

A Model Selection Approach to Interference*

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Abstract

In many social science applications, a process of interest occurring in one unit has consequences for the outcomes of other units, a phenomenon known as interference. Current methods to analyze interference or spillovers from a causal inference perspective assume that the researcher knows the relevant pathways through which interference occurs and can use that information to identify which units are plausibly exposed to treatment. In most cases, this assumption is not justifiable, which means researchers must make modeling decisions that are only indirectly informed by theory. Moreover, the discipline currently lacks standards to evaluate the appropriateness of alternative operationalizations. Focusing on the case of converting distance metrics into treatment exposures, this paper suggests approaching the problem as a model selection task. Researchers can use the desired performance criterion, algorithm, and selection strategy to choose the most appropriate model of interference given the data and estimation target. This paper focuses on inverse probability weighting estimators, cross-validation, and the lasso family of methods, but the ideas are general enough to fit researchers' theoretical and analytical needs. I illustrate the effectiveness of this approach an application to a study of voter registration irregularities in Ghana and simulations.

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1 Introduction

In the causal inference framework, interference or spillovers occur when a unit’s potential outcome depends on the treatment assignment of other units (Cox 1958). This is a violation of the stable unit treatment value assumption (SUTVA) used to justify the implementation of common design-based estimators (Rubin 1990). Some scholarship aims at detecting interference (Aronow 2012) or recovering the ability to identify causal effects in its presence (Sävje, Aronow, and Hudgens 2019). However, in the social sciences, interference can be a phenomenon of interest by itself. For example, research on electoral fraud suggests that the presence of election observers reduces irregularities in treated units, but increases them in nearby localities (Ichino and Schündeln 2012; Asunka et al. 2017).

Detecting and estimating interference in the causal inference framework is an active research agenda (see Halloran and Hudgens 2016; Aronow et al. 2021; Ogburn and VanderWeele 2014 for overviews). Current approaches assume the researcher knows the pathway(s) through which interference occurs. For example, Aronow and Samii (2017) propose a general estimator of the average unit-level causal effect of experiencing different exposure regimes, which requires knowledge of what units are exposed to treatment.¹ Similarly, Hudgens and Halloran (2008) develop estimators for several quantities of interest under the assumption that interference occurs within, but not across, groups or strata. Beyond estimation, Bowers, Fredrickson, and Panagopoulos (2013) introduce a framework to test hypotheses of counterfactual causal effects under a theoretically informed model of interference. As with any application of mathematical models, this approach assumes a correct model specification.²

These type of assumptions are not verifiable, but researchers can justify them with research designs meant to capture interference, such as multilevel experiments (Sinclair, McConnell,

¹I use “exposure to treatment” as a shorthand for “being exposed to a treated unit.” This means we suspect that the outcome of the unit in question may be affected by the treatment status of those it is exposed to.

²See also Toulis and Kao (2013), Athey, Eckles, and Imbens (2018), and Base, Feller, and Toulis (2019) for alternative approaches with similar assumptions.

and Green 2012), saturation designs (Baird et al. 2018), or natural experiments (Keele and Titiunik 2018).

In many social science applications, these research designs are not feasible. If the known pathways assumption is not met, the resulting estimates may be biased (Aronow et al. 2021). This paper focuses on estimating interference effects when researchers' domain expertise suggests a pathway for interference, but does not indicate how units connect to each other. For example, we may know units' geographic location, but not how a distant treated unit interferes with the outcome of others. To make a statement about what units are exposed to treatment, we must convert observed pairwise distances into exposures. This conversion is a decision that follows from theory, but is not directly informed by it, and the discipline currently lacks standards to determine whether a specific conversion is more appropriate than alternative operationalizations.

I argue that we can approach this challenge as a model selection task. We can think of alternative conversions from pairwise distances to exposures as a set of alternative models, or variables within a model, among which the researcher can select the one that best satisfies a performance criterion, given an algorithm and selection strategy of choice. While this paper focuses primarily on inverse probability weighted difference in means (Aronow and Middleton 2013; Aronow and Samii 2017), cross-validation, and the lasso-family methods for model selection (see Ratkovic and Tingley 2017 for an overview), I propose a general protocol that researchers can adapt to fit their theoretical and estimation needs.

The choice of model selection strategy depends on two decisions. First, the researcher must decide whether the purpose is to estimate categorical (e.g. Aronow and Samii 2017) or marginal exposure effects (e.g. Hudgens and Halloran 2008). Second, whether the task is to estimate a single global effect or multiple local effects at different ranges. I illustrate how to navigate these decisions with a reanalysis of an experiment dedigned to capture the spillover effect of election observers on voter registration irregularities in Ghana (Ichino and

Schündeln 2012), as well as with simulations of hypothetical experiments on a road network in the same country (based on Bowers et al. 2018).

The main contribution of this paper is to develop standards to assist researchers in making informed decisions while modeling interference in experiments and observational studies when the known pathways assumption is not satisfied by design. The model selection approach described here is helpful in identifying the most appropriate model among alternatives stemming from one or more theoretically relevant pathways. It extends recent work on analyzing interference when the assumption of known pathways is not sustainable. For example, Egami (2020) develops sensitivity analysis for interference in the presence of unobserved networks, and Sävje (2019) replaces the assumption of known exposure in Aronow and Samii (2017) with the weaker condition of sufficiently controlled (and hence estimable) specification errors. It also expands on recent literature using statistical learning to improve causal inference (see Blakely et al. 2019 for a general treatment), especially in the context of using supervised learning model selection algorithms prior to estimation to increase efficiency (e.g. Belloni, Chernozhukov, and Hansen 2013; Bloniarz et al. 2016).

2 Causal Inference Approaches to Interference

2.1 Setting

This section follows Aronow et al. (2021) closely. Consider an experiment conducted in a sample of N units indexed by $i = \{1, 2, \dots, N\}$. Let \mathbf{Z} denote a transposed treatment assignment vector so that $\mathbf{Z} = \{Z_1, \dots, Z_N\}^\top$. For simplicity, assume a binary treatment variable, which implies unit i 's possible treatment status is $Z_i = \{0, 1\}$. The logic in this paper still applies to multiple and continuous treatments. Based on the experimental design, the probability of treatment assignment $Pr(\mathbf{Z} = \mathbf{z})$ is known for all possible treatment vectors $\mathbf{z} \in \{0, 1\}^N$.

Assuming no interference, unit i 's potential outcome $Y_i(\mathbf{z})$ depends on its treatment assignment only, which means its observed outcome is $Y_i = z_i Y_i(1) + (1 - z_i) Y_i(0)$, where z_i is the observed treatment status of unit i . To make the absence of interference more explicit, let \mathbf{z}_{-i} and \mathbf{z}'_{-i} denote two different treatment vectors that exclude unit i 's treatment status. If potential outcomes depend on treatment assignment only, we can claim that $Y_i(z_i, \mathbf{z}_{-i}) = Y_i(z_i, \mathbf{z}'_{-i})$.

Interference implies that $Y_i(z_i, \mathbf{z}_{-i}) \neq Y_i(z_i, \mathbf{z}'_{-i})$, so we need to account for the treatment status of other units to fully characterize unit i 's potential outcome. With a binary treatment, accounting for every unit's treatment status leads unit i to have 2^N possible potential outcomes. Since this is intractable in most applications, researchers need to impose some structure. When manipulation is feasible, researchers can implement saturation (Baird et al. 2018) or multilevel (Sinclair, McConnell, and Green 2012) designs so that both treatment assignment and exposure to treatment are known. Natural experiments can also provide such a setting (e.g. Keele and Titiunik 2018). In these cases, the researcher can assume that interference occurs only within the structure imposed by the research design.³ When manipulation is not feasible, structure can come from assumptions informed by theory or domain expertise. For example, we could assume that interference is more likely among legislators with similar ideology scores (Coppock 2014), or that the presence of election observers affects electoral irregularities within a given distance radius (Ichino and Schündeln 2012).

Different assumptions about the nature of interference inform different empirical strategies. The literature on causal inference considers two alternative approaches. First, If the researcher observes how units connect with each other in a network and assumes that said network is sufficient to capture all relevant information about how treatments propagate, then they can estimate interference as the contrast across different exposures. Second, if the researcher is willing to assume that interference happens within observed groups only, they

³Even with a research design meant to capture interference, this is still an assumption that may not be credibly justified in some applications.

can estimate marginal a marginal effect of being exposed to treatment within the group. This would capture the effect of treatment saturation or the strength of exposure.

2.2 Interference as contrast across exposures

Consider the case of estimating interference in randomized experiments when the researcher knows how units connect with each other. Aronow and Samii (2017) introduce the concept of exposure mapping to characterize all the possible treatment-exposure combinations that may emerge depending on what the researcher assumes about interference. Under this setting, $Y_i(d_k)$ denotes the potential outcome of unit i under exposure k .⁴ With this, we can express the unit-level average exposure effect as

$$\tau(d_k, d_{k'}) = \frac{1}{N} \sum_{i=1}^N Y_i(d_k) - \frac{1}{N} \sum_{i=1}^N Y_i(d_{k'}) \quad (1)$$

which is the difference in means between the potential outcomes under exposures k and k' , with k' denoting any exposure different from k . For example, if we want to express the effect of being exposed to treatment among control units, we would write

$$\tau(d_{01}, d_{00}) = \frac{1}{N} \sum_{i=1}^N Y_i(d_{01}) - \frac{1}{N} \sum_{i=1}^N Y_i(d_{00}) \quad (2)$$

with $Y_i(d_{01})$ denoting the potential outcome of unit i when assigned to control and exposed to treatment, and $Y_i(d_{00})$ denoting the potential outcome of i when assigned to control and not exposed to treatment.

Per the fundamental problem of causal inference (Holland 1986), we cannot observe unit i 's potential outcome in more than one exposure at a time. Moreover, if treatment assignment does not account for network structure, the probability of experiencing different exposures

⁴A different treatment status of unit i implies a different exposure. See Aronow and Samii (2017) for an extensive formalization of this approach.

varies across units. Aronow and Samii (2017) propose a Horvitz-Thompson inverse probability estimator of $\tau(d_k, d_{k'})$ that accounts for both issues.

$$\widehat{\tau}_{HT}(d_k, d_{k'}) = \frac{1}{N} \left[\sum_{i=1}^N \mathbf{I}(D_i = d_k) \frac{Y_i}{\pi_i(d_k)} - \sum_{i=1}^N \mathbf{I}(D_i = d_{k'}) \frac{Y_i}{\pi_i(d_{k'})} \right] \quad (3)$$

This is the difference in inverse probability weighted means between two exposures, with $\mathbf{I}(D_i = d_k)$ denoting the units for which we observe exposure k , and $\pi_i(d_k)$ denoting the probability of unit i experiencing exposure k . The notation is analogous for k' . For a randomized experiment, $\pi_i(d_k)$ is the expected proportion of treatment assignments that induce unit i to experience exposure k , which can be computed exactly in relatively small samples or approximated through simulation otherwise.

See Aronow and Samii (2017) for a subsequent discussion of asymptotic properties, implementation, and variance estimation. For the purposes of this paper, the important part is that the estimator $\widehat{\tau}_{HT}(d_k, d_{k'})$ is unbiased under the known pathways assumption. Therefore, when this assumption is not satisfied by design, any operationalization of interference, even if informed by theory, may inadvertently introduce bias. From a model selection perspective, the task to find an operationalization that minimizes this bias in expectation.

2.3 Stratified interference

Another way to impose structure under interference is to assume that it occurs only within observed groups or strata. For example, Get Out the Vote campaigns may affect the voting behavior of untreated individuals living in treated households (Nickerson 2008), or that of individuals in other households in the neighborhood (Sinclair, McConnell, and Green 2012). With this restriction, unit i does not have 2^N different potential outcomes, but rather 2^{n_g} , with n_g denoting the number of units in group g .⁵ Capturing exposure-specific effects under

⁵This notation is different from the one in Hudgens and Halloran (2008). They denote the group as i and the individual as j .

this assumption may still be intractable in applications with large groups, so Hudgens and Halloran (2008) focus on marginal exposure effects instead. These include, for example, the effect of one additional treated unit within the group, or that of being exposed to different proportions of treated units within the group.

They define four quantities of interest at the individual, group, and population level: the direct, indirect, total, and overall causal effects. For simplicity, I only describe individual level effects.⁶ The average direct causal effect for individual i in group g is

$$\tau_{ig}^D(\psi) = \bar{Y}_{ig}(0; \psi) - \bar{Y}_{ig}(1; \psi) \quad (4)$$

which is the difference in means between treatment conditions, holding exposure regime ψ constant. The individual average indirect causal effect is

$$\tau_{ij}^I(\phi, \psi) = \bar{Y}_{ij}(0; \phi) - \bar{Y}_{ij}(0; \psi) \quad (5)$$

which is the difference in means between exposures regimes ϕ and ψ under the control condition. The individual average total causal effect is

$$\tau_{ig}^T(\phi, \psi) = \bar{Y}_{ig}(0; \phi) - \bar{Y}_{ig}(1; \psi) \quad (6)$$

which is the same as the sum of direct and indirect effects on individual i . Finally, the individual average overall causal effect is:

$$\tau_{ig}^O(\phi, \psi) = \bar{Y}_{ig}(\phi) - \bar{Y}_{ig}(\psi) \quad (7)$$

⁶In general, the group and population level causal effects are the aggregation of their individual level counterparts. See Hudgens and Halloran (2008) for details.

which is equivalent to the difference in means across two different treatment regimes.

Under Bernoulli random assignment with probability ψ ,⁷ an unbiased estimator of unit i 's outcome in group g under treatment assignment $z = \{0, 1\}$ and exposure regime ψ is

$$\hat{Y}_g(z; \psi) = \frac{\sum_{i=1}^{n_g} Y_{ig}(Z_g) I[Z_{ig} = z]}{\sum_{i=1}^{n_g} I[Z_{ig} = z]} \quad (8)$$

which is the average of observed outcomes in a group under the same treatment condition and treatment regime \mathbf{Z}_g . This informs the population-level estimators of direct, indirect, total, and overall causal effects. For example, the estimator for the population average indirect effect is $\hat{\tau}^I(\phi, \psi) = \hat{Y}(0; \phi) - \hat{Y}(0; \psi)$.

These estimators are unbiased under the partial interference assumption, which states that unit i 's potential outcomes depend only on the treatment assignment of units within, but not across, groups (Sobel 2006). The assumption of stratified interference, which states that the potential outcomes of unit i depend on the proportion or number of treated units in group g , but not on which units within the group are treated, is sufficient but not necessary to identify causal effects.⁸

Aronow et al. (2021) show that violations of partial interference introduce bias in marginal exposure effect estimates. This violation is plausible in social science settings since individuals can interact through unobserved networks. Egami (2020) considers sensitivity analysis for the case in which the researcher observes a causally relevant network but has concerns over whether interaction in unobserved networks may violate partial interference. For example, the researcher may observe how treatments propagate in online social networks but may not be able to account for treatment propagation through face-to-face interaction.

⁷Hudgens and Halloran (2008) suggest that the estimator is unbiased with any randomization schedule, Sävje, Aronow, and Hudgens (2019) clarify that this is only true for Bernoulli random assignment.

⁸However, Hudgens and Halloran (2008) show that stratified interference is necessary for variance estimation.

More generally, bias may emerge in this setting because groups themselves are not properly defined. In experiments with individuals as the unit of analysis, the challenge is to identify the right reference group. For example, in an experiment that assigns treatments to individuals in their households, interference can occur within a household, or across households in a neighborhood. In experiments with administrative units, the task is to identify an upper bound that determines which localities can be considered part of the same group. This paper focuses on the latter case.

3 A Model Selection Approach

Both causal inference approaches to interference described in the previous section assume that the researcher knows and fully observes the pathway(s) through which treatments propagate. This is analogous to assuming no omitted variable bias, as it implies that all causally relevant networks are observed. An alternative way to think about violations of the known pathways assumption is to conceive an observed network as an approximation of the true, unobserved causally relevant network. From this perspective, the task is to ensure that the pathway of choice approximates the true network as close as possible. Previous work provides tools to assess the influence of unobserved networks in the form of sensitivity analysis (Egami 2020). Therefore, the remaining task is to develop tools to determine whether the operationalization of a chosen pathway is appropriate relative to alternatives.

Choosing the appropriate operationalization is most relevant in the case where theory or domain expertise suggest a causally relevant pathway, but they imply many alternative operationalizations for it. For example, if we suspect that assigning election observers to some localities affects voter registration irregularities nearby (Ichino and Schündeln 2012; Asunka et al. 2017), we need a statement of which localities are indirectly exposed to the intervention. If we believe that units' outcomes are affected by the treatment assignment of other within

a distance range, then we have multiple options for its upper bound.⁹ This is analogous to finding the appropriate reference group. For example, research on the spillover effects of Get Out the Vote interventions suggests that treated individuals may affect the behavior of others within their household or neighborhood (Nickerson 2008; Sinclair, McConnell, and Green 2012). In this context, researchers interested in minimizing bias have incentives to choose the right reference group.

In some applications, as in the case of choosing between household or neighborhood effects, the range of plausible operationalizations is limited and the cost of analyzing all alternatives is minimal. In others, as in the case of choosing an appropriate distance threshold, analyzing all plausible operationalizations can become restrictive. Even if the researcher can estimate all the alternatives, they are left with the question of which result is a better approximation to the true, unobserved quantity of interest.

The protocol I propose requires the researcher to express these alternative operationalizations as a function of one or more parameters. For example, Keele and Titiunik (2018) study interference in the context of a geographic natural experiment in which the outcome of control households depends on the density of treated units within a distance threshold.¹⁰ In their case, density and distance are parameters that govern different model specifications. While in the context of a geographic natural experiment the number of combinations to report is limited by the context, in other applications researchers may not be able to identify a discrete range of parameter values.

Expressing plausible operationalizations of interference as a function of one or more parameters allows researchers to apply model selection systematically. Table 1 summarizes the proposed model selection protocol. The first step is to identify the causally relevant path-

⁹An alternative approach is to assume that interference effects decrease as a function of distance. This overcomes the challenge of identifying a threshold, but requires further modeling assumptions (e.g. Bowers, Fredrickson, and Panagopoulos 2013) or granular enough data to characterize the effect of point interventions as a function of distance (Aronow, Samii, and Wang 2020).

¹⁰They actually consider an application in which control units can interfere with the outcome of those treated, but I reverse the language for the sake of clarity.

ways through which interference occurs, this is a decision that comes from theory, domain expertise, or knowledge of the research design or data generating process.

Second, the researcher expresses the chosen pathway as pairwise distances between units along a distance metric. These pairwise distances are straightforward when the theoretically relevant pathway is a continuous measure indicating units' placement in multidimensional space (e.g. location or ideology scores), in which case we can express distance as the difference between the values of any two units. When pathways indicate how units connect to each other in a discrete manner, as in a peer network, the distance can be expressed as the geodesic (the lowest number of edges connecting two nodes). In the context of choosing the right reference group, pairwise distances indicate whether the units belong to the same group.

As an illustration, consider the case of converting pairwise distances into binary exposures. Let $\mathbf{W} \in [0, +\infty)$ be an $M \times T$ distance matrix where M is the number plausibly exposed units and T is the number of treated units.

$$W = \begin{bmatrix} \infty & w_{12} & \cdots & w_{1T} \\ w_{21} & \infty & \cdots & w_{2T} \\ \vdots & \vdots & \ddots & \\ w_{M1} & w_{M2} & \cdots & \infty \end{bmatrix} \quad (9)$$

The dimensions of \mathbf{W} depend on the assumptions we make about the nature of interference. If exposure to treatment affects both treated and control units, then $M = N$, if only control units can be affected by the treatment assignment of others, then $M = (N - T)$.

The task is to convert the matrix \mathbf{W} into a matrix \mathbf{K} of binary indicators of whether unit i can be considered as exposed to treated unit j . Let κ denote a distance threshold so that

1. Identify relevant pathway(s) through which interference occurs
2. Express the pathway as pairwise distances between (plausibly) exposed and treated units along a distance metric
3. Use pairwise distances to inform plausible models of interference
4. Apply model selection algorithm of choice
5. Estimate interference using the model(s) that satisfy the algorithm’s criteria

Table 1: A model selection protocol for interference

$$k_{ij} = \begin{cases} 1 & \text{if } w_{ij} \leq \kappa \\ 0 & \text{otherwise} \end{cases} \quad (10)$$

When $k_{ij} = 1$, we say that unit i is exposed to unit j . With this information, the researcher can compute the explanatory variables of interest based on the desired estimation target. If the goal is to estimate categorical exposure effects, then they should record whether unit i is exposed to at least one treated unit. If the goal is marginal exposure effects or strength of exposure, the variables should indicate the number or proportion of treated units i is exposed to.

The third step is to use the information about pairwise distances to identify multiple plausible models of interference. Different values of κ imply different versions of \mathbf{K} . Once again, this decision depends on the estimation target. If the researcher seeks to identify a single global effect, then different values of κ inform alternative upper bounds, and hence different models, for which units can be considered as exposed to treatment. For example, Paluck, Shepherd, and Aronow (2016) argue that the effects of anti-conflict interventions in a school spread to those students who spend time with treated students. However, the intervention can also reach those who spend time with those who spend time with treated students. In this case, κ can record network degrees as plausible upper bounds for interference.¹¹

¹¹Aronow and Samii (2017) overcome this challenge theoretically by allowing an arbitrary number of exposure mappings. In their approach, the possibility of second degree effects implies an increase in the number of distinct exposures.

If the goal is to identify local exposure effects at different distance ranges, then different values of κ inform the construction of different variables among which an algorithm will select to identify the most appropriate model. For example, Ichino and Schündeln (2012) estimate the marginal effect of election observer visits on voter registration irregularities within the 0-5 km and 5-10 km distance ranges. From a model selection perspective, each one of these brackets is a different variable that responds to a different value of κ .

In the fourth step, the researcher applies the model or variable selection algorithm of choice. In this paper, I focus on supervised learning model selection algorithms because they allow researchers to entertain the possibility of multiple, equivalent models. However, researchers can implement any model selection procedure they prefer. For example, Bayesian approaches to model selection also accomplish the goal of incorporating uncertainty around what can be considered the most appropriate model (Hollenbach and Montgomery 2020).

As in the previous step, the choice of algorithm depends on the estimation target. Off-the-shelf variable selection algorithms are appropriate when the task is to select among multiple plausible local exposure effects. This paper focuses on the lasso-family of algorithms (see Ratkovic and Tingley 2017 for a review) since they are a straightforward extension of the regression models that researchers usually estimate in this setting. However, within the universe of supervised learning, the researcher may also use tree-based methods (Breiman 2001; Bleich et al. 2014; Speiser et al. 2019) or any other feature selection algorithm of choice.¹²

In this case, when the target is a single global effect, different values of κ inform a different version of the estimator, so the algorithm is the estimator itself, and the researcher can select the most appropriate model by searching over a range of values for κ using the resampling strategy and performance criterion of choice. For regression, a common strategy is to com-

¹²One caveat of using supervised learning model selection, or any other approach that relies on resampling, is that researchers should identify plausible operationalizations of interference before implementing these methods. Otherwise, they risk breaking the underlying network structure in the data.

pute mean squared error via k-fold cross-validation (Hastie, Tibshirani, and Friedman 2009). In this context, κ is a hyper-parameter, which value the researcher can tune searching over a manual grid. If the application suggests a computationally restrictive grid, random search is also an option (Bergstra and Bengio 2021).

The final step is to estimate the most appropriate model(s) suggested by the model selection procedure. The researcher can use the estimator of choice, including those discussed in the previous two sub-sections. In the case of supervised learning approaches, the protocol may suggest multiple models that satisfy the performance criteria. For example, several models can be within one standard deviation from the model that minimizes mean squared error, in which case the researcher can consider all of them as plausible definitions of nearby.¹³

4 Application

4.1 Election observers and voting registration irregularities in Ghana

This section illustrates the usefulness of the model selection approach to interference by reanalyzing an experiment on the spillover effect of election observers on voter registration irregularities in Ghana (Ichino and Schündeln 2012). Table 2 summarizes the two-stage research design. Before randomization, the authors group constituencies (legislative districts) into blocks according to the difference in vote shares between the two main parties in the country in the 2004 legislative election. At the first stage, one constituency per block was randomly assigned to treatment and two were assigned to control. In the second stage, roughly 25% of the electoral areas (ELAs), subdivisions of constituencies, were assigned to receive the visit of an election registration observer in the wake of the 2008 election.

¹³When supervised learning algorithms use current data to predict new data, the common practice to reduce overfitting is to select the model with the highest mean squared error within one standard deviation from the minimum. In the context of a model selection approach to interference, this usually translates into choosing the most parsimonious model.

Constituencies	Electoral areas (ELAs)	Observations
Control	Control	592
Treatment	Control	199
Treatment	Treatment	77

Table 2: Research design in Ichino and Schündeln (2012)

Note: Two-stage design. Constituencies are randomly assigned to treatment and control, then ELAs within treatment constituencies are randomly assigned to the visit of an election observer.

The main finding in this experiment is that election observers do not deter but rather displace irregularities, one additional ELA assigned to treatment within 5 kilometers leads to a 3% increase in irregularities, measured as the percent change in voter registration between 2004 and 2008, in control ELAs.¹⁴ The effect is indistinguishable from zero for the number of ELAs assigned to treatment in the 5-10 kilometer range.

The exercise from a model selection perspective is to determine whether the proposed protocol can recover the same substantive findings as an experiment designed to capture interference. I extend the original analysis using different 5 kilometer intervals to illustrate the case of multiple local marginal effects.

4.2 Lasso model selection

Assume that the researcher believes that geographic distance is a relevant distance metric and that election observers may have different effects as distance increases. To capture this, one may choose to analyze effects separately at increasing discrete distance ranges. To reproduce this, I count the number ELAs assigned to treatment at 5 kilometer intervals up to 50 kilometers. This translates to 10 variables or predictors among which to select.

I select among these predictors using lasso-family algorithms. The logic of lasso (Least Absolute Shrinkage and Selection Operator) methods is to add a penalty term to the the objective function of OLS regression, which is the residual sum of squares (see Tibshirani 1996; Ratkovic and Tingley 2017 for mathematical details). As the penalty term increases, the

¹⁴This is the intent-to-treat effect, which is the focus of this paper, the local average treatment effect for those ELAs that were visited by an election observer is similar. See Ichino and Schündeln (2012) for details.

resulting regression coefficients shrink toward zero, a coefficient that reaches zero is excluded from the estimation step. The size of the penalty term is determined by a tuning parameter λ , which for the frequentist lasso is tuned via cross-validation or another resampling strategy.

A shortcoming of the standard lasso is that it tends to select irrelevant predictors that correlate with relevant predictors. Figure 1 shows the correlation matrix for the variables involved in the reanalysis. Many predictors correlate positively with each other, which may create complications for variable selection in the lasso. Subsequent refinements to the lasso attempt to minimize the tendency to over-select predictors (see Ratkovic and Tingley 2017 for a review).

In this application, I focus on the following variants of the lasso:

1. Lasso (Tibshirani 1996)
2. Adaptive lasso (Zou 2006)
3. Lasso + OLS (Belloni and Chernozhukov 2013)
4. LASSOplus (Ratkovic and Tingley 2017)

The logic of the original lasso is described above. The adaptive lasso introduces more flexibility by allowing predictor-specific weights, resulting in a penalty term that varies across predictors (Zou 2006). Following standard practice, I weight each predictor by the multiplicative inverse of the absolute value of its coefficient in a multivariate OLS regression of the outcome against the predictors, so for predictor p the weight is $1/|\beta_p|$.

The LASSO + OLS variant seeks to improve upon the initial lasso fit by excluding non-zero predictors that exceed a threshold. In this application, I focus on the goodness of fit thresholding (also known as OLS post-fit Lasso) procedure proposed by Belloni and Chernozhukov (2013), which consists of fitting an OLS regression for all the subsets of the model suggested by the lasso, and then choosing the subset with a residual variance that resembles the residual variance of the suggested lasso fit.

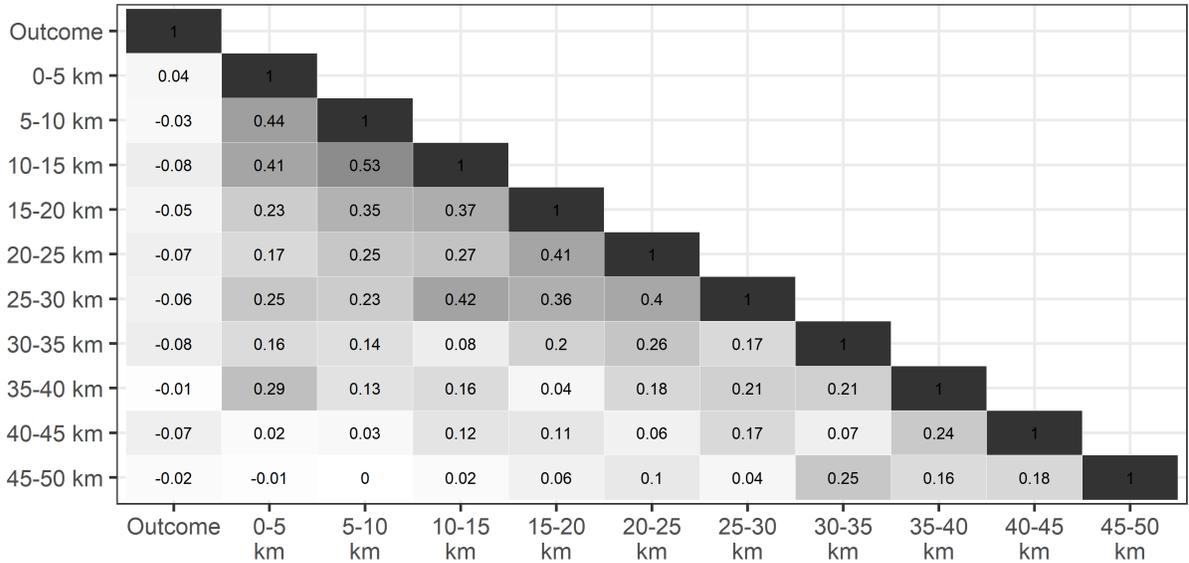


Figure 1: Correlation matrix for outcome and predictors

Note: The outcome is the 2004-2008 percent change in voter registration. The predictors count the number of ELAs assigned to treatment in the corresponding range. Numbers indicate the Pearson correlation coefficient between the intersecting variables. Darker shades of gray indicate more extreme values.

Lastly, the LASSOplus proposed by Ratkovic and Tingley (2017) is a Bayesian procedure that streamlines model selection and estimation. This method has three advantages. First, as a Bayesian method, it produces credible intervals analogous to the confidence intervals obtained by OLS regression, so it does not need an additional step for estimation like the frequentist variants do. The second advantage of LASSOplus is that it is a thresholding function that zeroes out small coefficients. Bayesian variants of the lasso tend to have better predictive performance (Casella et al. 2010), but are not sparse estimators in the sense that they do not automatically zero-out coefficients. Third, unlike standard lasso methods, LASSOplus can incorporate prior knowledge about the data generating process, which in the context of this paper translates to research design features. For example, LASSOplus can automatically incorporate the blocked structure of the Ichino and Schündeln (2012) experiment and adjust the posterior distribution accordingly.

For the frequentist variants of the lasso (standard, adaptive, and lasso + OLS), I tune

λ via 10-fold cross-validation using the `glmnet` R package and choose the most generous model among those implied by the range within one standard deviation from the value of λ that minimizes RMSE.¹⁵ I follow the default parameters of the `sparsereg` R package for LASSOplus, which estimates the model via MCMC via Gibbs sampling with 200 burn-in iterations, 200 posterior samples, and thinning every 10 samples.¹⁶

4.3 Results

Figure 2 summarizes the variables selected by each lasso variant and the resulting estimates from the selected models. Figures A1-B1 in the appendix show additional details for the frequentist lasso variants. The horizontal axis lists every variable selected by the corresponding lasso variant. For reference, the top frame denotes the original model selection in Ichino and Schündeln (2012), including the number of ELAs assigned to treatment within 0-5 kilometers and 5-10 kilometers, of which only the first has a non-zero effect. All the frequentist variants of the lasso correctly select this predictor, but also overselect every other predictor. This pattern emerges because continuous predictors tend to correlate with each other, and the lasso chooses to penalize one heavily and to leave the other untouched. LASSOplus, in turn, correctly selects the number of ELAs assigned to treatment within 0-5 kilometers as the only non-zero predictor, which aligns with the original findings.

Figure 2 also shows estimates from the models suggested by each lasso variant in separate frames. The first frame reproduces the original result in Ichino and Schündeln (2012). For the frequentist variants, estimation occurs after model selection following the original specification, which includes block fixed effects, a control for whether an ELA is in a treatment constituency, and clustered standard errors at the block level. Because in the frequentist variants of the lasso estimation occurs after selection, I compute 97.5% confidence intervals to control for the possibility of false coverage-statement rate (Benjamini and Yekutieli 2005).

¹⁵In this case, more generous implies selecting the model with the most predictors.

¹⁶These are the default parameters in the `sparsereg` package. It is a relatively small yet, as the results sub-section shows, sufficient number of iterations to yield satisfactory results.

Although all of the frequentist variants select irrelevant predictors, the estimation for each returns an effect similar to the original for the number of ELAs assigned to treatment in the 0-5 kilometer range. The remaining estimates are indistinguishable from zero, which still aligns with the conclusion that spillover effects do not occur beyond five kilometers.

For LASSOplus, the point estimate is the posterior mean of the same model used for variable selection, which includes the original research design features as prior information. Unlike the frequentist variants, LASSOplus only selects the number of ELAs assigned to treatment in the 0-5 kilometer range, and while the estimate is smaller than the original, the 95% credible interval is narrower than the confidence interval in the frequentist counterparts.

To summarize, both the frequentist variants of the lasso and LASSOplus arrive at the same substantive conclusion as an experiment intended to capture interference. As documented in previous work, the frequentist variants tend to select irrelevant effects that correlate with true non-zero effects (Ratkovic and Tingley 2017), a problem that LASSOplus overcomes in this application. Frequentist lasso-family methods arrive at the correct substantive conclusion despite over-selecting because, under regular conditions, the frequentist lasso and its variants satisfy the oracle inequality, which states that, asymptotically, the lasso selects at least a subset of the true model (Candès 2006).¹⁷ Therefore, both frequentist and Bayesian sparse estimation models are suitable for a model selection approach to interference.

5 Simulation

5.1 Setup

The previous section applies the model selection protocol to a specific case. This simulation study illustrates its properties more generally in the context of estimating interference as the contrast across exposures, with the goal of identifying a single global effect.

¹⁷The oracle inequality exists in contrast with the oracle property, which requires a variable selection procedure to asymptotically select the right model (Fan and Li 2001).

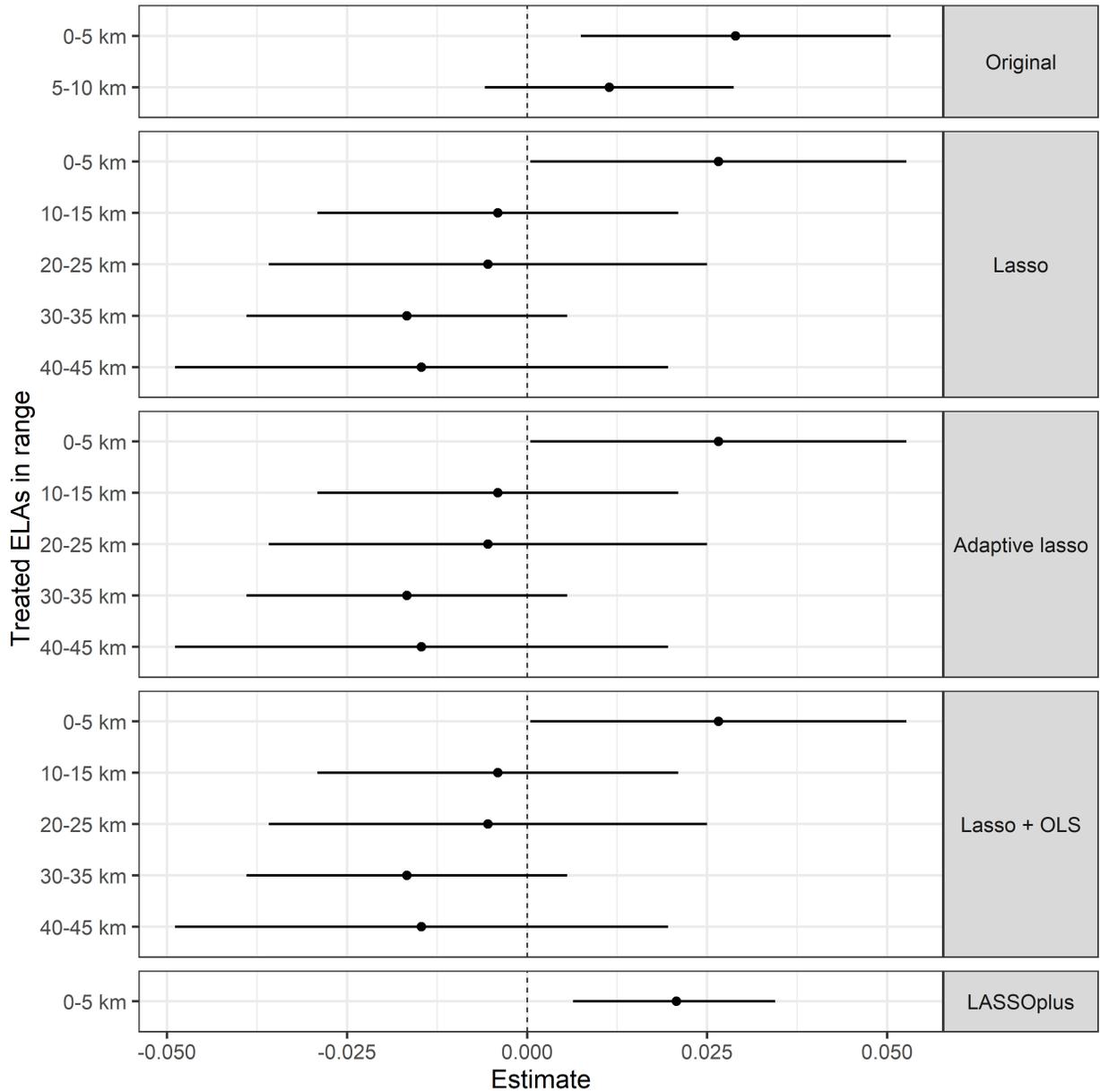


Figure 2: Estimates for the marginal effect of the number of ELAs assigned to treatment within selected distance ranges on voter registration irregularities

Note: Each frame denotes a different model with the variables selected by the corresponding model selection procedure. The first frame reproduces the original results. For the frequentist variants of lasso, the estimates come from post-selection OLS regression with block fixed effects and a control for whether an ELA is in a treatment constituency, with bars representing 97.5% false coverage-statement rate adjusted confidence intervals from block clustered standard errors. For LASSOplus, the point estimate is the posterior mean and the bars denote the 95% credible interval.

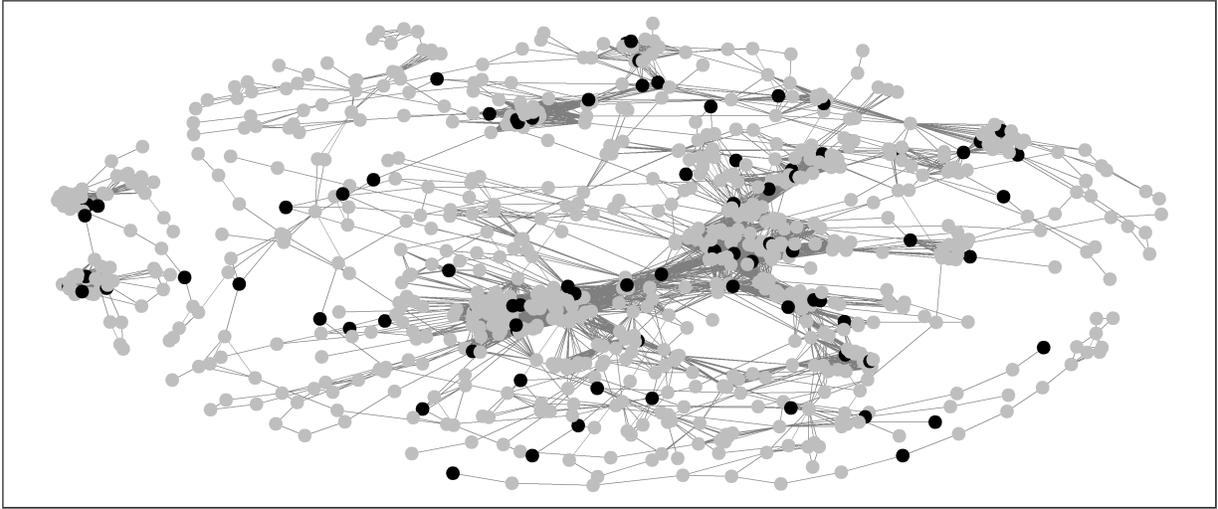
Consider a hypothetical experiment conducted in a network. I use the network in Bowers et al. (2018) since it reflects a realistic layout. Each node in this network is an ELA in Ghana ($N = 868$). Edges in this network denote whether a direct road connects two areas. The median number of direct connections is 22 (mean: 38, standard deviation: 41).

Bowers et al. (2018) focus on the case where interference occurs between adjacent nodes only. In this simulation exercise, interference may also occur at higher degrees. Therefore, the distance metric is the geodesic, or the number of edges in the shortest path between two nodes.

Z is a treatment assignment vector. $Z_i \sim \text{Bernoulli}(\alpha)$, which implies two possible treatment conditions $Z_i = \{0, 1\}$, which I refer to as control and treatment, respectively. One of the main conclusions in Bowers et al. (2018) is that experiments have higher power to detect interference when the proportion of units assigned to treatment is smaller than the usual even split across conditions. With this in mind, I set $\alpha \in [0.1, 0.4]$. Figure 3 shows one realization of the treatment assignment in the network with $\alpha = 0.1$.

Let $\mathbf{Y}(\mathbf{d}_{00})$ be the vector of potential outcomes under control and without exposure, $\mathbf{Y}(\mathbf{d}_{10})$ under treatment without exposure, $\mathbf{Y}(\mathbf{d}_{01})$ under control with exposure, and $\mathbf{Y}(\mathbf{d}_{11})$ under both treatment and exposure. I assume $\mathbf{Y}(\mathbf{d}_{00}) \sim U(0, 1)$ and $\mathbf{Y}(\mathbf{d}_{10}) = \mathbf{Y}(\mathbf{d}_{01}) = \mathbf{Y}(\mathbf{d}_{11}) = \lambda \mathbf{Y}(\mathbf{d}_{00})$ with the multiplicative treatment effect $\lambda \in \{0.26, 0.63\}$, which is about one and two standard deviations of the uniform distribution of the outcome, respectively. Under this setup, we can restrict our attention the effect of being exposed to treatment within control units, which is the contrast between $\mathbf{Y}(\mathbf{d}_{00})$ and $\mathbf{Y}(\mathbf{d}_{01})$.

To capture the idea that interference may occur within different distance ranges, I set $\kappa = \{1, 2, 3\}$ as the true interference upper bound. For example, with $\kappa = 2$ a node is exposed to treatment if it is within two or fewer edges away from a treated unit. Within this range, a node is infected with probability $\gamma \in [0.5, 1]$. Infected units exhibit the outcome under exposure $\mathbf{Y}(\mathbf{d}_{01})$, otherwise they exhibit $\mathbf{Y}(\mathbf{d}_{00})$. This reflects the scenario where treatments



Condition ● Treatment ● Control

Figure 3: Hypothetical experiment in a road network in Ghana

Note: Colors denote treatment assignment. Units are assigned to treatment with probability $\alpha = 0.1$.

propagate at different rates.

For each combination of the parameters α , λ , κ , and γ , I consider plausible upper bounds $k = \{1, 2, 3, 4\}$. k is the researcher’s guess of what the value of the true κ may be, with higher values reflecting a broader range within which control units are considered exposed to treatment. For each value of k , I consider the inverse probability weighted difference in means described in Equation 3 as both the algorithm and the estimator. I use 5-fold cross validation to compute the root mean squared error (RMSE) for each model and choose the one with the largest RMSE within one standard deviation of the mean. I denote the value of k in the chosen model as \bar{k} , and estimate the corresponding model.¹⁸

I repeat this process 1,000 times for each parameter combination and compare the protocol’s performance with an oracle that knows the value of κ ahead of time but does not know λ . I assess performance with bias, mean absolute deviation (as a measure of precision), power at a 0.05 false positive rate, and the mean value of \bar{k} .¹⁹

¹⁸This decision rule implies erring on the side of selecting a smaller \bar{k} .

¹⁹In some settings, treatment spreads too fast, which leads to implausible or rank-deficient estimates.

5.2 Results

To facilitate exposition, Figures 4 and 5 report performance in terms of bias and the mean value of \bar{k} at select parameter values $\alpha = \{0.1, 0.4\}$, $\gamma = \{0.5, 1\}$, and $\tau = 0.26$. Section B of the appendix reports simulation results in full. Figure 4 shows the bias of the estimator selected by the proposed supervised learning protocol against the oracle. Since the oracle knows κ ahead of time, but not the true treatment effect λ , it can produce biased estimates. Each value in the figure is based on 1,000 simulations. The protocol has similar bias than the oracle when treatment assignment probability α is low. When α is close to a coin flip ($\alpha = 0.4$), the protocol increases in bias with κ . In general, bias is higher when the infection probability γ is lower, but the difference between the protocol and the oracle as κ increases under high α is more pronounced when the infection probability γ is deterministic ($\gamma = 1$). Section B of the appendix leads to a similar conclusion for precision and power.

Figure 5 shows the mean of the selected upper bound \bar{k} , this statistic reflects the protocol’s average guess for κ across simulations. By definition, the oracle always selects the correct interference upper bound, so the protocol performs better when it resembles the oracle. This is the case under $\alpha = 0.1$ and $\gamma = 1$. In other scenarios, the protocol tends to overestimate the upper bound when κ is low, and underestimate it when κ is high. This reversion happens because at low κ the algorithm is more likely to err on the side of choosing a larger \bar{k} , with the opposite being the case when κ is high.

To summarize, the simulation exercise suggests that the protocol performs better when a relatively small proportion of units are assigned to treatment. This finding also appears in the simulations in Bowers et al. (2018). The underlying intuition is that when too many units are treated there is not enough information about the outcome of control units to assess the difference between those exposed to and isolated from treatment. For the same reason, performance tends to be worse when treatments travel too far, which is captured by κ . If

This occurs in roughly 3% of the simulations (out of a total of 288,000) and happens more often as α and κ increase. I exclude these from the analysis.

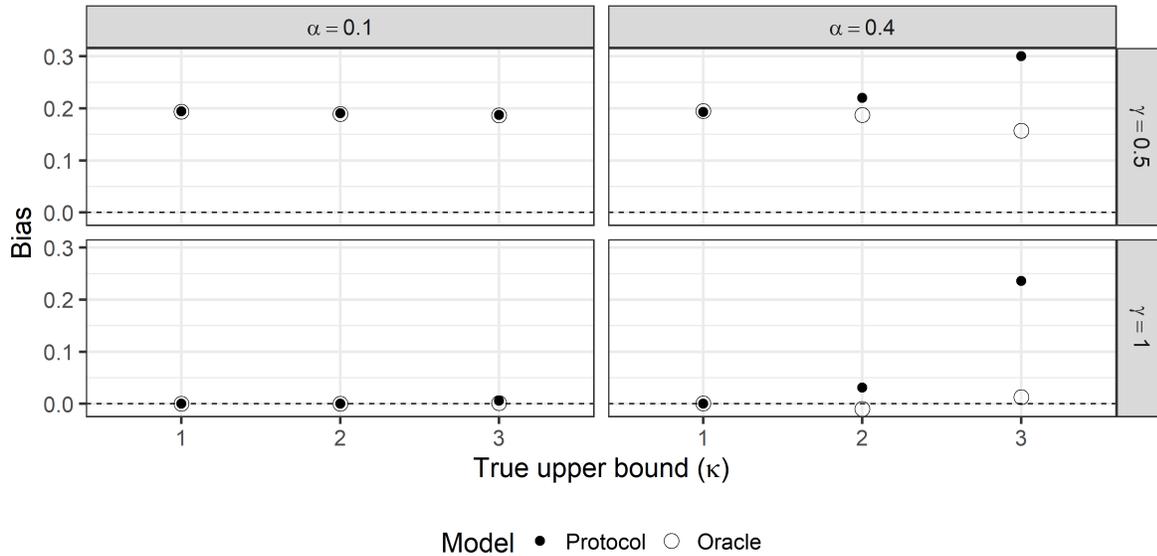


Figure 4: Comparing bias of the supervised learning model selection protocol against the oracle

Note: Each value is based on 1,000 simulations. When the treatment assignment probability α is low, the protocol and oracle have similar bias. When α is high, the bias of the protocol increases with the true upper bound κ . Bias is higher when the infection rate γ is a coin toss.

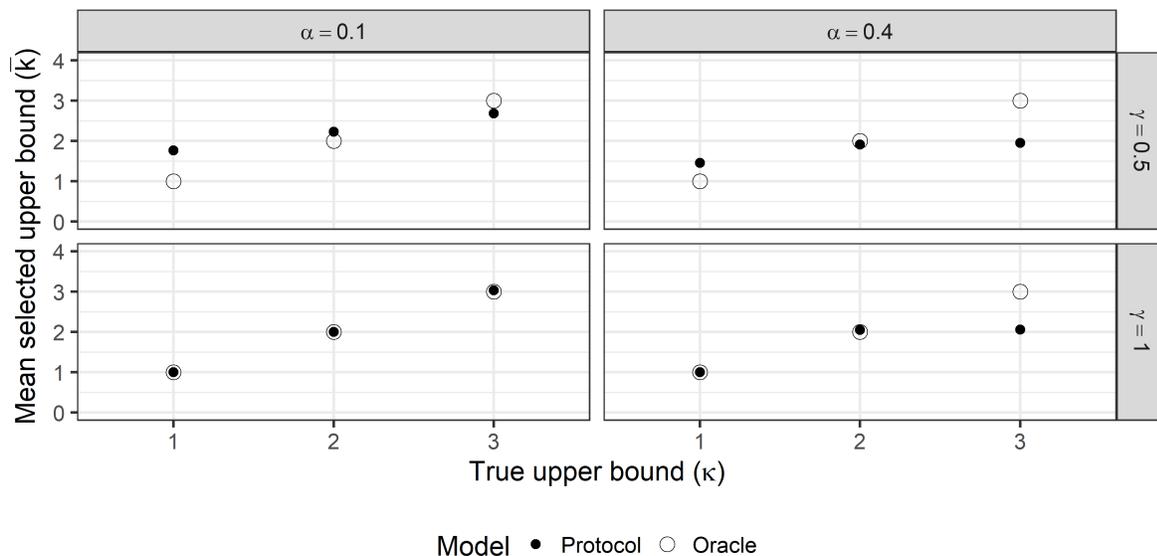


Figure 5: Comparing the mean selected upper bound of the supervised learning model selection protocol against the oracle

Note: Each value is based on 1,000 simulations. By definition the oracle always selects the right value of the true upper bound κ . In average, the protocol chooses the correct upper bound when the treatment assignment probability α is low and the infection rate γ is deterministic. Otherwise, the protocol tends to select a broader upper bound when κ is low and a narrower upper bound when κ is high.

too many units are exposed, then the researcher does not have enough information about those isolated.

Finally, performance also suffers when treatments spread in a probabilistic way. This is true for both the protocol and the oracle, which suggests that the problem does not lie in the supervised learning model selection approach, but rather in the theoretical decision to commit to the same upper bound across units. Future work may alleviate this problem by implementing more flexible distance metrics and algorithms that allow the interference upper bound to vary across units or clusters thereof.

6 Conclusion

This paper proposes a supervised learning model selection approach to study interference in contexts in which the identification assumptions of current design-based causal inference approaches cannot be satisfied. In such case, theory still guides modeling decisions, but it often implies multiple ways to operationalize interference, and the discipline currently lacks a standard to determine which model is more appropriate. This approach still puts the weight of justifying causal inference on what the researcher is willing to assume about the pathway through which interference occurs, but it provides tools to connect theoretical justification with modeling decisions.

The key intuition of the supervised learning model based approach is that, if the researcher can express a theory about interference in terms of a distance metric, then the metric can help in identifying plausible alternative operationalizations, among which the researcher can select using the algorithm, resampling strategy, and performance metric of choice.

Context-specific considerations aside, the choice of model selection approach depends primarily on two decisions about the estimation target. First, the researcher must determine whether the goal is to estimate categorical or marginal exposure effects. This informs whether

to record if a unit is exposed to a treatment condition or not, or to count the number of units assigned to a treatment condition within a certain range.

Second, the researcher must determine whether the task is to estimate a single global effect, or multiple local effects at different distance ranges. This informs the type of algorithm. In the case of a single global effect, the distance metric informs the different values of the upper bound of a range within which interference occurs, which in turns assists in identify alternative plausible operationalizations. For multiple local effects, the distance metric informs the construction of predictors among which the researcher can select using off-the-shelf algorithms for variable selection.

This paper illustrates the supervised learning model selection approach with simulations and the reanalysis of an experiment intended to capture interference. Focusing on the case of estimating the contrast across two exposures in a road network in Ghana, the simulations suggest that the proposed protocol performs better when a relatively small proportion of units is treated, when the probability of infection conditional on exposure is deterministic (as opposed to probabilistic), and when treatments do not spread too far along the theoretically relevant pathways. These conclusions align with previous simulations exercises (e.g. Bowers et al. 2018), which highlights the appropriateness of the approach. Similarly, the reanalysis of an experiment on the spillover effect of election observers on voter registration irregularities in Ghana (Ichino and Schündeln 2012) shows how the lasso-family of algorithms select models that lead to estimates that resemble the original findings, which also validates the usefulness of the approach in cases where the experimental structure was not designed to detect interference.

The simulations and reanalysis focus on model selection using cross-validation and the lasso family of methods, respectively. Similarly, the focus on the estimation side is on inverse probability weighted difference-in-means (Aronow and Samii 2017) and conventional design-based estimators for experimental data. However, the ideas in this paper are general enough

to accommodate for other model selection algorithms and estimation approaches.

A limitation of this approach is that it does not suit hypothesis testing approaches to interference. For example, the key intuition in Bowers, Fredrickson, and Panagopoulos (2013) is that we can test hypotheses about a range of parameter values in a theoretical model of interference. Supervised learning algorithms for variable selection operate under the assumption that a true effect exists and can be detected, even if unknown to the researcher. Testing approaches follow the idea that we can compute uncertainty for a range of hypothetical parameter values.

Future work should acknowledge this difference and develop standards to select among competing models in the context of hypothesis testing approaches to interference. Another area for future development is to develop guidelines on how to choose the appropriate distance metric. For example, the reanalysis of an experiment on the effect of election observers on voter registration irregularities in Ghana follows the authors' decision to count the number of treated units within 5 kilometer bins. However, in novel applications the choice of the number and size of bins (or whether to use bins at all) might be consequential for both the applicability and performance of a supervised learning algorithm.

Finally, future work should apply the ideas of the supervised learning model selection approach to the task of comparing the appropriateness of multiple plausible theoretical pathways. In such a case, the challenge is not only to determine which one is more appropriate, but also to assess and interpret whether alternative pathways are complementary.

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