Detecting Heterogeneous Treatment Effect with Instrumental Variables

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Abstract

There is an increasing interest in estimating heterogeneity in causal effects in randomized and observational studies. However, little research has been conducted to understand heterogeneity in an instrumental variables study. In this work, we present a method to estimate heterogeneous causal effects using an instrumental variable approach. The method has two parts. The first part uses subject-matter knowledge and interpretable machine learning techniques, such as classification and regression trees, to discover potential effect modifiers. The second part uses closed testing to test for the statistical significance of the effect modifiers while strongly controlling familywise error rate. We conducted this method on the Oregon Health Insurance Experiment, estimating the effect of Medicaid on the number of days an individual’s health does not impede their usual activities, and found evidence of heterogeneity in older men who prefer English and don’t self-identify as Asian and younger individuals who have at most a high school diploma or GED and prefer English.

1 Introduction

1.1 Motivation: Utilization of Medicaid in Oregon and the Complier Average Treatment Effect

In January of 2008, Oregon reopened its Medicaid-based health insurance plan for its eligible residents and, for a brief period, allowed a limited number of individuals to enroll in the program. Specifically, a household in Oregon was randomly selected by a lottery system run by the state and any eligible individual in the household can choose to enroll in the new health insurance plan; households that weren’t selected by the lottery could not enroll whatsoever.

For policymakers, Oregon’s randomized lottery system was a unique opportunity, specifically a natural experiment, to study Medicaid’s causal effect on a variety of health and economic outcomes, as directly randomizing Medicaid (or withholding it) to individuals would be infeasible and unethical. Finkelstein et al. (2012) used the randomized lottery as an instrumental variable (see Section 2.2 for details) to study the complier average treatment effect (CATE), or the effect of Medicaid among individuals who enrolled in Medicaid after winning
the lottery \cite{Angrist1996}. CATE reflects Medicaid’s impact among a subgroup of individuals, say the average effect of Medicaid in reducing medical debt among those who comply with their lottery result and enroll in Medicaid, and differs from the average treatment effect for the entire population (ATE) or the intent-to-treat (ITT) effect of the lottery itself on the outcome. In this paper, we focus on studying the CATE; see \cite{Imbens2010} and \cite{Swanson2013, Swanson2014} for discussions on CATE.

Often in studying CATE, the population of compliers is assumed to be homogeneous whereby two compliers are alike and have the same treatment effect. But, no two individuals are the same and it is plausible that some compliers may better benefit from the treatment than other compliers. For example, sick individuals who enroll in Medicaid after winning the lottery may benefit more from Medicaid than healthy individuals. Also, the perceived benefit of enrolling in Medicaid among sick versus healthy individuals creates heterogeneity in the compliance rate, i.e. the number of people who sign up when they win the lottery, with sick people presumably signing up more than healthy people. Alternatively, if people are equally likely to enroll in Medicaid if they win the lottery, those who are unemployed may benefit more from Medicaid in terms of reducing healthcare spending and medical debt than those who are employed. The theme of this paper is to explore these issues, specifically the heterogeneity of CATE and how to discover them in an honest manner.

1.2 Prior Work and Our Contributions

There are many recent works in causal inference using tree-based methods to estimate heterogeneity in the average treatment effect, with majority of them utilizing sample splitting or sub-sampling to obtain honest pointwise inference; see \cite{Su2009, Hill2011, Athey2016, Hahn2017, Wager2018, Athey2019} and references therein. \cite{Hsu2013} uses pair matching, classification and regression trees (CART) \cite{Breiman1984}, and the absolute value of the treatment difference between pairs to discover treatment heterogeneity and to conduct honest inference, all without sample splitting. A follow-up work by \cite{Hsu2015} formally showed that the proposal strongly controls the family wise error rate for testing heterogeneous treatment effects and subsequent works by \cite{Lee2018a, Lee2018b} extended this idea of using absolute value of the treatment-control difference to study effect heterogeneity.

There is also work on nonparametrically estimating treatment effects using instruments, mostly using likelihood, series, or moment-based approaches \cite{Abadie2003, Blundell2003, Newey2003, Hall2005, Darolles2011, Su2013, Athey2019}. Recently, \cite{BargagliStoffi2018} and \cite{BargagliStoffi2019} explore effect heterogeneity within IV context by using causal trees \cite{Athey2015} and Bayesian causal forests \cite{Hahn2017} to estimate heterogeneity in the ITT effect and dividing it by the compliance rate. However, to the best of our knowledge, none of the methods use matching, a popular, intuitive, and easy-to-understand method, as a device to nonparametrically estimate treatment heterogeneity in the context of IVs and guarantee strong familywise Type I error control, to ensure that only "truly" significant heterogeneity is detected. Works on using matching in IV context by
Baiocchi et al. (2010) and Kang et al. (2013, 2016) only focus on the population complier average treatment effect; they do not explore heterogeneous treatment effect with an IV. Also, aforementioned work by Hsu et al. (2013, 2015) using matching and CART to explore treatment heterogeneity were in non-IV contexts.

The goal of this paper is to propose a matching-based method to study treatment effect heterogeneity in IV settings. Specifically, the target estimand of interest is what we call the heterogeneous complier average treatment effect (H-CATE). A heterogeneous complier average treatment effect (H-CATE) is the usual complier average treatment effect, but for a subgroup of individuals defined by their pre-instrument covariates. At a high level, H-CATE explores treatment heterogeneity in the complier population, where we suspect that not all compliers in the data react to the treatment in the same way. Some subgroup of compliers may respond to the treatment differently than another subgroup of compliers, who may not respond to the treatment at all; some may even be more likely to be compliers if they believe the treatment would benefit them and they may actually benefit from the treatment. The usual complier average treatment effect (CATE) estimand obscures the underlying complier heterogeneity by averaging across these two types of compliers whereas H-CATE attempts to expose it. Also, in the case where the four compliance types in Angrist et al. (1996), compliers, never-takers, always-takers, and defiers, have identical effects, H-CATE can identify the heterogeneous treatment effect for the entire population by using an instrument. Section 2.3 formalizes H-CATE and provides additional discussions.

Methodologically, to study H-CATE, we combine the ideas of heterogeneous treatment effect estimation in non-IV matching contexts by Hsu et al. (2015) and matching with IVs by Kang et al. (2016). Specifically, we first follow Kang et al. (2016) and conduct pair matching on a set of pre-instrument covariates and test the CATE for each pair. Second, we follow Hsu et al. (2015) where we obscure treatment-control difference using absolute differences and CART to discover subgroups and novel H-CATEs without contaminating downstream inference. Third, we follow Hsu et al. (2015) and use closed testing to test H-CATE in different subgroups to find statistically significant subgroups, while strongly controlling for familywise error rate. Simulation studies are conducted to evaluate the performance of our proposed method under varying levels of compliance and effect heterogeneity. We illustrate its honest simultaneous discovery and inference while strongly controlling familywise error rate. We then analyze heterogeneity in the effect of Medicaid on increasing the number of days a complying individual’s health does not hamper their usual activities.

2 Method

2.1 Notation

Let $i = 1, \ldots, I$ index the $I$ matched pairs for individuals $j = 1, 2$, and $Z_{ij}$ denote a binary instrument for individual $j$ in matched pair $i$, so that one individual of the pair receives the instrument value $Z_{ij} = 1$ and the other receives the value $Z_{ij} = 0$. In the OHIE data, $Z_{ij} = 1$ and $Z_{ij} = 0$ denotes an individual winning or losing the lottery respectively to enroll in Medicaid. Let $Z$ be the vector of instruments, $Z = (Z_{11}, Z_{12}, \ldots, Z_{I1}, Z_{I2})$.
and $\mathcal{Z}$ denote an event of instrument assignments for all individuals.

For individual $j$ in matched pair $i$, let $d_{1ij}$ and $d_{0ij}$ denote the binary potential exposure, or treatment, values given the instrument value of $Z_{ij} = 1$ and $Z_{ij} = 0$ respectively. Further, define the potential response $r_{1ij}^{(d_{1ij})}$ for individual $j$ in matched set $i$ with exposure $d_{1ij}$ receiving instrument $Z_{ij} = 1$ and $r_{0ij}^{(d_{0ij})}$ similarly but with instrument $Z_{ij} = 0$. For the OHIE data, $d_{1ij}$ denotes whether an individual enrolled in Medicaid and $r_{1ij}^{(d_{1ij})}$ denotes the outcome, say the number of days not affected by one’s physical or mental health when they win the lottery $Z_{ij} = 1$. The observed response is defined as $R_{ij} = r_{1ij}^{(d_{1ij})}Z_{ij} + r_{0ij}^{(d_{0ij})}(1 - Z_{ij})$, and the observed exposure, or treatment, is defined as $D_{ij} = d_{1ij}Z_{ij} + d_{0ij}(1 - Z_{ij})$ for individual $j$ in matched set $i$. Define $\mathcal{F} = \{(r_{1ij}^{(d_{1ij})}, r_{0ij}^{(d_{0ij})}, d_{1ij}, d_{0ij}, X_{ij}, u_{ij}), i = 1, \ldots, I, j = 1, 2\}$ to be the set of potential outcomes, treatment levels, and covariates, both observed, $X_{ij}$, and unobserved, $u_{ij}$.

When partitioning the matched sets into subgroups for discovering treatment heterogeneity, the following notation is included. We define a "set of sets", or grouping, $\mathcal{G}$ which contains mutually exclusive and exhaustive subsets of the pairs $s_g \subseteq \{1, \ldots, I\}$, so that $\mathcal{G} = \{s_1, \ldots, s_G\}$. An appended subscript $s_g$ is used to denote an individual partitioned into the $g$th subset $s_g$. To avoid overloading the notation, the subscripts $s$ and $s_g$ will be used interchangeably when it isn’t necessary to specify a subgroup $g$. The set of potential outcomes, exposures, and covariates for subset $s_g$ are thus defined as $\mathcal{F}_s = \{(r_{1sij}^{(d_{1sij})}, r_{0sij}^{(d_{0sij})}, d_{1sij}, d_{0sij}, X_{sij}, u_{sij}), s_g \subseteq \{1, \ldots, I\}, i \in s_g, j = 1, 2\}$, where $\mathcal{F} = \bigcup_{s} \mathcal{F}_s$. For example, consider a grouping of two groups, $\mathcal{G} = \{s_1, s_2\}$ for $I = 10$ matched pairs. Then it may be that the first few pairs and last pair make up the first group and the rest are in the second group, $s_1 = \{1, 2, 3, 10\}$ and $s_2 = \{4, 5, 6, 7, 8, 9\}$. The set of potential responses, exposures, and observed and unobserved covariates for the first group is then $\mathcal{F}_{s_1} = \{(r_{1s1ij}^{(d_{1s1ij})}, r_{0s1ij}^{(d_{0s1ij})}, d_{1s1ij}, d_{0s1ij}, X_{s1ij}, u_{s1ij}), s_1 \subseteq \{1, 2, 3, 10\}, i \in s_1, j = 1, 2\}$. The observed response, binary instrument, and exposure for a given individual in subset $s_g$ is then denoted $Z_{sij}$, $R_{sij}$, and $D_{sij}$ respectively. The notation assumes that the Stable Unit Treatment Value Assumption (SUTVA) holds $[\text{Rubin (1980)}]$. 

2.2 Review: Matching, Instrumental Variables, and the Complier Average Treatment Effect (CATE)

Matching is a popular non-parametric technique in observational studies to balance the distribution of the observed covariates between treated and control individuals by grouping individuals based on the similarity between their covariates; see $[\text{Stuart (2010)}]$ and Chapters 3 and 8 of $[\text{Rosenbaum (2010)}]$ for overviews of matching. Pair matching is a specific type of matching where each treated individual is only matched to one control individual. In the context of instruments and pair matching, the IV serves as the treatment/control variable and the matching algorithm creates $I$ matched pairs indexed by $i = 1, \ldots, I$ where individuals $j = 1, 2$ in each matched pair $i$ are similar in their observed covariates $x_{ij}$ but one receives the instrument value $Z_{ij} = 1$ and the other receives the instrument value $Z_{ij} = 0$. Covariate similarity between individuals is typically measured by a rank-based Mahalanobis distance matrix with propensity score calipers to threshold distances exceeding a
certain value to infinity [Rosenbaum (2010)] and the optimal pair matching using optimal calipers can be found using the bigmatch R package [Yu (2019)] available on CRAN.

Instrumental variables (IV) is a popular approach to analyze causal effects when unmeasured confounding is present [Angrist et al. (1996); Angrist and Krueger (2001); Hernán and Robins (2006); Baiocchi et al. (2014)]. In an IV analysis, an instrument is utilized to extract variation free of unmeasured confounding in the treatment assignment and use this variation to identify causal treatment effects. To make claims of causality, the instrument must satisfy three core assumptions: (A1) the instrument is related to the exposure or treatment, \( \sum_{i=1}^{I} \sum_{j=1}^{J} (d_{1ij} - d_{0ij}) \neq 0; \) (A2) the instrument is not related to the outcome in any way except through the treatment, \( r_{0ij}^{(k)} = r_{1ij}^{(k)} \equiv r_{ij}^{(k)} \) for a fixed exposure \( k; \) (A3) the instrument is not related to any unmeasured confounders that affect the treatment and the outcome, \( P(Z_{ij} = 1|\mathcal{F}, Z) = \frac{1}{2} \) within each pair \( i \) (see Figure 1). If these core assumptions are satisfied, it is possible to obtain bounds on the average treatment effect. To further point identify a treatment effect, one needs to be willing to make an additional assumption. Here, we assume the (A4) monotonicity assumption to identify CATE, \( d_{0ij} \leq d_{1ij} \), so that no individuals act against the direction in which the instrument values pushes toward treatment, i.e. no defiers exist. See Hernán and Robins (2006) and Baiocchi et al. (2014) for discussion on other assumptions needed for point identification in an IV context.

In the Oregon Health Insurance Experiment, the lottery for individuals to have access to Medicaid is a plausible instrument. The lottery is randomized which ensures that the instrument is unrelated to unmeasured confounders satisfying (A3). Winning the lottery, on average, increased enrollment of Medicaid by 30% (Finkelstein et al., 2012) satisfying (A1). Assumption (A4) in the context of the OHIE states that there are no individuals who defy the lottery assignment to take or not take Medicaid if they lost or won the lottery respectively. This is guaranteed by the enforcement of the lottery, since an individual who loses cannot have access to Medicaid. However, we remark that Finkelstein et al. (2012) measure the exposure as whether or not an individual has ever had Medicaid during the study and a few individuals were already enrolled in Medicaid before the lottery winners were announced. Finally, assumption (A2), also referred to as the exclusion restriction assumption, is the only assumption potentially violated since individuals are not blinded to their lottery results, thereby allowing for lottery losers to seek other health insurance or lottery winners to make less healthy
decisions since they’re now able to be insured. These changes in an individual’s behavior could affect their outcome regardless of their treatment and so may violate the exclusion restriction assumption.

Let $N_{CO}$ be the total number of compliers in the population. Under the IV assumptions (A1)-(A4), the complier average treatment effect, defined as

$$
\lambda = \frac{\sum_{i=1}^{I} \sum_{j=1}^{2} (r_{1ij}^{(1)} - r_{0ij}^{(0)}) I(d_{1ij} = 1, d_{0ij} = 0)}{\sum_{i=1}^{I} \sum_{j=1}^{2} d_{1ij} - d_{0ij}} = \frac{1}{N_{CO}} \sum_{i=1}^{I} (r_{1ij}^{(1)} - r_{0ij}^{(0)}) I(ij \text{ is a complier})
$$

(1)

can be identified from data by taking the ratio of the ITT effect estimate, which is the difference in means of $R$ between instrument values 1 and 0, over the compliance rate, which is the difference in means of $D$ between instrument values 1 and 0 [Angrist et al. (1996)]. Statistical inference of CATE is usually via the delta method [Wooldridge (2010)]. Alternatively, in the context of matching and IV, [Rosenbaum (2002), Baiocchi et al. (2010) and Kang et al. (2016) proposed a test statistic for CATE by using the adjusted differences in outcomes

$$
T(\lambda_0) = \frac{1}{T(I-1)} \sum_{i=1}^{I} \sum_{j=1}^{2} (Z_{ij}(R_{ij} - \lambda_0 D_{ij}) - (1 - Z_{ij})(R_{ij} - \lambda_0 D_{ij}))
$$

(2)

along with an estimator for the variance of $T(\lambda_0)$,

$$
S^2(\lambda_0) = \frac{1}{T(I-1)} \sum_{i=1}^{I} \sum_{j=1}^{2} (Z_{ij}(R_{ij} - \lambda_0 D_{ij}) - (1 - Z_{ij})(R_{ij} - \lambda_0 D_{ij})) - T(\lambda_0))^2
$$

(3)

to test the null $H_0 : \lambda = \lambda_0$. Specifically, [Baiocchi et al. (2010) and Kang et al. (2016) showed that $\frac{T(\lambda)}{S(\lambda)}$ asymptotically follows the standard Normal distribution. Additionally, the same set of authors used the test statistic to propose a Hodges-Lehmann type estimator [Hodges Jr and Lehmann (1963)] for the effect ratio

$$
\hat{\lambda} = \frac{\sum_{i=1}^{I} \sum_{j=1}^{2} (Z_{ij} - \bar{Z}_i)(R_{ij} - \bar{R}_i)}{\sum_{i=1}^{I} \sum_{j=1}^{2} (Z_{ij} - \bar{Z}_i)(D_{ij} - \bar{D}_i)}
$$

where $\bar{Z}_i$, $\bar{R}_i$, and $\bar{D}_i$ are the averages of the pairs for the observed instrument, response, and exposure respectively. For a $(1 - \alpha)\%$ confidence interval for the effect ratio, the equation $T^2(\lambda) / S^2(\lambda) \leq z_{1-\alpha/2}$ is solved for $\lambda$, where $z_{1-\alpha/2}$ is the $(1 - \alpha/2)$ quantile of the standard Normal distribution. This turns out be equivalent to solving the roots of a quadratic equation; see Kang et al. (2016) and Kang et al. (2018) for details.

2.3 Heterogeneous Complier Average Treatment Effect (H-CATE)

We formally define the target estimand of interest in the paper, the heterogeneous treatment effect among the population of compliers, or H-CATE. Formally, H-CATE is defined as CATE for a subgroup of compliers with
a specific value of covariates

\[ \lambda(x) = \frac{\sum_{i=1}^{I} \sum_{j=1}^{2}(r_{1ij}^{(1)} - r_{0ij}^{(0)})I(d_{1ij} = 1, d_{0ij} = 0, X_{ij} = x)}{\sum_{i=1}^{I} \sum_{j=1}^{2}(d_{1ij} - d_{0ij})I(X_{ij} = x)} \]  

(4)

Because within each matched pair, two individuals are assumed to have identical covariate values, \( \lambda(x) \) can be rewritten as taking a subset of \( I \) matched pairs with identical covariates \( x \), say \( s \subseteq \{1, \ldots, I\} \)

\[ \lambda_s = \frac{\sum_{i \in s} \sum_{j=1}^{2}(d_{1sij} - d_{0sij})}{\sum_{i \in s} \sum_{j=1}^{2}d_{1sij} - d_{0sij}} \]  

(5)

Since each H-CATE, \( \lambda_s \), has the same form as the original CATE, we can apply the test statistic in Kang et al. (2016). Formally, consider the subset-specific hypothesis denoted \( H_{0s} : \lambda_s = \lambda_0 \) against \( H_{1s} : \lambda_s \neq \lambda_0 \). Then, we can use the test statistic (2) with variance (3) as described in Section 2.2 using the pairs specific to the subset in question.

We conclude this section by showing that the original CATE is equal to a weighted version of H-CATE:

**Lemma 1.** Suppose assumptions (A1)-(A4) hold. For a given mutually exclusive and exhaustive grouping \( G = \{s_1, \ldots, s_G\} \) of sets of pairs \( s_g \subseteq \{1, \ldots, I\} \), where there is at least one complier within each group \( s_g \), CATE is equivalent to a weighted average of H-CATEs where the weights are the proportion of compliers within subgroup \( s_g, g = 1, \ldots, G \) divided by the total number of compliers in the data.

\[ \lambda = \sum_{g=1}^{G} w_{s_g} \lambda_{s_g}, \quad w_{s_g} = \frac{\sum_{i \in s_g} \sum_{j=1}^{2}d_{1sij} - d_{0sij}}{N_{CO}} \]

An implication of Lemma 1 is that the typical analysis of CATE hides the underlying heterogeneity of CATE. For example, suppose there are two subgroups defined by a binary covariate, say male or female, and consider two scenarios. In the first scenario, among compliers, 80% are male and 20% are female, and the H-CATE of male is 1.25 and H-CATE of female is 0. In the second scenario, the male/female complier proportions remain the same, but H-CATE of male is now 1.5 and H-CATE of female is -1. In both cases, by Lemma 1, CATE is 1. But, in the second scenario, females have a negative treatment effect. By studying CATE only, as is typical in practice, the differential effects defined by H-CATE would have been masked. The next section presents a way to expose CATE and discover novel H-CATEs.

### 2.4 Discovering Novel H-CATE

A naive approach to finding novel H-CATE would be to exhaustively test every H-CATE for every subset of matched individuals and gradually aggregate matched pairs depending on their covariate similarities. However, the above procedure will not only lead to false discoveries of null treatment effects, but it will also be grossly underpowered.
Instead, based on the work by Hsu et al. (2015), we propose to use exploratory machine learning methods, such as CART, where the response going into the machine learning method is the absolute value of the difference in adjusted outcomes and the predictors for the machine learning method are the $X_i$ from each matched pair. CART will group matched pairs into subgroups with similar treatment effects, formulating groupings $G$ and use closed testing (Marcus et al., 1976) to not only test the effect heterogeneity in these groups, but also do so in a manner that strongly control for familywise error rate; see Algorithm 1 for details.

![Algorithm 1: Proposed method to discover and test effect heterogeneity in IV with matching](image)

We explain in some detail the key steps in the Algorithm. Similar to Fisher’s sharp null that there is no treatment effect for every individual (Fisher (1935)), we assume there is no instrument effect for every individual, $H_0: r_{ij}^{(d_{ij})} - \lambda d_{ij} = r_{ij}^{(d_{ij})} - \lambda d_{ij}$. This is equivalent to assuming that each individual has a treatment effect proportional to their treatment value, $H_0: r_{ij}^{(d_{ij})} - r_{ij}^{(d_{ij})} = \lambda (d_{ij} - d_{ij})$. Under this assumption, the absolute value of the difference in adjusted outcomes, $|Y_i| = |(Z_{i1} - Z_{i2})(R_{i1} - \lambda D_{i1} - (R_{i2} - \lambda D_{i2}))|$, between pairs obscures the instrument assignment of the pairs making $|Y_i| = |(d_{i1} - \lambda d_{i1}) - (r_{01}^{(d_{ij})} - \lambda d_{ij})|$, a function of $\mathcal{F}$ only, a fixed (and unknown) quantity. This is not the case if the adjusted outcomes, $Y_i$, were used without the absolute values, as $Y_i$ is a function of both $\mathcal{F}$ and $Z$, which is not a fixed quantity. Consequently, conditional on $\mathcal{F}$, building a CART tree based on $|Y_i|$ does not affect the distribution of $Z$; the distribution of $Z$ remains $1/2$ as stated in assumption (A3); see Section 3.1 for more details.

The algorithm also applies closed testing by conducting nested hypotheses tests constructed from CART’s grouping $\mathcal{G}$. Specifically, for a subset of the mutually exclusive and exhaustive $G$ groups $\mathcal{L} \subseteq \{1, \ldots, G\}$ and the hypothesis of the intersection of these groups $H_{0\mathcal{L}}$, closed testing rejects $H_{0\mathcal{L}}$ at level $\alpha$ if all of the valid $p$-values $p_{L'}$ (i.e. $p$-values from test statistics that control Type I error for that specific hypothesis), of the supersets $\mathcal{L}'$ of $\mathcal{L}$ are less than $\alpha$. That is, closed testing rejects $H_{0\mathcal{L}}$ if $p_{L'} \leq \alpha$ for all $\mathcal{L}' \supseteq \mathcal{L}$. Marcus et al. (1976) show that this closed testing procedure rejects at least one true hypothesis at level $\alpha$ if and only if the intersection of all true hypotheses is rejected, and therefore the familywise error rate is controlled to be at most $\alpha$. Proposition 1 shows this principle holds for Algorithm 1 using CART with absolute valued differences.

Proposition 1 (Familywise Error Rate Control of Algorithm 1). Under the assumption $H_0: r_{ij}^{(d_{ij})} - r_{ij}^{(d_{ij})} = \lambda (d_{ij} - d_{ij})$, the conditional probability given $(\mathcal{F}, Z, \mathcal{G})$ that Algorithm 1 makes at least one false rejection of
the set of hypotheses is at most $\alpha$.

Through the use of closed testing, our algorithm allows for strong control of the familywise error rate. It however does not describe the algorithm’s statistical power to detect effect heterogeneity. As a means of exploring the power of our method, we conduct simulation studies measuring the true discovery rate of H-CATE.

3 Simulations

The following three simulation settings are designed to (1) analyze the honesty of the simultaneous discovery and inference of the presented method, (2) analyze the proposed method’s performance as a function of constant compliance rate, and (3) again analyze the proposed method’s performance but with varying compliance rate between groups. We hope to see that our method, through CART, not only discovers that H-CATE only depends on certain covariates, but also tests the corresponding hypotheses generated from CART without inflating Type I error.

Each of the simulation settings use data generated in the form of a “God’s table”, which is a table of all the potential outcomes $r_{0ij}$ and $r_{1ij}$, potential treatments $d_{0ij}$ and $d_{1ij}$, and covariates $X_{ij}$ of each individual $j$ within each pair $i$ (see Table I). The observed treatment and outcome values are then taken from the table based on the value of the instrument (i.e. the lottery win), which is determined by a fair coin toss.

Following Hsu et al. (2015), there are six pre-instrument covariates, each generated from independent Bernoulli trials with 0.5 probability of success. At most two covariates, $x_1$ and $x_2$, modify the treatment effect. That is, H-CATEs defined by $\lambda(x_1, \ldots, x_6)$ in equation 3 are dependent on at most $x_1$ and $x_2$. Also, because both $x_1$ and $x_2$ are binary, there are at most four different H-CATEs $\lambda_{x_1 x_2}$, defined by the different combination of binary variables $\lambda_{00}$, $\lambda_{01}$, $\lambda_{10}$, and $\lambda_{11}$. Similar to the design of the OHIE, the data is generated under the assumption of one-sided compliance. This means that, for every individual, the potential treatment having not received the instrument is 0, $d_{0ij} = 0$. The potential treatment having received the instrument, $d_{1ij}$, is then a Bernoulli trial with success rate $\pi_{x_1 x_2}$. The notation implies the success rate, or compliance rate, may depend on the covariates capable of modifying the treatment effect, $x_1$ and $x_2$. Finally, the potential outcomes having not received the instrument $r_{0ij}$ are from a standard normal distribution $r_{0ij} \sim N(0, 1)$, and the potential outcomes having received the instrument $r_{1ij}$ are a function of the H-CATE and treatment value $r_{1ij} = r_{0ij} + d_{1ij} \lambda_{x_1 x_2}$.

Each simulations consists of $I = 2000$ pairs for a total of 4000 individuals. And, the regression trees are created in R using the package rpart. Unless specified otherwise, we use a complexity parameter of 0.005 (half of the default setting) and maintain the default settings for the rest of rpart’s parameters.
3.1 Honest Simultaneous Discovery and Inference

One advantage of our method is being able to use the entire data for discovering and testing effect modifiers. In order to simultaneously discover and draw inference on the sample, we use the absolute value of the pairwise differences $|Y|$ as the outcome of CART to obscure the sign of the difference in adjusted outcomes and preserve the original distribution of the instrumental variables (i.e. distribution based on assumption (A3)). We can then use this distribution to draw inference on our discovered potential effect modifiers. We study this phenomenon in two cases: (1) testing a single effect modifier (i.e. one hypothesis) and (2) testing multiple effect modifiers (i.e. multiple hypothesis).

In the first case, we are concerned about testing a single hypothesis and controlling the Type I error rate after discovering the hypothesis via CART. To investigate the effect of simultaneously discovering and drawing inference, we generate a “God’s table” with no treatment effect, $\lambda_{1,x_{1},x_{2}} = 0$ for all $x_{1},x_{2}$, and form potential effect modifiers for two different cases, (i) using $|Y|$ and (ii) $Y$ as the outcome for CART. The first leaf of each tree (or tree’s root if no leaves are formed) is then used to test the null hypothesis of no treatment effect. As a result of conducting CART to form a hypothesis 2000 times, Figure 2 shows the histogram of $p$-values when we use $|Y|$ as the outcome for CART versus $Y$ as the outcome for CART. Under $|Y|$, the $p$-values resemble a uniform distribution and hence, Type I error is controlled. However, under $Y$, the $p$-values are right-skewed implying that Type I error is inflated. In other words, the null hypothesis is rejected more frequently when using $Y$ as the outcome of CART, demonstrating the “winner’s curse” phenomena. Therefore, as predicted by Proposition 1, using $|Y|$ as the outcome in CART prevents the contamination of the $\alpha$ level of the hypothesis test and allow for simultaneous discovery and inference.

In the second case, with multiple hypotheses, we are concerned with the average Type I error rate and strong control of the familywise error rate rate when testing multiple hypotheses. To evaluate strong control of the familywise error rate, we generate the data where there is an effect in some groups and no effect in others, $\lambda_{00} = 2$, $\lambda_{01} = \lambda_{10} = 0 = \lambda_{11} = 0$. Furthermore, for rpart, we reduce the complexity parameter to 0.0001 to encourage more liberal splitting and set the max depth of the regression tree to be 4 to save on computational time. After data generation we randomly assign instrument values within pairs and split the data using $|Y|$
Figure 2: Histogram of $p$-values obtained from using $|Y|$ and $Y$ as the outcomes in CART in discovery of potential effect modifiers. The black dashed line denotes the alpha level of 0.05 of the hypothesis tests.

| Simulation Setting | Mean Type I error rate | Familywise error rate |
|-------------------|------------------------|-----------------------|
| $|Y|$              | 0.0008                 | 0.028                 |
| $Y$               | 0.0003                 | 0.028                 |

Table 2: Results of simulations analyzing strong control of familywise error rate.

and $Y$ 2000 times. Each hypothesis is tested for whether or not there is a treatment effect $H_0: \lambda = 0$, so true hypotheses are hypotheses of groups of pairs generated with $\lambda_{01} = \lambda_{10} = \lambda_{11} = 0$. The average Type I error rate is computed by taking the average of the proportion of false rejections from each of the 2000 simulated trees and the familywise error rate is computed by taking the average of any false rejections amongst the 2000 simulated trees.

The results of this simulation show that the average type I error rate and familywise error rate are below the $\alpha$ level of the hypothesis tests in both simulation settings $|Y|$ and $Y$. The average Type I error rate for $|Y|$ and $Y$ is 0.0008 and 0.0003, respectively. The familywise error rate for both $|Y|$ and $Y$ is 0.028 (See Table 2). This is surprising considering that closed testing requires that each hypothesis test be level $\alpha$ to strongly control the familywise error rate and using $Y$ as the outcome contaminates the test’s level, as seen in Section 3.1. Despite the theoretical underpinnings for this data generation process, closed testing seems to strongly control the familywise error rate regardless of whether or not the test’s size is preserved by a technique such as taking the absolute value. Upon closer investigation, it seems that the trees formed in both $Y$ and $|Y|$ cases are the same at the upper levels of the tree, as there is a particularly strong signal for a certain group $\lambda_{00} = 2$. This then leads to the same hypotheses in both settings resulting in similar Type I error rates and familywise error rates. Overall, the simulation suggests that in the case where there is one very strong signal, the difference between using $|Y|$ and $Y$ is minor. But, we do stress familywise error control is only guaranteed for the $|Y|$ case.
### 3.2 Weak Instrument with Constant Compliance

Instrument strength is a description of how large of a push the instrument gives towards or against treatment. If the probability of complying with the instrument’s nudge is high then the instrument is considered strong. Under noncompliance, the performance of statistical tests and estimation depends strongly on the strength of the instrument, particularly when the instrument is weak; see Staiger and Stock (1997) and Stock et al. (2002) and references therein for more details. It is our intention to understand how instrument strength affects estimating and inferring H-CATE.

We chose four heterogeneous treatment settings for consideration. The four settings are referred to as (a) no heterogeneity, (b) similar heterogeneity, (c) strong heterogeneity, and (d) complex heterogeneity, and each of the four settings have an overall complier average treatment effect of \( \lambda = 0.5 \). The settings are defined as (a) there are no effect modifiers resulting in one subgroup with equal treatment effects, \( \lambda_{00} = \lambda_{01} = \lambda_{10} = \lambda_{11} = 0.5 \); (b) there is one effect modifier resulting in two subgroups with similar but different treatment effects, \( \lambda_{00} = \lambda_{01} = 0.7 \) and \( \lambda_{10} = \lambda_{11} = 0.3 \); (c) there is one effect modifier resulting in two subgroups with dissimilar treatment effects, \( \lambda_{00} = \lambda_{01} = 0.9 \) and \( \lambda_{10} = \lambda_{11} = 0.1 \); and (d) there are two effect modifiers resulting in three subgroups, one with a strong effect, two with no effect, and the last group with the average effect, \( \lambda_{00} = 1.5, \lambda_{01} = \lambda_{10} = 0 \) and \( \lambda_{11} = 0.5 \). These definitions are concisely provided in Table 3. We note that each group has the same compliance rate.

![Table 3: Heterogeneous treatment effect settings.](image)

To further measure and understand the performance of the proposed method, we measure the ability of CART to correctly partition the pairs into groups defined in Table 3. For each pair \( i \), we know their treatment effect \( \lambda_i \), which depends on the pairs of covariates \( x_1 \) and \( x_2 \), so we’re able to define a perfect partition based on the treatment effects in the leaves of CART. Let \( \bar{\lambda}_g = |s_g|^{-1} \sum_{i \in s_g} \lambda_i \) denote the average treatment effect of the \( g \)th subgroup \( s_g \), or leaf, in \( G \). A perfect tree is then defined as the case when \( \lambda_i = \bar{\lambda}_g \) for all \( i \in s_g \) for every \( g \), which is the case that CART partitions the subgroups to having the same identifying treatment effects.

The metric used to measure how close a given tree is to a perfect tree is

\[
\phi_G = \frac{\sum_{g=1}^{G} \sum_{i \in s_g} (\lambda_i - \bar{\lambda}_g)^2 + \sigma_i^2}{\sum_{g=1}^{G} \sum_{i \in s_g} \sigma_i^2}
\]

which is the fractional increase in mean squared error from grouping \( G \) compared with a perfect grouping, used by Hsu et al. (2015). Here, \( \sigma_i^2 = 1 \) for all individuals as \( r_{d(i)}^{(a)} \sim N(0, 1) \) in the “God’s table”. A perfect tree has \( \phi_G = 1 \). From hereon, \( \phi_G \) is referred to as tree accuracy.
The simulations are conducted within each treatment heterogeneity setting. We first generate the data in the form of a “God’s table” for a given compliance rate, as described above. Then, we (i) randomly assign the instrument within each pair \(i\), (ii) calculate \(|Y_i|\), (iii) form grouping \(G\) using CART, and (iv) finally conduct hypothesis tests using closed testing. We repeat (i)-(iv) 2000 times and measure two quantities, the average true discovery rate and the average Type I error. The true discovery rates are computed as the number of true rejections of false null hypotheses divided by the total number of false null hypotheses per simulation and the average is taken across the 2000 simulations. Similarly, the Type I error rate is calculated as the total number of false rejections of true null hypotheses divided by the total number of true null hypotheses and the average taken across the 2000 simulations. We remark that the null hypothesis is that of no treatment effect and, since all treatment heterogeneity settings have an overall effect of \(\lambda = 0.5\), only hypotheses consisting of pairs generated with \(\lambda_{x_1x_2} = 0\) are true null hypotheses.

![Figure 3](image-url)

**Figure 3:** True discovery rate as a function of overall compliance rate for the no heterogeneity and slight heterogeneity settings. The dot size denotes how tree accuracy, where a smaller dot implies greater accuracy.

Figures 3 and 4 show the true discovery rate under the four treatment heterogeneity settings as a function of instrument strength, as measured by the overall compliance rate. We see that as compliance with treatment grows, the true discovery rate of our method grows for all of the treatment heterogeneity settings. This aligns with our expectations, since as more individuals comply with their treatment there is a stronger signal of treatment effect. We further see that the tree becomes more accurate as the compliance rate increases, since the size of the dots denote the average tree accuracy for the regression trees formed. Recall that a values closer to 1 denotes greater accuracy. The size ranges from smallest, a tree accuracy of \(\phi_G = 1\) to largest, \(\phi_G \approx 1.4\). In Figure 3, which presents the no heterogeneity and the slight heterogeneity setting, there is a minor difference in the true discovery rate and tree complexity. The size of the dots in this figure represent \(\phi_G = 1\) for the no heterogeneity setting and range from \(\phi_G \approx 1.02\) to \(\phi_G \approx 1.04\) in the slight heterogeneity setting.

In Figure 4 we observe a counter-intuitive dip in true discovery rate as compliance rate grows. To investigate
Figure 4: True discovery rate as a function of overall compliance rate for the strong heterogeneity and complex heterogeneity settings. The dot size denotes how tree accuracy, where a smaller dot implies greater accuracy. The shades of gray denote a single subgroup's treatment effect, where a darker shade denotes the stronger treatment effect.

this drop, we also plot in shades of gray the true discovery rate of single subgroups formed by CART, and the darker shade of gray denotes leaves containing pairs with a stronger treatment effect. For example, in the strong heterogeneity setting, the darker gray represents pairs formed by $\lambda_{00} = \lambda_{01} = 0.9$, and the lighter gray represents pairs formed by $\lambda_{10} = \lambda_{11} = 0.1$. For the complex heterogeneity setting, the darker gray denotes pairs generated by $\lambda_{00} = 1.5$, and a lighter gray isn’t shown because CART fails to form a group consisting of only pairs generated by $\lambda_{11} = 0.5$. By comparing the curves, we see that the drop in the true discovery rate is due to the formation of leaves with smaller treatment effects as the compliance rate grows. This can be seen from the size of the dots decreasing at the start of the dip, indicating that the tree is getting more accurate. Specifically, tree accuracy ranges from $\phi_G = 1$ to $\phi_G = 1.15$ for the strong heterogeneity setting and $\phi_G = 1.03$ to $\phi_G = 1.36$ for the complex heterogeneity setting. Because the compliance rate is large enough, these small effects are beginning to be detected by CART. But, the power to detect these effects are much smaller than the large effects represented by the darker grey curves and the overall true discovery rate, which is roughly the average of these two curves, dips at the lower end of the compliance rate. However, As the compliance rate grows, we see the true discovery rate of our method begin to climb again, as more signal for the smaller H-CATE groups is gained.

3.3 Weak Instruments with Varying Compliance

Up until now, the simulation setting has assumed constant compliance rates across the groups, but it is possible that the compliance rates vary between groups. Therefore, we further consider four varying compliance rate settings as an extension of understanding the method’s performance. These four different compliance settings are referred to as (a) same, (b) similar, (c) different (1), and (d) different (2) and are functions of the overall
Table 4: Varying compliance rate settings when $\pi \leq 0.5$.

| Compliance Setting | $\pi_{00}$ | $\pi_{01}$ | $\pi_{10}$ | $\pi_{11}$ |
|--------------------|------------|------------|------------|------------|
| Same               | $\pi$      | $\pi$      | $\pi$      | $\pi$      |
| Similar            | $0.9\pi$   | $0.9\pi$   | $1.1\pi$   | $1.1\pi$   |
| Different (1)      | $0.5\pi$   | $0.5\pi$   | $1.5\pi$   | $1.5\pi$   |
| Different (2)      | $0.7\pi$   | $0.5\pi$   | $1.1\pi$   | $1.7\pi$   |

Compliance rate $\pi$. Each are categorized based on the distance from the overall compliance rate. If the overall compliance is less than a half, $\pi \leq 0.5$, a group’s compliance rate is $\pi_{x_1x_2} = \pi + c_{x_1x_2}\pi$, and if $\pi > 0.5$, a group’s compliance rate is $\pi_{x_1x_2} = \pi + c_{x_1x_2}(1 - \pi)$ for some constant $c_{x_1x_2} \in [0, 1]$. The four settings are then defined by the constants $c_{x_1x_2}$: (a) same compliance $c_{00} = c_{01} = c_{10} = c_{11} = 0$; (b) similar compliance $c_{00} = c_{01} = -0.1$ and $c_{10} = c_{11} = +0.1$; (c) different (1) compliance $c_{00} = c_{01} = -0.5$ and $c_{10} = c_{11} = +0.5$; and different (2) compliance $c_{00} = -0.3$, $c_{01} = -0.5$, $c_{10} = +0.1$, and $c_{11} = +0.7$. The compliance settings for when $\pi \leq 0.5$ are concisely shown in Table 4. When combined with Table 3, we have a total of 16 possible settings of heterogeneity in H-CATE. We also remark that subgroups experiencing a larger H-CATE have a reduced compliance rate.

Figure 5 shows the true discovery rate of the four compliance types for each treatment heterogeneity setting. The gray lines now denote the different compliance types, where the darker shade of gray represents a more dissimilar compliance rate between groups. So, the lightest shade of gray represents the same compliance setting and the darkest shade represents the different (2) compliance setting. As the compliance rates get more different, reducing the signal of the stronger H-CATE group, we observe a reduction in the true discovery rate. This is most noticeable in the strong heterogeneity setting, where we see pronounced differences in the true discovery rate amongst the different compliance settings. In this setting, we also see a change in true discovery rate between the more different and more similar compliance groups; the more different compliance groups have an increased true discovery rate after an overall compliance rate of $\pi \approx 0.45$. At this point, the dot sizes of the lighter gray lines are smaller, implying the trees are becoming more accurate at lower overall compliance rates. This is due to the lower compliance rate in the groups with stronger H-CATE obscuring the signal for which CART uses to split on. As the overall compliance rate grows, so too does the subgroup-specific compliance rates, and so the true discovery rates of the compliance settings converge. This is evidence that our method’s true discovery rate relies on both the subgroup-specific size of H-CATEs and subgroup-specific compliance rates.

Our simulation studies show that our method strongly controls for familywise error rate while remaining able to detect a variety of treatment heterogeneity. The use of $|Y|$ as the outcome of CART prevents an increase in Type I error, preserving the level $\alpha$ of our hypothesis tests. However, we did note that in the presence of strong signal, closed testing with $|Y|$ and $Y$ had little differences in Type I error rate. Our analysis of our method’s power showed that the true discovery rate is a function of both the size of subgroup’s H-CATE and subgroup’s compliance rate.
Figure 5: True discovery rate as a function of overall compliance rate for the four treatment heterogeneity settings. The dot size denotes tree accuracy, where a smaller dot implies greater accuracy. The smallest dot is a tree accuracy of $\phi_G = 1$ and the largest dot is a tree accuracy of $\phi_G = 1.3$. The shade of gray denotes the compliance setting, getting darker as the compliance gets less similar between groups.

4 Oregon Health Insurance Experiment Example

4.1 Data Description

We use our method to analyze the differential effects of Medicaid on the number of days an individual’s physical or mental health prevent their usual activities from the OHIE study. In brief, the OHIE collected administrative data on hospital discharges, credit reports, and mortality, survey data on health care utilization, financial strain, and overall health, and prerandomization demographic data. A total of 74,922 individuals were included in the study. Of these individuals, there were 11,808 lottery winners and 11,933 controls with publicly available survey data for a total sample size of 23,741 individuals for our analysis; see Finkelstein et al. (2012) for details.

We matched on demographic, prerandomization variables recorded by Finkelstein et al. (2012): sex, age, whether they preferred English materials when signing up for the lottery, whether they lived in a metropolitan statistical area (MSA), their education level (less than high school, high school diploma or GED, vocational or 2-year degree, 4-year college degree or more), and self-identified race (as the individual reported in the survey). Since some of the covariates had missing data, namely self-identifying as Hispanic or Black and their level of education, we also match on indicators of these covariates; see Section 9.4 of Rosenbaum (2010) for details. We used R package bigmatch [Yu (2019)] to generate our optimal pair matched set using optimal calipers, where the caliper is optimal in the sense that it is the smallest caliper such that an optimal match exists. The covariate similarity between lottery winners and losers is calculated using a robust rank-based Mahalanobis distance as in Yu (2019). The performance of the matched set is assessed by checking covariate balance in Figure 6.

For the majority of covariates, the matching algorithm did little to change the absolute standard differences
between lottery winners and controls, which is not surprising given that the lottery was randomized. However, the indicator for missingness in education, self-identified American Indian, and Black were made to be more similar after matching. An absolute standardized difference of 0.25 is deemed trustworthy \cite{rubin2001, stuart2010}, which our covariates satisfy after matching.

### 4.2 Analysis and Results

In this paper, we examine the effect of enrolling in Medicaid on the number of days an individual’s physical or mental health did not prevent them from their usual activities, in the past 30 days of their survey response. The absolute value of the difference in adjusted outcomes are calculated and used by CART to form a tree partitioning of the groups. Our formed tree, shown in Figure 7, was created using the R package \texttt{rpart} \cite{therneau2015} with a complexity parameter of 0 and maximum depth of 4. The depth of the tree was chosen by forming trees of larger depth and then pruning back until a more interpretable tree was obtained.

For each node of the CART, we test for whether or not there is an effect of enrolling in Medicaid $H_0: \lambda_s = 0$. In Figure 7, a solid lined box denotes a hypothesis that was rejected and a dashed lined box denotes a hypothesis that was failed to be rejected, both by the closed testing procedure. Each node contains its corresponding estimated H-CATE $\hat{\lambda}_s$, its 95% confidence interval, the number of pairs $I_s$, and compliance rate $\pi_s$. Here, a positive H-CATE implies a decrease in the number of days where the individual’s physical and mental health prevented them from their usual activities, and a negative value implies an increase. Note, some nodes imply a significant effect of Medicaid at the alpha level of 0.05, but are enclosed in a dashed lined box. This is due to the closed testing procedure; an intersection of hypotheses containing the node in question was failed to be rejected, and so any hypotheses in this intersection cannot be rejected.

From the CART results, we can see evidence of heterogeneous treatment effects amongst the complier population. Complying men, over the age of 36, who do not identify as Asian, and prefer English have a
stronger effect of Medicaid on the number of days an individual’s physical or mental health did not prevent them from their usual activities. Furthermore, complying individuals younger than 36, who prefer English, and with no more than a high school diploma or GED have a stronger effect of Medicaid on increasing the number of days not impeded upon by their physical and mental health. Lastly, it’s possible that CART overfits the data and suggests heterogeneity where it doesn’t exist, but our method controls for this by conducting honest familywise statistical inference and retaining the null if there is truly no treatment effect.

Figure 7: Results of our proposed method of the effect of Medicaid on the number of days physical or mental health prevented usual activities. Here, positive effects are beneficial to the individual. Solid lined boxes denote hypothesis tests that were rejected and dashed lined boxes denote hypotheses that were failed to be rejected by closed testing. Within each box, the subgroup-specific estimated H-CATE $\hat{\lambda}$, its 95% confidence interval, sample size of pairs $I_s$, and compliance rate $\pi_s$ are provided. Here less educated refers to pairs with at most a high school diploma or GED and more educated refers to pairs with a higher education.

We also note that there is some variation in the compliance rates amongst groups, although most of them are minor. The minor variation suggests that while some groups are more likely to be compliers than others, most of the effect heterogeneity is likely driven by the variation in how the treatment responds to these subgroups; a bit more formally, most of the effect heterogeneity in the data is likely arising from the numerator of H-CATE rather than the denominator of H-CATE.

5 Summary

We propose a method to detect treatment effect heterogeneity using an IV. Under the usual IV assumptions, our method discovers and tests heterogeneity in H-CATEs by using matching, CART, and closed testing, all without the need to do sample splitting. The latter is achieved by taking the absolute value of the adjusted pairwise differences to conceal the instrument assignment. Our method was shown to strongly control the familywise error rate. We conducted a simulation study to examine the power of our method under varying degrees of
compliance and effect heterogeneity and showed that our method can detect wide variety of heterogeneity. Our method was used to study the effect of Medicaid on the number of days an individual's physical or mental health did not prevent their usual activities where we used the lottery selection as an instrument. It was found that Medicaid has a larger impact on improving the number of days not impeded upon by their health for complying, older, non-Asian men who selected English materials at lottery sign-up and for complying, younger, less educated individuals who selected English materials at lottery sign-up.
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Appendix

**Lemma 1** Suppose assumptions (A1)-(A4) hold. For a given mutually exclusive and exhaustive grouping \( G = \{s_1, \ldots, s_G\} \) of sets of pairs \( s_g \subseteq \{1, \ldots, I\} \), CATE is equivalent to a weighted average of H-CATES where the weights are the proportion of compliers within subgroup \( s_g \), \( g = 1, \ldots, G \) divided by the total number of compliers in the data.

\[
\lambda = \sum_{g=1}^{G} w_{s_g} \lambda_{s_g}, \quad w_{s_g} = \frac{\sum_{i \in s_g} \sum_{j=1}^{2} d_{1sij} - d_{0sij}}{N_{CO}}
\]

*Proof.* The monotonicity (A4) assumption states that \( d_{0ij} \leq d_{1ij} \), so for a given a mutually exclusive and exhaustive grouping of \( G = \{1, \ldots, G\} \) of sets of pairs \( s_g \subseteq \{1, \ldots, I\} \), the monotonicity assumption is equivalently written as \( d_{0sij} \leq d_{1sij} \). The number of compliers can then be written as

\[
N_{CO} = \sum_{g=1}^{G} \sum_{i \in s_g} \sum_{j=1}^{2} d_{1sij} - d_{0sij}
\]

We then see that,

\[
\sum_{g=1}^{G} w_{s_g} \lambda_{s_g} = \sum_{g=1}^{G} \frac{\sum_{i \in s_g} \sum_{j=1}^{2} d_{1sij} - d_{0sij}}{\sum_{g=1}^{G} \sum_{i \in s_g} \sum_{j=1}^{2} d_{1sij} - d_{0sij}} \lambda_{s_g}
\]

\[
= \sum_{g=1}^{G} \frac{\sum_{i \in s_g} \sum_{j=1}^{2} d_{1sij} - d_{0sij}}{\sum_{g=1}^{G} \sum_{i \in s_g} \sum_{j=1}^{2} d_{1sij} - d_{0sij}} \left( \frac{\sum_{i \in s_g} \sum_{j=1}^{2} r_{1sij} - r_{0sij}}{\sum_{i \in s_g} \sum_{j=1}^{2} d_{1sij} - d_{0sij}} \right)
\]

\[
= \sum_{g=1}^{G} \frac{\sum_{i \in s_g} \sum_{j=1}^{2} r_{1sij} - r_{0sij}}{\sum_{i \in s_g} \sum_{j=1}^{2} d_{1sij} - d_{0sij}}
\]

\[
= \lambda
\]

\( \square \)

**Proposition 1** (Familywise Error Rate Control of Algorithm 1). For the hypotheses \( H_{0\mathcal{C}}, \mathcal{L} \subseteq \{1, \ldots, G\} \), generated by closed testing, The conditional probability given \( (\mathcal{F}, \mathcal{Z}, \mathcal{G}) \) that Algorithm 1 makes at least one false rejection is at most \( \alpha \).

*Proof.* Refer to Algorithm 2 for the additional details required for the proof of the proposition, where the additional details are the included specifics of the closed testing procedure. Following the logic of both Marcus et al. (1976) and Hsu et al. (2015), define \( h \subseteq \{1, \ldots, I\} \) to be the union of all groups of pairs for which the null hypothesis is true; the groups of pairs of individuals which have an effect ratio of \( \lambda_0 \). In order to have a notion of type I error, some hypothesis or hypotheses must be true, so we assume that \( h \neq \emptyset \) and that hypothesis \( H_{0\mathcal{C}} : \lambda_s = \lambda_0 \) for \( s = \bigcup_{g \in \mathcal{K}} s_g \) is true. Note that by definition of \( h \), in order for \( H_{0\mathcal{K}} \) to be true, the groups in \( \mathcal{K} \) are also contained in \( h \), \( s \subseteq h \). To make a type I error and reject hypothesis \( H_{0\mathcal{K}} \), algorithm 1 must
reject the intersection of all true hypotheses \( H_{0T} \), where \( h = \bigcup_{g \in T} \) and \( K \subseteq T \). Yet, rejecting \( H_{0T} \) requires
\[
\left| \frac{T(\lambda_0)}{S(\lambda_0)} \right| \geq z_{1-\alpha/2}, \text{ where } P \left( \left| \frac{T(\lambda_0)}{S(\lambda_0)} \right| \geq z_{1-\alpha/2} | F, Z, G \right) = \frac{\alpha}{2}. \]
Therefore, to make a type I error and reject \( H_{0K} \), one must reject \( H_{0T} \) which is a level \( \alpha \) test.

Given:
- Observed outcome \( R \)
- Binary instrument \( Z \)
- Exposure \( D \)
- Covariates \( X \)
- Hypothesized null value \( \lambda_0 \)
- Desired familywise error rate \( \alpha \)

1. Pair match on observed covariates
2. Calculate absolute value of pairwise differences
   \[
   |Y_i| = |(Z_{i1} - Z_{i2})(R_{i1} - \lambda D_{i1} - (R_{i2} - \lambda D_{i2}))|
   \]
3. Construct mutually exclusive and exhaustive grouping \( G = \{s_1, \ldots, s_G\} \) using an exploratory machine learning method, such as CART. Here, CART takes \( |Y_i| \) as the outcome and \( X_i \) from each matched pair as the predictors
4. for \( \mathcal{L} \subseteq \{1, \ldots, G\} \) do
   - if \( H_{0\mathcal{L}} \) has not been accepted or rejected then
     - Calculate \( T_s(\lambda_0) \) and \( S_s(\lambda_0) \) for \( s = \bigcup_{g \in \mathcal{L}} s_g \)
     - if \( \left| \frac{T_s(\lambda_0)}{S_s(\lambda_0)} \right| \geq z_{1-\alpha/2} \) then
       - Accept the null hypothesis \( H_{0\mathcal{K}} : \lambda_K = \lambda_0 \) for all \( \mathcal{K} \subseteq \mathcal{L} \subseteq \{1, \ldots, G\} \)
     - end
   - else
     - Reject \( H_{0\mathcal{L}} \)
   - end
5. end

Algorithm 2: Detailed method to discover and test effect heterogeneity in IV with matching