed using `rstan` [Stan Development Team 2023], in which we obtain a posterior distribution over the model parameters of interest (using the default weakly informative priors provided by `rstan`).

We present the results in terms of 90% and 95% credible intervals over the estimated model parameters. For the treatment effects associated with CHANGE and DC, we also show the posterior over the relative risk, which averages out over the distribution of other covariates in the study population to obtain the average risk of a given outcome in participants in the treatment arm in question compared to the control group. For example, a relative risk of 80% indicates that, on average, a participant in the given treatment arm has 80% of the probability of a given behavior compared to a participant in the control group, all other features held equal.

Results are known only for youth who completed the follow-up surveys, leading to missing data due to participant attrition (as is expected for a study enrolling YEH). Of the 713 participants who completed the baseline survey, 245 (34%) missed the 1-month follow-up, 300 (42%) missed the 3-month follow-up, and 180 (25%) missed both follow-ups. However, missingness had no statistically significant association with CAS or CVS, indicating that youth were not significantly over or under represented in the follow-up data based on their baseline level of risk behavior.

Results

We now present the main results of the statistical analysis, shown in Figure 2. As shown in the figures, for both outcomes there is little evidence of a baseline difference between the arms or of an intervention-independent improvement over time (i.e., the credible intervals for all such estimated parameters include 0).

We find that CAS reduced in the CHANGE group over time, with a posterior median relative risk of 0.58 (95% CrI: 0.35-0.93). The relative risk of 0.58 indicates that, in the model estimates, a youth who is enrolled in the CHANGE arm of the study has 42% lower probability to engage in CAS than if they were enrolled in the observation-only group. That is, on average a youth who is enrolled in CHANGE has 42% lower probability to engage in CAS post-intervention than a youth with identical starting characteristics (including baseline rate of CAS) who did not receive the intervention. For the DC group, the posterior median of 0.70 relative risk indicated a tendency towards improvement, though the 95% credible interval did not exclude 1 (95% CrI: 0.39, 1.15) and so an improvement cannot be demonstrated with high probability.

Moving to the second outcome, the model estimated that the median relative risk for CVS in the CHANGE group was 0.73, with credible interval narrowly inclusive of 1 (95% CrI: 0.50, 1.01). The 90% credible interval excluded 1, as shown in Figure 2. For the DC group, the median relative risk was 0.84 (95% CrI: 0.54, 1.21).

We conclude from the analysis that CHANGE produced an improvement in HIV risk behaviors with high probability (at least 97.3% probability of improvement in the posterior for both outcomes). DC showed a tendency towards improvement in these behaviors but a neutral or negative effect could not be excluded at the 90% credible interval level. Since the

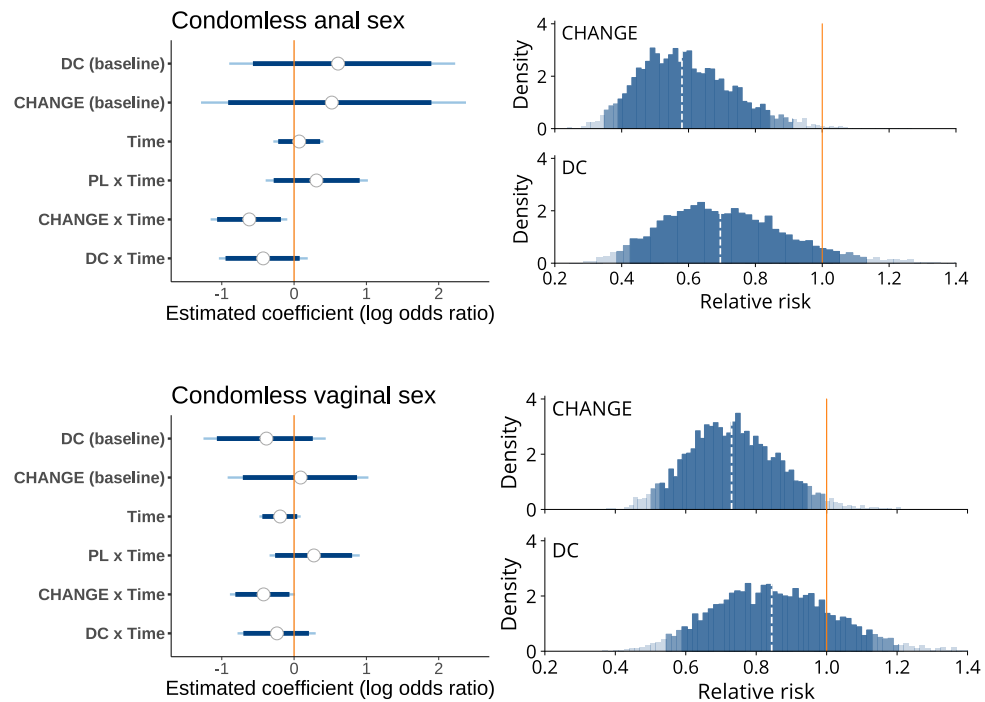


Figure 2: Posterior estimates for the CAS (top) and CVS (bottom) outcomes. Left: credible intervals for estimated coefficients in the linear mixed effects model. Thick lines denote 90% credible intervals, thin lines denote 95% credible intervals, and circles denote the posterior median. Right: posterior distribution of the relative risk post-intervention for each treatment arm. Shaded regions denote the 90% and 95% credible intervals, with the dashed line giving the posterior median. In the left-hand figure, the “baseline” category measures pre-existing differences between the groups (relative to the observation-only group) on enrollment in the study. The “Group x Time” category measures the estimated per-unit-time impact of participating in each arm of the intervention (relative to the observation-only group, and after controlling for both demographics and baseline behaviors). “PL x Time” refers to improvement over time in youth selected to be peer leaders across either arm of the intervention. “Time” gives the estimated contribution of a trend over time independent of which arm of the study a participant was enrolled in.

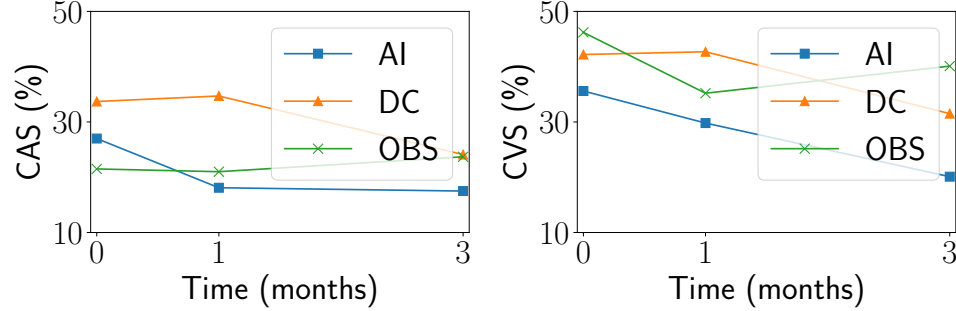


Figure 3: Average value of each outcome variable at each point in time for the three arms. These plots show the results without any statistical processing, while the analysis above attempts to control for pre-existing differences between participants in each arm.

analysis controlled for the selection of youth as peer leaders, estimated improvements can be attributed to changes across the entire group, including youth who were not selected as peer leaders. This provides evidence that the intervention created improvements via spillovers from the directly treated peer leaders to the youth who were not selected, as hoped.

Direct examination of the average values of the outcome variables for each arm at each point in time (Figure 3) shows another interesting trend. Improvements in the CHANGE group happen faster than the DC group: most of the improvement for CHANGE occurs by the one-month survey, while improvements in the DC group are not fully realized until month three. Fast results are important for two reasons. First, rapid adoption of protective behaviors helps to immediately curtail transmission in a high-risk population. Second, high transience among YEH means that a non-negligible portion of youth will have left the center by the time a three-month intervention is completed. We conclude that the AI-augmented intervention implemented with CHANGE has an additional potential advantage over an intervention where peer leaders are selected with the standard DC method.

Discussion

This project provides evidence that AI methods can be used to improve the effectiveness of social network interventions in public health: significant reductions in HIV risk behaviors were observed in groups where our CHANGE method was used to plan the intervention, with no significant changes in behavior when the status quo method (selecting high degree nodes) was employed. More broadly, we hope that our experiences over the course of the project can provide generalizable lessons about how AI research can be successfully employed for social good. There have been recent attempts by others to synthesize principles for AI for Social Good research [Floridi et al. 2020, Tomašev et al. 2020]. We offer a complementary

perspective shaped by the process of deploying a specific community-level intervention. In particular, existing discussions of best practice often focus in large part on ethics, data privacy, and building trust with stakeholders. While such considerations are indispensable, it is also important for the research community to investigate the on-the-ground components of developing and deploying an impactful intervention. We highlight five points.

First, the starting point was to listen to domain experts and understand where in the problem domain AI could be most impactful. We did not approach this project with a preexisting intention to apply influence maximization to the choice of peer leaders. Rather, this emerged organically from discussions between the AI and social work sides of the research team as a topic where an AI-augmented intervention was both technically feasible and likely to improve outcomes. *Success is less likely when AI researchers start with a favored technique and search for an application.*

Second, data was overwhelmingly the bottleneck to the AI component of the intervention. Computational work on influence maximization to date had largely assumed a great deal of information would be known – the structure of the graph, the model for information diffusion, etc. None of this information was in fact available for YEH (or would likely be available in other public health settings). Moreover, gathering this data is itself time-consuming and costly, requiring unsustainable effort on the part of an agency wishing to deploy the intervention on their own. Much of the technical focus of the research consisted of finding ways to reduce the amount of data which needed to be gathered for the intervention to succeed. *Finding ways to reduce or eliminate data needs through improved algorithm design is an important part of producing deployable AI interventions in a community health context.*

Third, simplicity is valuable. As an example, prior to developing CHANGE, we designed a much more theoretically sophisticated algorithm for collecting network data which enjoyed provable guarantees for certain families of graphs [Wilder et al. 2018a]. However, it quickly became apparent that this algorithm would be difficult to deploy in practice because it required a large number of sequential queries (the node which is queried on step 1 determines the node who is to be queried on step 2, and so on). This was impractical in the context of a program working with YEH where any given youth may be difficult to find, interrupting the entire process. More generally, if the algorithm requires tight coupling with the outside world (many steps where information is input, the algorithm recommends a very specific action, more information is input, and so on) then there are more things that can go wrong which are not captured in the computational formalization of the problem. This poses a contrast to the way that simplicity is often operationalized in AI for social good work as either *explainability* [Floridi et al. 2020] or as *methodological* simplicity [Tomašev et al. 2020] (e.g., using well-developed techniques instead of a new algorithm). Both explainability and methodological simplicity are of course valuable in many settings but in our experience neither was first-order requirement: the algorithm can solve a complex optimization problem internally so long as

the way that it interacts with the outside world is simple and robust. *We believe that this operational simplicity is an under-emphasized design criterion for AI for Social Good.*

Fourth, smaller pilot tests were a valuable part of the project prior to embarking on a larger clinical trial. We conducted several such tests, each of which consisted of a deployment at a single drop-in center, in order to test earlier versions of our system [Wilder et al. 2018b, Yadav et al. 2016b, 2017c]. This helped reveal key issues which needed to be addressed. For example, we quickly discovered that a plan to collect network information via Facebook was not viable with this population and that manual collection of network data entailed a great deal of effort. We also quickly observed that peer leaders often did not attend the training, requiring on-the-fly adjustments over the course of the program. Addressing such issues was necessary to the success of the overall project (and turned out to provide much of the technical challenge involved). *It would have been very difficult to identify these challenges without piloting algorithms in the actual environment where they will be used.* It was also helpful for computer scientists on the research team to be regularly present onsite during the pilot deployments to learn more about the environment and help coordinate the initial attempts at using the algorithm.

Fifth, community engagement and trust was essential to the success of the project. Beyond the research team, a number of stakeholders needed to be involved in the process. For example, we needed buy-in from each of the drop-in centers to conduct the study at the center, enroll their clients, and use their facilities. We regularly convened a community advisory board with representatives from each of the drop-in centers along with members of the research team to provide information about the study progress, explain the methods being used, and share information which could be helpful to other center activities. Just as critical as the center leadership though, were the youth themselves. We asked youth to disclose sensitive information, including their HIV risk behaviors and social contacts. Especially for the YEH population, which is less inclined than most to engage with authority figures, building trust is essential. We found two factors to be especially important in establishing this trust. First, the social work portion of the research team had deep roots in the community, having regularly offered services at these drop-in centers for the past ten years. Second, transparency about why information was being collected was critical. We observed substantially increased willingness to disclose information related to social contacts when researchers explained how this information would be used in the study (i.e., that a computer program would be used to select some people as peer leaders based on their contacts) than when such an explanation was not proactively given. *A critical part of the peer change agent model is empowering youth to make a difference in their community, and this philosophy extends to the way that AI should be used in a community setting.*

Our hope is that this project provides one example towards a broader research agenda aiming at AI techniques which can be successfully used to improve health and equity within our communities. A great deal of work remains. Just within the context of social network inter-

vention, future work should explore other intervention designs (e.g., interventions which attempt to modify network structure by fostering supportive relationships), methods for further reducing data requirements (e.g., by using administrative data to infer social connections), and more deeply investigate the relationship between information diffusion and behavioral change. However, the results from this clinical trial provide evidence that AI can substantially improve the quality of services offered to the most vulnerable among us.

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