Propensity Score Weighting for Causal Inference with Multi-valued Treatments

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ABSTRACT

This article proposes a unified framework, the balancing weights, for estimating causal effects with multi-valued treatments using propensity score weighting. These weights incorporate the generalized propensity score to balance the weighted covariate distribution of each treatment group, all weighted toward a common pre-specified target population. The class of balancing weights include several existing approaches such as inverse probability weights and trimming weights as special cases. Within this framework, we propose a class of target estimands based on linear contrasts and their corresponding nonparametric weighting estimators. We further propose the generalized overlap weights, constructed as the product of the inverse probability weights and the harmonic mean of the generalized propensity scores, to focus on the target population with the most overlap in covariates. These weights are bounded and thus bypass the problem of extreme propensities. We show that the generalized overlap weights minimize the total asymptotic variance of the nonparametric estimators for the pairwise contrasts within the class of balancing weights. We also develop two new balance check criteria and a sandwich variance estimator for estimating the causal effects with generalized overlap weights. We illustrate these methods by simulations and apply them to study the racial disparities in medical expenditure.

KEY WORDS: balancing weights, equipoise, generalized propensity score, generalized overlap weights, pairwise comparison, sandwich variance estimator

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1 Introduction

Unconfounded comparisons between groups in non-randomized studies often require adjustment for differences in pre-treatment covariates. Standard parametric regression adjustment may be sensitive to model misspecification when there is limited overlap in covariate distributions between groups. The propensity score plays a central role in estimating the causal effects in such settings (Rosenbaum and Rubin [1983]). With binary treatments, the propensity score summarizes the multi-dimensional covariates into a scalar score and balancing this score balances all covariates. To accommodate the increasingly common multi-valued treatments in observational studies, Imbens (2000) has developed the generalized propensity score method; the key insight is that the scalar generalized propensity score of each treatment level can be exploited to separately estimate the average potential outcomes at that level.

With the generalized propensity score device, matching and subclassification have been discussed extensively; see, for instance, Lechner (2002); Zanutto et al. (2005); Rassen et al. (2013); Yang et al. (2016); Lopez and Gutman (2017a,b). An alternative strategy, propensity score weighting, has also been generalized to multi-valued treatments (Robins et al., 2000; Feng et al., 2012; McCaffrey et al., 2013; Rose and Normand, 2018), with much focus on the pairwise average treatment effect (ATE) based on inverse probability weighting (IPW). However, with the prevalent use of convenience samples in observational studies, the automatic focus on ATE may be questionable because the available data may not represent a scientifically appropriate target population. Moreover, multi-valued treatments exacerbate the overlap issues as different treatments may be applicable only to certain subpopulations. Regardless of the number of treatment options, extreme propensity scores close to zero or one will likely result in bias and excessive variance of the IPW estimators (Li, Thomas, and Li, 2018b). Crump et al. (2009) proposed an optimal trimming procedure that focuses on regions with good overlap and thus improves the efficiency of the IPW estimator for binary treatments; Yang et al. (2016)
extended the trimming rule to multi-valued treatments. Though easy to implement, propensity trimming often corresponds to an ambiguous target population and may discard a large number of units.

In this article, we present a unified framework for weighting-based causal inference applicable to multi-valued treatments. Specifically, we generalize the balancing weights framework for binary treatments (Li, Morgan, and Zaslavsky, 2018a) to balance the distribution of covariates from multiple treatment groups according to a pre-specified target population. Within this framework, we propose a class of target estimands based on linear contrasts and their corresponding nonparametric weighting estimators. We derive several asymptotic results on these nonparametric estimators, based on which we develop the generalized overlap weights, constructed as the product of the inverse probability weights and the harmonic mean of the generalized propensity scores. The generalized overlap weights emphasize the target population with the most overlap in covariates, that is, the subpopulation with substantial probabilities to be assigned to all treatments. Under mild conditions, we show that the generalized overlap weights minimize the total asymptotic variance of the nonparametric estimators for the pairwise contrasts within the class of balancing weights. These weights are strictly bounded between zero and one, and thus automatically avoid the issue of extreme weights.

The rest of the paper is organized as follows. Section 2 introduces the general framework of balancing weights. In Section 3 we propose the generalized overlap weights for pairwise comparisons with nominal treatments, discuss balance check criteria and variance estimation. A simulation study is conducted in Section 4 to examine the finite-sample performance of the proposed methods, followed by an illustrative data example in Section 5. Section 6 concludes.
2 Balancing Weights for Multi-valued Treatments

2.1 Basic Setup

We consider a sample of \( n \) units, each belonging to one of \( J \) (\( \geq 3 \)) groups for which covariate-balanced comparisons are of interest. Let \( Z_i \in \mathbb{Z} = \{1, \ldots, J\} \) denote the treatment group membership, and \( D_{ij} = \mathbb{1}\{Z_i = j\} \) the indicator of receiving treatment level \( j \). For each unit, we observe an outcome \( Y_i \) and a set of \( p \) pre-treatment covariates \( X_i = (X_{i1}, \ldots, X_{ip})' \). The generalized propensity score is the probability of being assigned to each group given the covariates [Imbens 2000]:

\[
e_j(X) = \Pr(Z = j | X), \quad j = 1, \ldots, J.
\] (1)

By definition, the sum-to-unity restriction \( \sum_{j=1}^{J} e_j(X) = 1 \) holds for all \( X \) in support \( \mathbb{X} \), and hence each unit’s propensity can be uniquely characterized by \( J - 1 \) scalar scores.

Under the Stable Unit Treatment Value Assumption (SUTVA), each unit has a potential outcome \( Y_i(j) \) mapped to each treatment level \( j \in \mathbb{Z} \), among which, only the one corresponding to the received treatment, \( Y_i = Y_i(Z_i) \), is observed. We define the conditional expected potential outcomes in group \( j \) as \( m_j(X) = \mathbb{E}[Y(j) | X] \). Assuming weak unconfoundedness [Imbens 2000], that is, \( Y(j) \perp \mathbf{1}\{Z = j\} | X, \forall j \in \mathbb{Z} \), (2)

we have \( m_j(X) = \mathbb{E}[Y | Z = j, X] \), which is estimable from observed data. We further require the overlap or positivity assumption, that is, \( e_j(X) > 0 \) for all \( j \) and \( X \in \mathbb{X} \), which restricts the study population to the covariate space where the probability of receiving any treatment is strictly bounded away from zero. The propensity score methods are also applicable to unconfounded descriptive (non-causal) comparisons where the group membership is a non-manipulable state, such as different races or years. In these cases, the common objective is
to compare the expected observed outcomes, \( m_j(\mathbf{X}) = \mathbb{E}[Y \mid Z = j, \mathbf{X}] \); for example, when \( J = 2 \), Li, Zaslavsky, and Landrum (2013) defined the contrast between \( m_1(\mathbf{X}) \) and \( m_2(\mathbf{X}) \) averaged over a population the average controlled difference (ACD). Below we develop our framework in the context of causal inference, but the discussion applies also to unconfounded descriptive comparisons.

### 2.2 Balancing Weights

Assume the marginal density of the covariates, \( f(\mathbf{X}) \), exists, with respect to a base measure \( \mu \). In causal studies, the interest is on the average effects of units in a target population, whose density (up to a normalizing constant) we represent by \( f(\mathbf{X})h(\mathbf{X}) \), with \( h(\mathbf{X}) \) being a pre-specified function of covariates or equivalently a tilting function. We first define the expectation of the potential outcomes over the target population \( f(\mathbf{X})h(\mathbf{X}) \):

\[
\hat{m}_j = \frac{\int_{\mathbf{X}} m_j(\mathbf{X}) f(\mathbf{X})h(\mathbf{X}) \mu(d\mathbf{X})}{\int_{\mathbf{X}} f(\mathbf{X})h(\mathbf{X}) \mu(d\mathbf{X})}.
\]

(3)

Then we can define a class of estimands as a linear combination of the above expectations, with coefficients \( a = (a_1, \cdots, a_J)' \):

\[
\tau^h(a) = \sum_{j=1}^J a_j \hat{m}_j.
\]

(4)

The causal estimand \( \tau^h(a) \) generalizes the definition of weighted average treatment effect (WATE) in binary treatments (Hirano et al., 2003) where \( J = 2 \) and \( a = (1, -1) \). As will be seen in due course, \( \tau^h(a) \) includes several existing causal estimands for multi-valued treatments as special cases.

We next define the class of balancing weights. Let \( f_j(\mathbf{X}) = f(\mathbf{X} \mid Z = j) \) be the density of \( \mathbf{X} \) in the \( j \)th group over its support \( \mathbb{X}_j \), we have \( f_j(\mathbf{X}) \propto f(\mathbf{X})e_j(\mathbf{X}) \). Given any pre-specified function \( h \), we can weight the group-specific density \( f_j(\mathbf{X}) \) to the target population
using the following weights, proportional up to a normalizing constant:

\[ w_j(X) \propto \frac{f(X)h(X)}{f(X)e_j(X)} = \frac{h(X)}{e_j(X)}, \quad j = 1, \ldots, J. \]  

(5)

It is straightforward to show that the class of weights defined in Equation (5) balance the weighted distributions of the covariates across \( J \) comparison groups:

\[ f_j(X)w_j(X) = f(X)h(X), \quad \forall \ j = 1, \ldots, J. \]  

(6)

To apply the above framework, a key is to specify the coefficients \( a \) and the tilting function \( h \), with the former defining the causal contrast and the latter representing the target population. We focus on the case of nominal treatments, where the scientific interest usually lies in pairwise comparisons. More specifically, the choice of \( a \) is contained in the finite set \( \mathbb{S} = \{ \lambda_{j,j'} = \lambda_j - \lambda_{j'} : j < j' \} \), where \( \lambda_j \) is the \( J \times 1 \) unit vector with one at the \( j \)th position and zero everywhere else. In principle, the tilting function \( h \) can take any form, each leading to a unique type of balancing weights; statistical, scientific and policy considerations all play into the specification of \( h \). We illustrate specifications of \( a \) and \( h \) by connecting the general definition (4) with existing estimands in the literature of multi-valued treatments.

When \( h(X) = 1 \), the corresponding target population \( f(X) \) is the combined population from all groups and the weights become the standard inverse probability weights, \( \{1/e_j(X), \ j \in Z\} \); the target estimand is the pairwise ATE (Feng et al., 2012). When \( h(X) = e_j(X) \), the target population is the subpopulation receiving treatment \( Z = j \), and the weights,

\[ \{e_j(X)/e_1(X), \ldots, e_j(X)/e_J(X)\}, \]

are designed to estimate the average treatment effect for the treated (ATT). Define

\[ \underline{e}_j = \max_{1 \leq l \leq J} \min_{X \in X_l} \{e_j(X)\}, \]

\[ \bar{e}_j = \min_{1 \leq l \leq J} \max_{X \in X_l} \{e_j(X)\}, \]

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and an eligibility function $E_j(X) = \{ e_j \leq e_j(X) \leq \bar{e}_j \}$ for all $j \in \mathbb{Z}$. When $h(X) = e_j(X) \prod_{l=1}^{j} E_l(X)$, the target population is the subpopulation receiving treatment $Z = j$ but remaining eligible for all other treatments (Lopez and Gutman 2017b). Define a threshold $\alpha$ as the largest value such that

$$\alpha \leq 2 \mathbb{E} \left[ \sum_{j=1}^{J} 1/e_j(X) \middle| \sum_{j=1}^{J} 1/e_j(X) \leq \alpha \right] / \Pr \left( \sum_{j=1}^{J} 1/e_j(X) \leq \alpha \right). \quad (7)$$

When $h(X) = 1\{X \in \mathbb{C}\}$ with $\mathbb{C} = \{X \in \mathbb{X}| \sum_{j=1}^{J} 1/e_j(X) \leq \alpha \}$, the target population is characterized by the subpopulation $\mathbb{C}$, and the inverse probability weights are formulated after applying the optimal trimming rule proposed in Yang et al. (2016). Finally, when $h(X) = \min_{1 \leq j \leq J} \{e_j(X)\}$, one arrives at the generalized matching weights (Yoshida et al. 2017)—an extension of the matching weights of Li and Greene (2013) to multi-valued treatments. The matching weights is a weighting analogue to exact matching and the causal comparisons are made for the matched population. Moreover, one could choose indicator functions for $h$ that directly involves covariates of a subpopulation of interest, such as a specific gender or a range of age.

For ordinal treatments where the treatment levels are ordered categories, target estimands may differ from the pairwise comparisons and thus require different choice of $a$. For instance, one may be interested in the quadratic contrasts between unit increases in the treatment level, namely $(m_{j+1}^h - m_j^h) - (m_j^h - m_{j-1}^h)$. In other cases, one may be interested in the weighted average of unit increase in the treatment level, $\sum_{j=1}^{J-1} \pi_j (m_{j+1}^h - m_j^h)$, or the accumulative effect of the maximum treatment, $m_J^h - m_1^h$. In this article, we focus on nominal treatments, but note that our weighting framework is also applicable to ordinal treatments.
2.3 Transitivity

With multi-valued treatments, a desirable property of a given class of estimands is transitivity. For pairwise comparisons, lack of transitivity often implies that comparisons of treatments are based on different populations. Non-transitivity may lead to incompatible pairwise contrasts; for example, it is possible that treatment 1 is favored over treatment 2, treatment 2 is favored over treatment 3, but treatment 3 is found to better than treatment 1 at the same time. Below we provide a formal definition of transitivity and two related remarks.

**Definition 1** The class of causal estimands \( T(h, A) = \{ \tau^h(a) : a \in A \subset \mathbb{R}^J \} \) is transitive if the following equivariance relationship holds: \( \tau^h(a) + \tau^h(a') = \tau^h(a'') \) whenever \( a, a', a'' \in A \) and \( a + a' = a'' \).

**Remark 1** Fixing a tilting function \( h \), the class of estimands specifying all pairwise contrasts, namely, \( T(h, S) \) is transitive. For example, with \( h(X) = 1 \), the class of pairwise ATE estimands is transitive; with \( h(X) = e_j(X) \prod_{j=1}^J E_l(X) \), the class of ATT estimands in Lopez and Gutman (2017b) is also transitive.

**Remark 2** The union of \( T(h_1, S) \) and \( T(h_2, S) \) or that of their subsets is generally non-transitive for \( h_1 \neq h_2 \). This explains why several existing classes of estimands are non-transitive, including the class of ATT estimands of Lechner (2001). \( \{ \mathbb{E}[Y_i(j) - Y_i(j') | Z_i = j \text{ or } Z_i = j'] : j < j' \} \). The reason is that each individual estimand corresponds to a distinct tilting function \( h_{j,j'}(X) = (e_j(X) + e_{j'}(X))/e_1(X) \), and therefore this class of estimands is the union of \( \binom{J}{2} \) elements, each of which is contained in \( T(h_{j,j'}, S) \) for some \( j < j' \).
2.4 Large-sample Properties of Nonparametric Estimators

For any pre-specified vector \( a \) and tilting function \( h \), we could first use the plug-in sample estimator to obtain the expectation of the potential outcomes among the target population

\[
\hat{m}_j^h = \sum_{i=1}^{n} D_{ij} Y_i w_j(X_i) / \sum_{i=1}^{n} D_{ij} w_j(X_i),
\]

and then estimate \( \tau^h(a) \) by a linear combination,

\[
\hat{\tau}^h(a) = \sum_{j=1}^{J} a_j \hat{m}_j^h,
\]

where the sum is over a sample drawn from density \( f(X) \). Below we establish three large-sample results of \( \hat{\tau}^h(a) \) and present the proofs in Appendix A.

**Proposition 1** Given any \( h \) and \( a \), \( \hat{\tau}^h(a) \) is a consistent estimator of \( \tau^h(a) \).

Denote the collection of treatment assignment \( Z = \{Z_1, \ldots, Z_n\} \) and covariate design points \( X = \{X_1, \ldots, X_n\} \). The next two results concern the variance of the sample estimator, which is decomposed as

\[
\mathbb{V}[\hat{\tau}^h(a)] = \mathbb{E}_Z \mathbb{V}[\hat{\tau}^h(a)|Z, X] + \mathbb{V}_Z \mathbb{E}[\hat{\tau}^h(a)|Z, X].
\]

The first term is the variation due to residual variance in \( \hat{\tau}^h(a) \) conditional on the design points. The second term arises from the dependence of the expectation of the plug-in estimator on the sample, and estimating it involves the outcome model (associations between \( Y_j \) and \( X \)). As individual variation is typically much larger than conditional mean variation, the benefit of further optimizing the weights by a preliminary look at the outcomes, which mixes the design and analysis, would usually not justify the risk of biasing model specification to attain desired results (Imbens, 2004). Hence, we focus on the first term.

**Proposition 2** Given \( a \), suppose the family of residual variances \( \{\mathbb{V}[\hat{\tau}^h(a)|Z, X], n \geq 1\} \) is uniformly integrable. Then the expectation of the conditional variance converges

\[
n \cdot \mathbb{E}_Z \mathbb{V}[\hat{\tau}^h(a)|Z, X] \to Q(a, h) \equiv \int_X \left( \sum_{j=1}^{J} a_j^2 w_j(X) / e_j(X) \right) h^2(X) f(X) \mu(dX) / C_h^2,
\]

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where \( v_j(X) = \nabla[Y(j)|X] \) and \( C_h \equiv \int_X h(X)f(X)\mu(dX) \) is a constant.

When the residual variance of the potential outcome is homoscedastic across all groups such that \( v_j(X) = v \), then the limit \( Q(a,h) \) can further simplify and the following result holds.

**Proposition 3** Under homoscedasticity, the function \( \tilde{h}(X) \propto (\sum_{j=1}^{J} a_j^2 / e_j(X))^{-1} \) gives the smallest asymptotic variance for the weighted estimator \( \hat{\tau}^h(a) \) among all \( h \)'s, and \( \min_h Q(a,h) = v/C_{\tilde{h}}. \)

A more general result of Proposition 3 can be obtained under heteroscedasticity. In that case, the optimal tilting function, \( \tilde{h}(X) \propto (\sum_{j=1}^{J} a_j^2 v_j(X) / e_j(X))^{-1} \), explicitly depends on the residual variances of the potential outcomes. Although estimates of \( v_j(X) \) can be obtained by outcome regression modeling in the analysis stage, it is rarely the case that accurate prior information is available in the design stage. Therefore, such a tilting function is difficult to specify for design purposes and may find limited use without peaking at the outcomes (mixing the design and analysis). For such considerations, we motivate the generalized overlap weights in Section 3 under homoscedasticity. Overall, these asymptotic results generalize those for binary treatments in Li et al. (2018a); they are also connected to the asymptotic results on propensity score trimming in Yang et al. (2016), who have similarly assumed homoscedasticity and restricted the class of tilting functions to indicator functions.

## 3 Generalized Overlap Weighting for Pairwise Comparisons

### 3.1 The Generalized Overlap Weights

For nominal treatments, scientific interest often lies in comparing outcomes between each pair of treatment groups in a common target population. In this case, as \( a \in S \), we propose to choose
the tilting function $h$ that minimizes the total asymptotic variance of the sample estimators for all pairwise comparisons; in other words, the objective function is

$$\sum_{j<j'} Q(\lambda_{j,j'}, h) \propto Q(1_{J \times 1}, h). \tag{10}$$

According to Proposition 3, the function $h(X) = \left( \sum_{j=1}^{J} 1/e_j(X) \right)^{-1}$—the harmonic mean of the generalized propensity scores—minimizes $Q(1_{J \times 1}, h)$ among all $h$. Based on this optimal tilting function $h$, we define the generalized overlap weights for $j = 1, \ldots, J$:

$$w_j(X) \propto \frac{1/e_j(X)}{\sum_{k=1}^{J} 1/e_k(X)}. \tag{11}$$

For binary treatments $(J = 2)$, the generalized overlap weights reduce to the overlap weights in Li et al. (2018a), namely the propensity of assignment to the other group: $w_1(X) \propto 1 - e_1(X) = e_2(X)$, $w_2(X) \propto 1 - e_2(X) = e_1(X)$.

The maximum of the harmonic mean function $h$ is attained when $e_j(X) = 1/J$ for all $j$, that is, when the units have the same propensity to each of the treatments. Heuristically, the tilting function $h$ gives the most relative weight to the covariate regions in which none of the propensities are close to zero. Similar to the overlap weights for binary treatments, we can interpret the corresponding target population to be the subpopulation with the most overlap in covariates among all groups. Therefore, we call the corresponding target estimand as the pairwise average treatment effect among the overlap population (ATO). We argue this causal estimand is of policy and clinical relevance because it emphasizes the population close to equipoise for whom the choice of treatment remains uncertain and the comparative information is most needed.

Besides its optimality in asymptotic efficiency, the generalized overlap weights have several additional attractive features. First, the harmonic mean function $h$ is strictly bounded between $\min_{1 \leq l \leq J} \{e_l(X)\}/J$ and $\min_{1 \leq l \leq J} \{e_l(X)\}$, and thus the weighting scheme is robust to extreme weights, in contrast to the traditional IPW. Second, the target population defined by the
generalized overlap weights is adaptive to the covariate distributions among the \( J \) comparison groups. For example, when the propensity of assignment to treatment \( j \) is small compared to others so that \( e_j(X) \approx 0 \), the tilting function \( h(X) \propto \prod_{l=1}^{J} e_l(X) / \sum_{k=1}^{J} \prod_{l \neq k} e_l(X) \approx \prod_{l=1}^{J} e_l(X) / \prod_{l \neq j} e_l(X) = e_j(X) \), suggesting that the target population is similar to the \( j \)th treatment group and the associated estimands approximate the ATTs. On the other hand, if the treatment groups are almost balanced in size and covariate distribution so that \( e_j(X) \approx 1/J \) for all \( j \), we have \( h(X) \propto 1 \) and the target estimands approximate the pairwise ATEs. Arguably this adaptiveness enables the generalized overlap weighting scheme to define a scientific question that may be best answered nonparametrically by the available data. Finally, the generalized matching weights (Yoshida et al., 2017)—defined by \( h(X) = \min_{1 \leq j \leq J} \{ e_j(X) \} \)—share some of the above advantages, but these weights are not asymptotically efficient and are non-smooth in \( X \), which renders closed-form variance calculation more complex.

3.2 Estimate Propensity Scores and Balance Check

In practice, usually the propensity scores are not known and must be estimated from the data. For multiple nominal treatments, the generalized propensity scores are often modeled by a multinomial logistic regression,

\[
e_1(X_i) = \frac{1}{1 + \sum_{k=2}^{J} \exp(\alpha_k + X_i^T \beta_k)},
\]

\[
e_j(X_i) = \frac{\exp(\alpha_j + X_i^T \beta_j)}{1 + \sum_{k=2}^{J} \exp(\alpha_k + X_i^T \beta_k)}, \quad j = 2, \ldots, J,
\]

(12)

where the covariate vector \( X \) could contain higher-order moments, splines and interactions. Model parameters \( \theta = (\alpha_2, \ldots, \alpha_j, \beta_2^T, \ldots, \beta_j^T)^T \) can be estimated by standard maximum likelihood, from which we obtain the estimated propensity scores. To assess the fit of the propensity score model, we check the weighted covariate balance in the target population. We propose two ways for balance check motivated by the population balancing constraint (6). First,
constraint (6) implies the weighted covariate balance between each group and the target population. Therefore, we inspect, for each treatment level, the weighted covariate mean deviation from that of the target population. Specifically, we define

\[ \bar{X}_j = \frac{n}{\sum_{i=1}^{n} D_{ij} w_j(X_i)}, \]

as the weighted mean of covariate \( X \) from the \( j \)th group and \( S^2_{X,j} \) as the unweighted variance.

Further, we define

\[ \bar{X}_p = \frac{n}{\sum_{i=1}^{n} \sum_{l=1}^{J} D_{il} h(X_i)}, \]

as the average value of covariate \( X \) in the target population and \( S^2_X = J^{-1} \sum_{j=1}^{J} S^2_{X,j} \) as the averaged unweighted variance. The population standardized difference (PSD) is then defined for each covariate and each treatment level as

\[ \text{PSD}_j = |\bar{X}_j - \bar{X}_p| / S_X. \] (13)

Similar to McCaffrey et al. (2013), we then use \( \max_j |\text{PSD}_j| \) as the balance metric for each covariate \( X \) and inspect the adequacy of the propensity score model. If a covariate was not well balanced in one group, interaction terms of that variable with other variables can be added to the model, and the new model is re-fit and re-evaluated until balance is deemed satisfactory. On the other hand, the population balance constraint (6) also implies pairwise balance \( f_j(X)w_j(X) = f_{j'}(X)w_{j'}(X) \), and so we could alternatively assess balance by checking the pairwise absolute standardized differences (ASD),

\[ \text{ASD}_{j,j'} = |\bar{X}_j - \bar{X}_{j'}| / S_X. \] (14)

Similarly, the balance metric for each covariate can be specified as \( \max_{j < j'} |\text{ASD}_{j,j'}| \). In practice, the two balance criteria perform similarly and we will illustrate both in Section 5.
In real applications, a rich propensity score model is often preferable because the ultimate goal of weighting-based causal inference is to remove bias through balancing the covariates in the target population, rather than to maximize the predictive utility of the propensity score model. Therefore, the above balance check constitutes a crucial step for diagnosing propensity score models and the traditional goodness-of-fit diagnostics are minimally relevant. However, the richness of the propensity score model will be capped by the bias-variance tradeoff: when the propensity score model becomes saturated and discovers a separating plane in the data, the variance of the weights will likely increase and reduce the precision of the effect estimates.

Finally, an attractive property of the overlap weights with binary treatments is exact balance, that is, when the propensities scores are estimated from a logistic model, the standardized difference of all the covariates entering the propensity model is zero (Li et al., 2018a, Theorem 3). However, this exact balance property is due to the happenstance that the logistic score equations exploit the covariate-balancing moment conditions, and does not extend to the generalized overlap weights with \( J \geq 3 \) when the propensity score is estimated by a multinomial logistic model. Therefore, we still recommend to use the conventional iterative fitting-checking procedure to improve the propensity model.

### 3.3 Variance Estimation

The asymptotic variance results in Section 2.4 are not directly useful for calculating the sample variance of \( \hat{\tau}^h(\lambda_{j,j'}) \) in practice because the \( v_j(X) \)'s are not known. Moreover, one has to account for the additional uncertainty in estimating the propensities in the variance estimation. Here we derive an empirical sandwich variance estimator (Stefanski and Boos, 2002) that accounts for the uncertainty in estimating the generalized overlap weights from the multinomial logistic model (12). Under standard regularity conditions, we show that the weighting
estimator is asymptotically normal (complete derivation is presented in Appendix B),

\[ \sqrt{n} \{ \hat{\tau}^h(\lambda_{j,j'}) - \tau^h(\lambda_{j,j'}) \} \overset{d}{\rightarrow} N \left( 0, \frac{\mathbb{E} \{ \psi_{ij} - \psi_{ij'} \}^2}{\mathbb{E} \{ h(X) \}^2} \right), \]

where

\[ \psi_{ij} = D_{ij}(Y_i - m_{ij}^h)w_j(X_i) + \mathbb{E} \left\{ D_{ij}(Y_i - m_{ij}^h) \frac{\partial}{\partial \theta^T} w_j(X_i) \right\} I_{\theta \theta}^{-1} S_{\theta,i}, \quad \text{(15)} \]

and \( S_{\theta,i}, I_{\theta \theta} \) are the individual score and information matrix of \( \theta \), respectively. Denote \( \hat{\theta}, \hat{S}_{\theta,i}, \hat{I}_{\theta \theta} \) as the maximum likelihood estimator of \( \theta \), the plug-in consistent estimators for the individual score and information matrix, the empirical sandwich variance estimator the estimated pairwise ATO is obtained as

\[ \hat{\psi}[\hat{\tau}^h(\lambda_{j,j'})] = \frac{\sum_{i=1}^{n} \left( \hat{\psi}_{ij} - \hat{\psi}_{ij'} \right)^2}{\left[ \sum_{i=1}^{n} \left( \sum_{k=1}^{J} 1/\hat{e}_k(X_i) \right)^{-1} \right]^2}, \quad \text{(16)} \]

where

\[ \hat{\psi}_{ij} = D_{ij}(Y_i - \hat{m}_{ij}^h)w_j(X_i; \hat{\theta}) + \left\{ \frac{1}{n} \sum_{i=1}^{n} D_{ij}(Y_i - \hat{m}_{ij}^h) \frac{\partial}{\partial \theta^T} w_j(X_i; \hat{\theta}) \right\} \hat{I}_{\theta \theta}^{-1} \hat{S}_{\theta,i}, \]

is a consistent estimator of \( \psi \).

The true generalized propensity score is generally unknown in applications and will be substituted by its sample analogue. Hirano et al. (2003) suggested that a consistent estimator of the propensity score leads to more efficient estimation of the WATE with binary treatments than the true propensity score. Our derivation of the variance estimator reinterprets their findings in the context of multi-valued treatments. Specifically, with a consistent estimator for the generalized propensity score, the influence function for estimating \( m^h_j \), \( \psi_{ij} / \mathbb{E} \{ h(X) \} \), can be viewed as the residual of \( D_{ij}(Y_i - m^h_j)w_j(X_i) / \mathbb{E} \{ h(X) \} \)—the influence function for estimating \( m^h_j \) using the true propensity score—after projecting it onto the nuisance tangent space of \( \theta \) (Tsiatis, 2006). Therefore, the efficiency implications from Hirano et al. (2003) naturally carry over to our pairwise comparisons emphasizing the overlap population.
4 A Simulation Study

We conduct a simulation study to examine the finite-sample performance of the generalized overlap weights (G-OW) relative to existing methods for estimating pairwise causal effects with multi-valued treatments. To quantify the confounding bias in each simulation scenario, we first report the raw difference in means (DIF). For comparison, besides G-OW, we consider three weighting approaches: inverse probability weighting (IPW), IPW with optimal trimming rule (7) (IPW-TM), and the generalized matching weights (G-MW). Each of these weighting approach corresponds to a specific choice of $h$ and a target population, as explained in Section 2.2. With binary treatments, IPW is known to be sensitive to extreme propensity scores induced by lack of overlap; such a problem is likely exacerbated with multi-valued treatments as there are $J$ scalar scores per unit. To address this problem, trimming methods exclude units with extreme propensities, whereas G-MW and G-OW down-weight those units. We also examine the generalized propensity score matching proposed by Yang et al. (2016), both with and without the optimal trimming step (GPSM and GPSM-TM). GPSM separately exploits each scalar propensity score for estimating the average potential outcomes and thus resolves the issue of matching on high-dimensional propensity score vector.

Our data generating process follows the one in Yang et al. (2016) except that we consider nonzero pairwise average treatment effect among the considered target populations. We generate covariates $X_{1i}$, $X_{2i}$ and $X_{3i}$ from a multivariate normal distribution with mean vector $(2, 1, 1)$ and covariances of $(1, -1, -0.5)$; $X_{4i} \sim \text{Uniform}[-3, 3]$; $X_{5i} \sim \chi^2_1$ and $X_{6i} \sim \text{Bernoulli}(0.5)$, with the covariate vector $X_i^T = (X_{1i}, X_{2i}, X_{3i}, X_{4i}, X_{5i}, X_{6i})$. The assignment mechanism follows the multinomial logistic regression

$$(D_{i1}, \ldots, D_{ij}) \sim \text{Multinom}(e_1(X_i), \ldots, e_J(X_i)),$$
where $D_{ij}$ is the treatment indicator defined in Section 2.1 and

$$e_j(X_i) = \exp(\alpha_j + X_i^T \beta_j) / \sum_{k=1}^J \exp(\alpha_k + X_i^T \beta_k)$$

is the true generalized propensity score with $\alpha_1 = 0$, $\beta_1^T = (0, 0, 0, 0, 0)$. In the first simulation with $J = 3$ treatment groups, $\beta_2^T = \kappa_2 \times (1, 1, 1, -1, -1, 1)$ and $\beta_3^T = \kappa_3 \times (1, 1, 1, 1, 1)$. We set $(\kappa_2, \kappa_3) = (0.2, 0.1)$ to simulate a scenario with adequate covariate overlap and $(\kappa_2, \kappa_3) = (0.8, 0.4)$ to induce lack of overlap with strong propensity tails, i.e.,

the propensity to receive certain treatment is close to zero for specific design values. We further choose $\alpha_2$ and $\alpha_3$ so that the overall treatment proportions are fixed at $(0.3, 0.4, 0.3)$. The potential outcomes are generated from $Y_i(j) = (1, X_i^T) \gamma_j + \epsilon_i$ with $\epsilon_i \sim N(0, 1)$, $\gamma_1^T = (-1.5, 1, 1, 1, 1, 1, 1)$, $\gamma_2^T = (-4, 2, 3, 1, 2, 2, 2)$ and $\gamma_3^T = (3, 3, 1, 2, -1, -1, -1)$. In the second simulation with $J = 6$ groups, we specify $\beta_2^T = \kappa_2 \times (1, 1, 2, 1, 1, 1)$, $\beta_3^T = \kappa_3 \times (1, 1, 1, 1, -5)$, $\beta_4^T = \kappa_4 \times (1, 1, 1, 1, 5)$, $\beta_5^T = \kappa_5 \times (1, 1, -2, 1, 1)$ and $\beta_6^T = \kappa_6 \times (1, 1, -2, -1, 1)$. We use $(\kappa_2, \kappa_3, \kappa_4, \kappa_5, \kappa_6) = (0.1, 0.15, 0.2, 0.25, 0.3)$ to simulate a scenario with adequate overlap and $(\kappa_2, \kappa_3, \kappa_4, \kappa_5, \kappa_6) = (0.4, 0.6, 0.8, 1, 1.2)$ to represent a challenging scenario with strong propensity tails. The intercepts are chosen so that the marginal treatment proportions are $(0.12, 0.16, 0.12, 0.25, 0.2, 0.15)$. Finally, the coefficients for the outcome model is specified as $\gamma_1^T = (-1.5, 1, 1, 1, 1, 1, 1)$, $\gamma_2^T = (-4, 2, 3, 1, 2, 2, 2)$, $\gamma_3^T = (4, 3, 1, 2, -1, -1, -4)$, $\gamma_4^T = (1, 4, 1, 2, -1, -1, -3)$, $\gamma_5^T = (3, 5, 1, 2, -1, -1, -2)$ and $\gamma_6^T = (3, 5, 6, 1, 2, -1, -1, -1)$. The total sample size is fixed at $n = 1500$ for $J = 3$ and $n = 6000$ for $J = 6$.

For each scenario, we simulate 1000 replicates and estimate the pairwise causal effects using the seven estimators described above. Because the target population may differ in different estimators, we assess the accuracy of estimators relative to their corresponding target estimands. Specifically, the target estimands of DIF, IPW and GPSM are pairwise ATE
for the combined population and are analytically determined from the true potential outcome model, whereas the target estimands for G-MW, G-OW, IPW-TM and GPSM-TM are defined for specific subpopulations and evaluated numerically based on Monte Carlo integration. For each replicate, we estimate the generalized propensity scores based on the correct multinomial logistic regression model including all covariates. The 95% confidence intervals were obtained using: 2.5 and 97.5 quantiles of 1000 bootstrap samples for DIF and G-MW; point estimates $\pm 1.96 \times \text{(empirical sandwich variance)}^{1/2}$ for IPW and G-OW; point estimates $\pm 1.96 \times \text{(Abadie and Imbens variance)}^{1/2}$ for GPSM (Abadie and Imbens, 2012). The empirical sandwich variance estimators for G-OW and IPW are computationally convenient and take into account the uncertainty in estimating the generalized propensity scores. By contrast, the weight function $w_j(X)$ for G-MW is not everywhere differentiable and fails to satisfy the regularity conditions for deriving a sandwich variance. Because it is generally difficult to smoothly approximate $w_j(X)$ around its infinite-many non-differentiable points, we resort to the computationally-intensive bootstrap approach for interval estimation. Similar to our sandwich variance, the Abadie and Imbens variance for GPSM takes into account the uncertainty involving in both the matching process and propensity score estimation. Finally, whenever trimming is used (IPW-TM and GPSM-TM), the generalized propensity scores are re-estimated based on the trimmed sample as refitting generally improves the finite-sample performance of the resulting estimators (Li et al., 2018b); accordingly, variance calculation is carried out based on the trimmed sample.

Table 1 and 2 summarize the absolute bias, root mean squared error (RMSE) and coverage of each estimator with $J = 3$ groups. As expected, DIF shows substantial bias and under-coverage, characterizing the strong confounding in the simulations. All other approaches perform reasonably well when there is adequate overlap. However, with lack of overlap, IPW and GPSM are sensitive to extreme propensities and produce biased point estimates. The optimal
Table 1: Simulation results with $J = 3$ treatment groups and adequate overlap. In this case, the optimally trimming excludes at most 2% of the total sample.

|                | $\tau(\lambda_{1,2})$ | $\tau(\lambda_{1,3})$ | $\tau(\lambda_{2,3})$ | $\tau(\lambda_{1,2})$ | $\tau(\lambda_{1,3})$ | $\tau(\lambda_{2,3})$ | Coverage of 95% CI |
|----------------|------------------------|------------------------|------------------------|------------------------|------------------------|------------------------|-------------------|
| DIF            | 0.46                   | 0.60                   | 0.14                   | 0.55                   | 0.65                   | 0.37                   | 0.64              |
| IPW            | 0.02                   | 0.01                   | 0.01                   | 0.20                   | 0.16                   | 0.26                   | 0.92              |
| IPW-TM         | 0.01                   | 0.002                  | 0.01                   | 0.16                   | 0.16                   | 0.23                   | 0.94              |
| GPSM           | 0.02                   | 0.01                   | 0.01                   | 0.26                   | 0.22                   | 0.31                   | 0.99              |
| GPSM-TM        | 0.02                   | 0.004                  | 0.01                   | 0.25                   | 0.23                   | 0.31                   | 0.98              |
| G-MW           | 0.02                   | 0.01                   | 0.02                   | 0.17                   | 0.18                   | 0.27                   | 0.95              |
| G-OW           | 0.01                   | 0.001                  | 0.01                   | 0.15                   | 0.15                   | 0.22                   | 0.94              |

Table 2: Simulation results with $J = 3$ treatment groups and lack of overlap. In this case, the optimal trimming rule excludes 19% to 30% of the total sample.

|                | $\tau(\lambda_{1,2})$ | $\tau(\lambda_{1,3})$ | $\tau(\lambda_{2,3})$ | $\tau(\lambda_{1,2})$ | $\tau(\lambda_{1,3})$ | $\tau(\lambda_{2,3})$ | Coverage of 95% CI |
|----------------|------------------------|------------------------|------------------------|------------------------|------------------------|------------------------|-------------------|
| DIF            | 0.43                   | 0.64                   | 0.21                   | 0.50                   | 0.68                   | 0.38                   | 0.65              |
| IPW            | 0.19                   | 0.02                   | 0.17                   | 1.04                   | 0.61                   | 1.16                   | 0.79              |
| IPW-TM         | 0.03                   | 0.01                   | 0.01                   | 0.38                   | 0.28                   | 0.47                   | 0.93              |
| GPSM           | 0.25                   | 0.10                   | 0.15                   | 0.86                   | 0.51                   | 0.90                   | 0.88              |
| GPSM-TM        | 0.08                   | 0.02                   | 0.05                   | 0.53                   | 0.37                   | 0.60                   | 0.95              |
| G-MW           | 0.001                  | 0.01                   | 0.01                   | 0.29                   | 0.24                   | 0.36                   | 0.95              |
| G-OW           | 0.01                   | 0.01                   | 0.003                  | 0.28                   | 0.23                   | 0.35                   | 0.95              |
trimming method excludes 19% to 30% of the total sample, reduces the bias and improves efficiency and coverage in estimating the subpopulation causal effects. By down-weighting extreme units, both G-MW and G-OW provide unbiased point estimates with nominal coverage. Overall, IPW-TM, G-MW and G-OW are associated with the smallest RMSE and are more efficient than the other methods. Among them, G-OW is the most efficient with the smallest RMSE, matching the theoretical predictions in Section 2.4.

Figure 1 and 2 present the simulation results with $J = 6$ groups. With adequate overlap, all methods have good control of confounding bias, produce unbiased estimates and close to nominal coverage. G-MW and G-OW provide the lowest RMSE, with the latter demonstrating higher efficiency for estimating most of the causal contrasts (the ratio of total MSE is 1.18). With lack of overlap, the clear separation of covariate space makes it challenging to simultaneously remove all confounding for estimating the 15 pairwise contrasts. By discarding more than half of the sample, the optimal trimming method improves the bias, efficiency and coverage properties over IPW and GPSM, both of which are subject to bias and excessive variance with extreme propensities. G-MW and G-OW further improve the efficiency and coverage properties upon trimming by down-weighting the extreme units. As expected from the large-sample theory, G-OW produces more efficient estimates than G-MW for 12 out of 15 causal contrasts (the ratio of total MSE is 1.17). In this challenging scenario, the bootstrap CI for G-MW has slightly better finite-sample coverage than the closed-form CI for G-OW based on the empirical sandwich variance, but the closed-form CI estimator for G-OW demonstrates the best coverage among all the considered closed-form CI estimators. However, the biggest gain of G-OW over G-MW is the computational time: for each simulation, the bootstrap interval estimates for G-MW with 1000 resamples require more than 80 times longer running time than that of the closed-form G-OW interval estimates, which can be very significant for large data sets.
Figure 1: Simulation results with $J = 6$ treatment groups and $(\kappa_2, \kappa_3, \kappa_4, \kappa_5, \kappa_6) = (0.1, 0.15, 0.2, 0.25, 0.3)$, i.e., with adequate overlap. Optimal trimming excludes $3\% \sim 7\%$ of the total sample. For a given approach, each one of the 15 causal comparisons is represented by the contrast $\lambda_{j,j'}$ for notational simplicity.
Figure 2: Simulation results with $J = 6$ treatment groups and $(\kappa_2, \kappa_3, \kappa_4, \kappa_5, \kappa_6) = (0.4, 0.6, 0.8, 1, 1.2)$, i.e., with strong propensity tails. Optimal trimming excludes $52\% \sim 74\%$ of the total sample. For a given approach, each one of the 15 causal comparisons is represented by the contrast $\lambda_{j,j'}$ for notational simplicity.
5 Application to the Racial Disparities in Medical Expenditure

We study the racial disparities in medical expenditure for adult respondents aged 18 years and older based on the 2009 Medical Expenditure Panel Survey (MEPS) data. Our sample resembles the one examined by Lê Cook et al. (2010) and contains health care expenditure information for four racial groups: 9830 non-Hispanic Whites, 1446 Asians, 4020 Blacks, 5150 Hispanics. The goal is to estimate the disparity in health care expenditure among these racial groups after balancing confounding variables. Li et al. (2018a) examined a similar data set using separate binary-group comparisons. Here, we focus on the simultaneous multiple-group comparisons facilitated by defining a common target population. Since race is non-manipulable, these comparisons are descriptive but share the same nature with causal comparisons with respect to confounding control. Focusing on the pairwise ATE (equivalently with IPW) would force one to consider a hypothetical target population defined by the combined population from all four racial groups. This combined population may not only be an infeasible target of inference due to the lack of overlap, but also lack policy relevance for tracking disparities since it may emphasize individuals atypical for their own racial group. Instead, we use the generalized overlap weights to emphasize the subpopulation with the most overlap across all racial group, namely the individuals who, based on their observed characteristics, could easily be either White or from other minority groups.

There are 25 covariates of individual demographics and self-reported health information. We estimate the generalized propensity scores using a multinomial logistic regression including the main effects of each covariate. The distributions of the estimated scores are presented in Figure 3. There is a moderate lack of overlap especially regarding the Asian group, with the largest inverse propensity weight normalized to be 0.32, accounting for almost one third of
Figure 3: Distribution of the estimated generalized propensity scores for all racial groups in the MEPS data.
the total weights out of 1446 Asians. This weight corresponds to a 78-year-old Asian female with a very high BMI of 55.4 (atypical value among Asians) and consequently an extreme generalized propensity score close to zero. On the other hand, the largest generalized overlap weight is normalized to be only 0.0017. The lack of overlap is also evident when applying the optimal trimming methods, which excludes 18.5% of the sample (2125 Whites, 44 Asians, 1001 Blacks and 603 Hispanics; 3773 individuals in total). Figure 4 shows boxplots of $\max_j |\text{PSD}_j|$ and $\max_{j<j'} |\text{ASD}_{j,j'}|$, which are two criteria defined in Section 3.2 to examine covariate mean balance in the weighted population. Due to the extreme propensities, IPW results in even worse covariate balance than no weighting, yielding substantial imbalance of several covariates. By contrast, optimal trimming, the generalized matching weights, and generalized overlap weights lead to satisfactory balance in their respective target populations, with the best balance achieved by generalized overlap weights. The two balance criteria perform similarly in this application.

We estimate the (weighted) average controlled difference in total health care expenditure between all pairs of racial groups, and present the point estimates and 95% confidence intervals in Table 3. Estimates differ substantially between different methods. For example, the weighted average difference between Whites and Asians in health care expenditure is estimated as $2402 and $1818 from IPW and matching. The optimal trimming reduces the White-Asian disparity estimates for IPW and GPSM ($1335 and $1402) and tightens the interval estimates, whereas the White-Asian disparity estimates are even smaller ($1112 and $1160) according to G-MW and G-OW. The same pattern is also observed for Asian-Black disparity estimates. Further, IPW and GPSM report much higher expenditure for Hispanics compared to Asians (a statistically significant difference is reported by GPSM with $p = 0.022$), while G-OW reverses the sign and reports slightly higher ($p = 0.825$) expenditure for Asians that are most comparable to other racial groups. By emphasizing the subpopulation where each racial group have the most similar characteristics, we find via generalized overlap weighting that Whites are associ-
Figure 4: Boxplots for the population standardized difference (PSD) and absolute standardized difference (ASD) for all covariates corresponding to each weighting method. The gray horizontal line indicates adequate balance at 0.1.
Table 3: Weighted average controlled difference in total health care expenditure (dollars). W: non-Hispanic Whites; A: Asians; B: Blacks; H: Hispanics. All 95% confidence intervals are obtained using the same methods described in the simulation study.

|       | W-A | W-B | W-H | A-B | A-H | B-H |
|-------|-----|-----|-----|-----|-----|-----|
| DIF   | 2764| 786 | 2651| -1978| -113| 1865|
|       | (2317, 3216)| (346, 1234)| (2288, 2997)| (-2499, -1461)| (-566, 335)| (1426, 2328) |
| IPW   | 2402| 908 | 719 | -1494| -1683| -189|
|       | (530, 4274)| (505, 1311)| (129, 1309)| (-3385, 397)| (-3621, 255)| (-836, 459) |
| IPW-TM| 1335| 1148| 1257| -187| -77| 109|
|       | (671, 1999)| (781, 1511)| (129, 1309)| (-872, 499)| (-812, 657)| (-375, 594) |
| GPSM  | 1818 | 827 | 902 | -991| -916| 74|
|       | (1091, 2545)| (334, 1320)| (439, 1364)| (-1796, -185)| (-1700, -132)| (-504, 652) |
| GPSM-TM| 1402| 1147| 1392| -255| -10| 245|
|       | (814, 1989)| (689, 1605)| (927, 1856)| (-922, 411)| (-680, 660)| (-314, 804) |
| G-MW  | 1112 | 839 | 1234| -273| 122| 395|
|       | (648, 1569)| (455, 1239)| (813, 1623)| (-737, 281)| (-385, 621)| (-100, 820) |
| G-OW  | 1160 | 886 | 1221| -274| 61| 335|
|       | (660, 1661)| (518, 1253)| (849, 1593)| (-813, 264)| (-479, 601)| (-82, 752) |
ated with the highest expenditure ($4097), while Blacks have the second highest expenditure ($3212), followed by Asians ($2937) and Hispanics ($2876). Statistically significant disparities are found between White and each minority group ($p < 0.001$ for all three comparisons), but not between the minority groups. Similar to the simulations, G-MW provides point and interval estimates close to G-OW in this application, but again computing its bootstrap intervals takes much longer time than the closed-form intervals of G-OW.

Table 4: Effective sample size (ESS) of each weighted group according to different weighting methods.

|                | Whites | Asians | Blacks | Hispanics | Total |
|----------------|--------|--------|--------|-----------|-------|
| Unweighted     | 9830   | 1446   | 4020   | 5150      | 20446 |
| IPW            | 8371   | 10     | 2549   | 2482      | 13412 |
| Unweighted (Trimmed) | 7705   | 1402   | 3019   | 4547      | 16673 |
| IPW-TM         | 6524   | 695    | 2183   | 3071      | 12473 |
| G-MW           | 4937   | 1285   | 1875   | 3176      | 11273 |
| G-OW           | 6015   | 1166   | 2234   | 3756      | 13171 |

To further compare the different weighting methods, we calculate the effective sample size (ESS) of each racial group according to each weighting scheme. The ESS for group $j$ is defined as (McCaffrey et al., 2013)

$$\text{ESS}_j^h = \left( \frac{\sum_{i=1}^{n} \sum_{j=1}^{J} D_{ij} w_j(X_i)}{\sum_{i=1}^{n} \sum_{j=1}^{J} D_{ij} w_j^2(X_i)} \right)^2 / \sum_{i=1}^{n} \sum_{j=1}^{J} D_{ij} w_j^2(X_i).$$

(17)

As weighting generally increases the variance compared to the unweighted estimates based on the same sample, the ESS may serve as a conservative measure to characterize the variance inflation or precision loss due to weighting. Table 4 presents the ESS (estimated by plugging in the estimated weights in the definition) and the total ESS. It is evident that all weighting
methods reduce the ESS compared to the original sample. However, IPW results in a very small value of ESS for Asians relative to the original group size, signaling the presence of extreme weights and lack of overlap. This observation further underlies the wide confidence intervals for pairwise differences associated with IPW. By contrast, G-MW, G-OW and trimming result in relatively balanced ESS across groups. Among them, G-OW reports the largest total ESS, which further supports its efficiency optimality.

6 Discussion

In this article, we propose a unified framework, the balancing weights, for estimating causal effects with multi-valued treatments. Within this framework, we focus on pairwise comparisons for nominal treatments and develop the generalized overlap weights to emphasize the target population with the most covariate overlap across all groups. We show that the generalized overlap weights minimize the total asymptotic variance of the nonparametric estimators for the pairwise contrasts within the balancing weights family. We derived an empirical sandwich variance formula for its associated nonparametric estimator, the interval estimator based on which shows satisfactory coverage in the simulation study.

One limitation of the generalized overlap weighting method is that, similar to existing propensity score weighting methods, requires a correctly specified propensity score model. Another limitation is that the nonparametric sample estimator \( \hat{m}^{h} \) does not exploit smoothness of the outcome in each level of the treatment and thus may not achieve semiparametric efficiency. Following Cattaneo (2010), one could in fact construct, for each choice of the balancing weights, a regression-augmented estimator for the expectation of the potential outcomes among the target population as

\[
\hat{m}_{j}^{h,\text{aug}} = \hat{m}_{j}^{h} - \frac{\sum_{i=1}^{n}(D_{ij} - e_{j}(X_{i}))w_{j}(X_{i})\hat{m}_{j}(X_{i})}{\sum_{i=1}^{n}h(X_{i})},
\]
where \( \hat{m}_j(X_i) = \hat{E}[Y(j)|X] \) is the outcome regression function. It can be shown that, under weak unconfoundedness, \( \hat{m}_{j, \text{aug}} \) achieves the semiparametric efficiency bound for estimating \( m_j \) when both the generalized propensity score model and the regression function are correctly specified. Of note, when the tilting function \( h(X_i) = 1 \), \( \hat{m}_{j, \text{aug}} \) has an additional double-robustness property such that it is consistent to \( \mathbb{E}[Y(j)] \) when either the generalized propensity score model or the regression function is correctly specified, but not necessarily both \( \text{[Linden et al., 2016]} \). However, this robustness property does not hold in general for \( \hat{m}_{j, \text{aug}} \) concerning other choices of \( h \) and balancing weights, including the generalized overlap weights. Nevertheless, additional work is warranted to study the efficiency property of the augmented generalized overlap weighting estimator with multi-valued treatments; for example, one can consider more flexible semiparametric regression models as in \( \text{[Mercatanti and Li, 2014]} \).

### Appendix A: Proof of Propositions

For proving the Propositions, we assume regularity conditions on \( m_j(X) = \mathbb{E}[Y(j)|X] \) and \( v_j(X) = \mathbb{V}(Y(j)|X) \) necessary to ensure that the integrals are well defined.

**Proof of Proposition 1**

By definition of the generalized propensity score, we must have \( \mathbb{E}[1\{Z = j\}/e_j(X)|X] = 1 \) for all \( j \in \mathbb{Z} \). Then the average of the potential outcomes in target population \( h \)

\[
\begin{align*}
m^h_j &= \frac{\int_X m_j(X)f(X)h(X)\mu(dX)}{\int_X f(X)h(X)\mu(dX)} \\
&= \frac{\int_X \mathbb{E}[1\{Z = j\}Y(j)(h(X)/e_j(X))|X]f(X)\mu(dX)}{\int_X \mathbb{E}[1\{Z = j\}(h(X)/e_j(X))|X]f(X)\mu(dX)} \\
&= \frac{\int_X \mathbb{E}[1\{Z = j\}Y(j)w_j(X)|X]f(X)\mu(dX)}{\int_X \mathbb{E}[1\{Z = j\}w_j(X)|X]f(X)\mu(dX)}
\end{align*}
\]

(18)

where the second equation holds due to the weak unconfoundedness assumption, \( Y(j) \perp 1\{Z = j\}|X \) \( \text{[Imbens, 2000]} \). Because \( D_{ij} = 1\{Z_i = j\} \), it follows that the estimators,
Proof of Proposition 2

By SUTVA, we write
\[
\hat{\tau}^h(a) = \sum_{j=1}^{J} a_j \frac{\sum_{i=1}^{n} D_{ij} Y_i w_j(X_i)}{\sum_{i=1}^{n} D_{ij} w_j(X_i)} = \sum_{j=1}^{J} a_j \frac{\sum_{i=1}^{n} D_{ij} Y_i w_j(X_i)}{\sum_{i=1}^{n} D_{ij} w_j(X_i)}.
\]

Conditional on the assignment \(Z\) and sample design \(X\), only the potential outcomes are random. Therefore the residual variance of \(\hat{\tau}^h(a)\) is
\[
\mathbb{V}[\hat{\tau}^h(a)|Z, X] = \sum_{j=1}^{J} a_j^2 \frac{\sum_{i=1}^{n} v_j(X_i) D_{ij} w_j^2(X_i)}{[\sum_{i=1}^{n} D_{ij} w_j(X_i)]^2}
= \sum_{j=1}^{J} a_j^2 \frac{\sum_{i=1}^{n} \{v_j(X_i)/e_j(X_i)\} \{D_{ij}/e_j(X_i)\} h^2(X_i)}{[\sum_{i=1}^{n} \{D_{ij}/e_j(X_i)\} h(X_i)]^2}.
\]

Averaging over the joint distribution of \(Z\) and \(X\), we observe by the Weak Law of Large Numbers that
\[
\frac{1}{n} \sum_{i=1}^{n} \{D_{ij}/e_j(X_i)\} h(X_i) \overset{p}{\to} \int_X \mathbb{E}[\mathbb{1}\{Z=j\}/e_j(X)|X] h(X) f(X) \mu(dX) = C_h,
\]
and
\[
\frac{1}{n} \sum_{i=1}^{n} \{v_j(X_i)/e_j(X_i)\} \{D_{ij}/e_j(X_i)\} h^2(X_i)
\overset{p}{\to} \int_X \mathbb{E}[\mathbb{1}\{Z=j\}/e_j(X)|X] h^2(X) f(X) \mu(dX)
= \int_X \{v_j(X)/e_j(X)\} h^2(X) f(X) \mu(dX).
\]

An application of the Slutsky’s Theorem shows \(n \cdot \mathbb{V}[\hat{\tau}^h(a)|Z, X] \overset{p}{\to} Q(a, h)\), where \(Q(a, h)\) is a constant defined in Proposition 2. The uniform integrability of the family of random variables \(\{\mathbb{V}[\hat{\tau}^h(a)|Z, X], n \geq 1\}\) then gives the desired \(L_1\) convergence result.
Proof of Proposition 3

For notational simplicity, we use the $\mathbb{E}[]$ operator to represent $\int_{\mathcal{X}} f(X) \mu(dX)$. Under homoscedasticity, $v_j(X) = v$.

$$Q(a, h) = \left(\frac{v}{C_h}\right) \int_{\mathcal{X}} \left(\sum_{j=1}^{J} a_j^2/e_j(X)\right) h^2(X) f(X) \mu(dX)$$

$$= \left(\frac{v}{C_h}\right) \mathbb{E}\left\{ h^2(X) \left(\sum_{j=1}^{J} a_j^2/e_j(X)\right) \right\}.$$

Applying the Cauchy-Schwarz inequality, we have

$$C_h^2 = \left[\mathbb{E}\{h(X)\}\right]^2 = \left[ \mathbb{E}\left\{ h(X) \left(\sum_{j=1}^{J} a_j^2/e_j(X)\right)^{1/2} \left(\sum_{j=1}^{J} a_j^2/e_j(X)\right)^{-1/2}\right\} \right]^2$$

$$\leq \mathbb{E}\left\{ h^2(X) \left(\sum_{j=1}^{J} a_j^2/e_j(X)\right) \right\} \mathbb{E}\left\{ \left(\sum_{j=1}^{J} a_j^2/e_j(X)\right)^{-1}\right\},$$

and the equality is attained when $h = \tilde{h}(X) \propto \left(\sum_{j=1}^{J} a_j^2/e_j(X)\right)^{-1}$. This implies that

$$\mathbb{E}\left\{ h^2(X) \left(\sum_{j=1}^{J} a_j^2/e_j(X)\right) \right\} / C_h^2 \geq \left[ \mathbb{E}\left\{ \left(\sum_{j=1}^{J} a_j^2/e_j(X)\right)^{-1}\right\} \right]^{-1} = C_h^{-1},$$

which gives $Q(a, \tilde{h}) = v/C_h$.

Appendix B: Variance Estimation

From the multinomial logistic model, we have for $i = 1, \ldots, n$,

$$e_1(X_i) = Pr(Z_i = 1 | X_i) = \frac{1}{1 + \sum_{k=2}^{J} \exp(\alpha_k + X_i^T \beta_k)}.$$

$$e_j(X_i) = Pr(Z_i = j | X_i) = \frac{\exp(\alpha_j + X_i^T \beta_j)}{1 + \sum_{k=2}^{J} \exp(\alpha_k + X_i^T \beta_k)}, \quad j = 2, \ldots, J.$$

Since $D_{ij} = 1\{Z_i = j\}$, it is straightforward to show that the log likelihood function

$$l(\theta) = \sum_{i=1}^{n} l_i(\theta) = \sum_{i=1}^{n} \left[ \sum_{j=2}^{J} D_{ij} (\alpha_j + X_i^T \beta_j) \right] - \log \left\{ 1 + \sum_{k=2}^{J} \exp(\alpha_k + X_i^T \beta_k) \right\}$$

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When the estimation of model parameters is carried out by maximum likelihood, the first-order condition is obtained by differentiating the log likelihood with respect to $\theta$,

$$0 = S_\theta = \sum_{i=1}^{n} S_{\theta,i} = \sum_{i=1}^{n} \frac{\partial}{\partial \theta} l_i(\theta) = \sum_{i=1}^{n} \left( \frac{\partial}{\partial \alpha_2} l_i(\theta), \ldots, \frac{\partial}{\partial \alpha_J} l_i(\theta), \frac{\partial}{\partial \beta_2^T} l_i(\theta), \ldots, \frac{\partial}{\partial \beta_J^T} l_i(\theta) \right)^T,$$

(19)

where for $l = 2, \ldots, J$,

$$\frac{\partial}{\partial \beta_l} l_i(\theta) = X_i \frac{\partial}{\partial \alpha_l} l_i(\theta) = X_i\{D_{il} - e_l(X_i)\}. \quad (20)$$

We further let $I_{\theta\theta} = -E\left[\frac{\partial^2}{\partial \theta \partial \theta^T} l_i(\theta)\right]$ be the information matrix, whose exact form can be expressed in a similar fashion but is omitted here for brevity. We denote a consistent estimator for this information by $\hat{I}_{\theta\theta}$. For application purposes, we usually don’t have to worry about its exact form since a consistent estimator could be directly obtained from standard software output (e.g., the `multinom` routine in the R package `nnet` or the `PROC CATMOD` routine in SAS). Under standard regularity conditions (Lehmann, 1983), the stochastic expansion for the maximum likelihood estimator is

$$\sqrt{n}(\hat{\theta} - \theta) = I_{\theta\theta}^{-1} \frac{1}{\sqrt{n}} \sum_{i=1}^{n} S_{\theta,i} + o_p(1),$$

where $o_p(1)$ is asymptotically negligible as $n \to \infty$.

With the multinomial logistic model, the generalized overlap weights are expressed as functions of $\theta$:

$$w_1(X_i) = w_1(X_i; \theta) = \frac{1}{1 + \sum_{k=2}^{J} \exp(-\alpha_k - X_i^T \beta_k)}$$

$$w_j(X_i) = w_j(X_i; \theta) = \frac{\exp(-\alpha_j - X_i^T \beta_j)}{1 + \sum_{k=2}^{J} \exp(-\alpha_k - X_i^T \beta_k)}, \quad j = 2, \ldots, J,$$

and the derivative of the weights takes the form

$$\dot{w}_j(X_i) \equiv \frac{\partial}{\partial \theta} w_j(X_i) = \left( \frac{\partial}{\partial \alpha_2} w_j(X_i), \ldots, \frac{\partial}{\partial \alpha_J} w_j(X_i), \frac{\partial}{\partial \beta_2^T} w_j(X_i), \ldots, \frac{\partial}{\partial \beta_J^T} w_j(X_i) \right)^T.$$
where for \( j = 1, \ldots, J \) and \( l = 2, \ldots, J \),
\[
\frac{\partial}{\partial \beta_l} w_j(X_i) = X_i \frac{\partial}{\partial \alpha_l} w_j(X_i) = X_i \{ w_j(X_i) w_l(X_i) - \delta_{jl} w_l(X_i) \},
\]
and \( \delta_{jl} = 1 \{ j = l \} \).

For \( j = 1, \ldots, J \), the plug-in weighting estimator \( \hat{m}_j^h \) can be regarded as the solution of the following estimating equation
\[
\sum_{i=1}^{n} U(\hat{m}_j^h, \hat{\theta}) = \sum_{i=1}^{n} D_{ij}(Y_i - \hat{m}_j^h) w_j(X_i; \hat{\theta}) = 0.
\]

Under certain regularity conditions (van der Vaart, 1998), a first-order Taylor expansion of the unbiased estimating equations around the truth leads to
\[
\sqrt{n}(\hat{\tau}_j^h - \tau_j^h) = \frac{1}{\sqrt{n}} \left\{ \frac{1}{\sqrt{n}} \sum_{i=1}^{n} U(m_j^h, \theta) + H_j^T \sqrt{n}(\theta - \theta) \right\} + o_p(1)
\]
\[
= \frac{1}{\sqrt{n}} \sum_{i=1}^{n} \left\{ D_{ij}(Y_i - m_j^h) w_j(X_i) + H_j^T I_{\theta\theta}^{-1} S_{\theta,i} \right\} + o_p(1),
\]
where \( \varpi = \mathbb{E}[D_{ij} w_j(X_i)] = \mathbb{E}[h(X_i)], \) and \( H_j = \mathbb{E}[D_{ij}(Y_i - m_j^h) \hat{w}_j(X_i)] = \mathbb{E}[(Y_i - m_j^h) e_j(X_i) \hat{w}_j(X_i)] \). Therefore, given any fixed coefficient \( a = (a_1, \ldots, a_J)' \), we have
\[
\sqrt{n}(\hat{\tau}_j^h(a) - \tau_j^h(a)) = \frac{1}{\sqrt{n}} \sum_{i=1}^{n} \left\{ \frac{1}{\varpi} \sum_{j=1}^{J} a_j \psi_{ij} \right\} + o_p(1),
\]
where we define \( \psi_{ij} = D_{ij}(Y_i - m_j^h) w_j(X_i) + H_j^T I_{\theta\theta}^{-1} S_{\theta,i} \). Since the triplets \( \{Y_i, X_i, Z_i\}'s \) are assumed i.i.d., an application of CLT gives,
\[
\sqrt{n}(\hat{\tau}_j^h(a) - \tau_j^h(a)) \overset{d}{\to} \mathcal{N}(0, \varpi^{-2} \mathbb{E} \left\{ \sum_{j=1}^{J} a_j \psi_{ij} \right\}^2).
\]

In practice, we use the empirical sandwich estimator to consistently estimate the large-sample variance (Stefanski and Boos, 2002); the variance of \( \hat{\tau}_j^h(a) \) is estimated by
\[
\frac{1}{(n \varpi)^2} \sum_{i=1}^{n} \left\{ \sum_{j=1}^{J} a_j \hat{\psi}_{ij} \right\}^2,
\]

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where

\[ \hat{\psi}_{ij} = D_{ij}(Y_i - \hat{m}^h_j)w_j(X_i; \hat{\theta}) + \hat{H}_j^T \hat{I}_\theta^{-1} \hat{S}_{\theta,i}, \]

\[ \hat{\omega} = \frac{1}{n} \sum_{i=1}^{n} \left\{ \sum_{k=1}^{J} 1/\hat{e}_k(X_i) \right\}^{-1}, \]

\[ \hat{H}_j = \frac{1}{n} \sum_{i=1}^{n} D_{ij}(Y_i - \hat{m}^h_j)\hat{w}_j(X_i; \hat{\theta}), \]

and \( \hat{S}_{\theta,i} \) is the estimated individual score function \([19]\) from the propensity model. For pairwise comparisons, we substitute \( a \) with \( \lambda_{j,j'} \) to obtain the form of the variance estimator in the manuscript. Finally, we offer three remarks regarding variance estimation.

**Remark 3** One could similarly characterize the asymptotic distribution of a collection of estimators specified by different contrast coefficients. Briefly, let the coefficient matrix \( A_{J \times R} = (a_1, \ldots, a_R) \), where the vector \( a \)'s are distinct from one another. For pairwise comparisons, each vector \( a \) is a distinct element in the set \( S \). Write \( \tau = (\tau^h(a_1), \ldots, \tau^h(a_R))' \), and \( \hat{\tau} = (\hat{\tau}^h(a_1), \ldots, \hat{\tau}^h(a_R))' \) as the corresponding weighting estimators. Further denote \( \psi_i = (\psi_{1i}, \ldots, \psi_{Ji})' \), and it can be shown that

\[ \sqrt{n}(\hat{\tau}^h - \tau^h) = \frac{1}{\sqrt{n}} \sum_{i=1}^{n} \tau^h A^T \psi_i + o_p(1) \xrightarrow{d} N(0, \omega^{-2} A^T \mathbb{E}\{\psi_i \psi_i^T\} A). \]

The covariance for \( \hat{\tau}^h \) can then be estimated by the empirical sandwich estimator

\[ \hat{\mathbb{V}}(\tau^h) = (n \hat{\omega})^{-2} A^T \left\{ \sum_{i=1}^{n} \hat{\psi}_i \hat{\psi}_i^T \right\} A. \]

**Remark 4** Although the above derivation focuses on the generalized overlap weights, a more general presentation for other members of the balancing weights is possible, provided that the balancing weights is a differentiable function in the generalized propensity scores. This differentiability condition rules out the generalized matching weights, which is smooth but not everywhere differentiable and so closed-form variance requires additional considerations \([35]\).
and Greene (2013). In particular, if we choose the balancing weights as the inverse probability weights, in which case $h(X) = 1$ and the target population is the combined population from all groups, the above derivation can be repeated by substituting the correct forms of $w_j(X_i)$ and $\dot{w}_j(X_i)$. For example, the inverse probability weights are

$$w_1(X_i) = 1/e_1(X_i) = 1 + \sum_{k=2}^{J} \exp(\alpha_k + X_i^T \beta_k)$$

$$w_j(X_i) = 1/e_j(X_i) = \frac{1 + \sum_{k=2}^{J} \exp(\alpha_k + X_i^T \beta_k)}{\exp(\alpha_j + X_i^T \beta_j)}, \quad j = 2, \ldots, J,$$

and the derivative of the weights takes the form

$$\frac{\partial}{\partial \beta_l} w_j(X_i) = X_i \frac{\partial}{\partial \alpha_i} w_j(X_i) = X_i \{ w_j(X_i)/w_l(X_i) - \delta_{jl} w_l(X_i) \},$$

for $j = 1, \ldots, J$ and $l = 2, \ldots, J$. Of note, the resulting empirical sandwich variance for $h(X) = 1$ extends the one proposed by Lunceford and Davidian (2004) for binary treatments to multi-valued treatments, and is used to obtain the interval estimates in the simulation study presented in Section 4 of the main text.

**Remark 5** We have focused on the case with a multinomial logistic propensity score model, but in fact the derivation can be made more general to accommodate other propensity score models that admit a regular and asymptotically linear estimator for the model parameters (Tsiatis, 2006). This condition permits a stochastic expansion for $\sqrt{n}(\hat{\theta} - \theta)$, which can then be substituted into (21) to obtain the corresponding sandwich variance estimator. In particular, one could replace the multinomial logistic model with a multinomial Probit model, which is another commonly used regression model to accommodate categorical responses.
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