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Baseline Inequivalence and Matching

B oth randomized controlled trials (RCTs) and quasi-experimental designs (QEDs) can provide evidence of intervention impacts in Teen Pregnancy Prevention (TPP) effectiveness studies. However, for an RCT or a QED to convince a skeptical reader that the intervention caused the observed impact, the intervention and comparison groups in the impact analysis sample should be equivalent on key characteristics measured before the study began (that is, baseline characteristics) that influence outcomes.¹ In this brief, we discuss why baseline equivalence is important, how to assess it, and how to address baseline inequivalence, paying particular attention to meeting the requirements of the current **HHS Evidence Standards for TPP Interventions.**

Baseline inequivalence in impact evaluations and why it is a problem

In theory, the RCT and QED designs currently being used by TPP grantees to estimate intervention impacts can produce rigorous evidence of intervention effects, provided that the two groups being compared in either design are comparable at baseline on characteristics that influence the outcomes of interest.

In a well-executed RCT, the study sample is randomly divided into the intervention and comparison groups and, therefore, will be similar on all measured and unmeasured characteristics at baseline (any differences will be due to random sampling errors). As a result, any intervention-comparison group differences in outcomes can be attributed as the effect of the intervention.

In a well-executed QED, the intervention and comparison groups are not created by randomly dividing the study sample into the two groups. Although the intervention and comparison groups in a well-executed QED can be shown to be similar on key characteristics measured at baseline, there is a possibility that the two groups differ on unmeasured characteristics. Therefore, we are less confident (than we are with an RCT) that differences in outcomes between the two groups in a QED solely reflect the effect of the intervention—they may also reflect unmeasured differences between the two groups that affect outcomes. Therefore, the evidence from a QED is considered lower in quality than the evidence from a well-executed RCT.

In practice, two issues—which relate to study setup and sample loss—can render the study groups in both an RCT and a QED inequivalent and thus can undermine the strength of the evidence they produce.

The first issue is that problems with the **initial study setup** can either cause nonrandom allocation of the sample in an RCT or result in mismatched groups in a QED, as follows:

- Nonrandom allocation of sample in an RCT. In a random assignment study, if the process used to assign study participants to conditions is not effectively random, or the random assignment is undermined by intervention staff or participants, then there is no guarantee that the process will produce groups of youth that are equivalent on all measured and unmeasured variables. For example, intervention staff involved in random assignment might selectively choose participants who seem more willing to change their behavior to participate in the intervention condition (even if they are assigned to the comparison group), which invalidates the random assignment process. The sample members may actually be inequivalent on measured variables that are expected to influence outcomes, which could invalidate the assertion that any post-intervention differences in outcomes are attributable to the intervention.
- **Mismatched groups in a QED.** In a QED, if the initially assigned groups are drawn from substantially different populations, the groups may differ on key measured or unmeasured baseline characteristics that influence outcomes. In this case, any comparison of outcomes across conditions will produce a biased test of the intervention, due to the differences in the baseline characteristics of the groups. For example, if students drawn from a low-income area were offered the intervention, and students from a more affluent area served as the comparison group, the intervention-comparison group difference in outcomes would conflate intervention effects with the systematic differences in the composition of the intervention and comparison conditions.

A second issue that can create baseline inequivalence problems is **sample loss** as a result of nonresponse.² The intervention may affect whether or not an individual will participate throughout the study period and complete a follow-up assessment. For example, some intervention group members may drop out of a

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study soon after experiencing the program because they do not find the services useful. As a result, in both RCTs and QEDs in which the initially assigned groups were equivalent on key baseline variables, sample loss can produce final samples that are not comparable. Therefore, when outcomes are compared in the final samples (which will be *subsets* of the samples originally assigned to condition), the resulting impact estimates will be biased due to underlying differences between the intervention and comparison groups being used to estimate the impacts.

In the rest of this brief, we focus on assessing and establishing equivalence of the *analysis (or analytic) sample*. Establishing baseline equivalence on the analysis sample is necessary (according to HHS evidence standards) for estimating credible program impacts. Doing so can mitigate concerns about baseline inequivalence threatening the internal validity of the study's evidence.

The analysis sample is the sample of youth with observed data for the outcome of interest at the point at which program intervention impacts are to be estimated. Establishing the equivalence of the intervention and comparison groups in this sample is necessary to convince skeptical readers that an impact estimate from this sample is credible.

There may be multiple analysis samples within a study if there are outcomes examined at several time periods.³ In that case, baseline equivalence must be established for each analysis sample (corresponding to the follow-up period). If there are varying sample sizes for two or more outcomes *within a specific follow-up* we recommend constructing a single analysis sample of youth who have complete data for all outcomes in that follow-up period. Using that sample, you then would demonstrate equivalence between groups and estimate impacts for all outcomes in that follow-up period. If, however, there are substantially different response rates across outcomes within a follow-up period, you could consider creating two or more analysis samples for the follow-up period.

Baseline inequivalence in the analytic sample is a problem for TPP evaluations hoping to meet HHS evidence standards

Measured differences in outcomes between the intervention and comparison groups may result from the intervention's impacts, but may also be attributable to differences between the groups at baseline, before receipt of the intervention (that is, baseline inequivalence). HHS evidence standards recognize that baseline inequivalence can affect impacts; hence, they stipulate that a study with substantive baseline inequivalence is at risk of being unable to convincingly demonstrate the effectiveness of the intervention and, therefore, receiving the lowest evidence rating. In particular, RCTs with high levels of sample attrition at the unit of assignment or QEDs with statistically significant interventioncomparison group differences on a key baseline measure can receive the lowest possible evidence rating, due to these threats to internal validity.⁴ The rest of this brief describes the steps a researcher would take to demonstrate equivalent samples for studies with these problems, and to create equivalent samples if baseline inequivalence between groups is a concern.

Step 1. Deciding what variables to examine when assessing baseline equivalence

In general, to convince a skeptical reader that the intervention is solely responsible for the intervention-comparison group differences in outcomes, it is necessary to show that the two groups are equivalent on key baseline characteristics that are expected to influence the outcomes of interest. The HHS evidence standards have clear minimum requirements for demonstrating baseline equivalence:

"... in order to receive the moderate study rating, quasiexperimental comparison group studies and random assignment studies with high attrition [at the unit of assignment] are required to demonstrate that the intervention and comparison groups were similar at baseline (p > .05, two-tailed test) on three key demographic characteristics: age or grade level, gender, and race/ethnicity. For studies with sample members at least 14 years old at baseline (or eighth grade or higher), the study authors must also establish baseline equivalence on at least one behavioral outcome measure (for example, rates of sexual initiation). This criterion is not applied to studies with younger sample members because rates of sexual risk behaviors are typically low for this age group."

(HHS evidence standards, p. 7)⁵

We also suggest assessing baseline equivalence on other key variables that are expected to influence outcomes, if such baseline data are available. For example, the study might assess equivalence on attitudes toward sex, knowledge about contraception and pregnancy, other measures of risky behavior (alcohol and drug use), or other variables that have been shown to correlate with sexual behaviors among teens. Since these variables are expected to influence outcomes, whenever possible, they should be examined for baseline equivalence to ensure that differences in these variables are not confounded with intervention impacts.

Step 2. Documenting baseline equivalence of the analytic sample

According to HHS evidence review standards, any statistically significant differences in the baseline averages of these key variables indicate a potential baseline inequivalence problem in an analysis sample. It is also good practice to examine other summary statistics for each baseline measure separately for the intervention and comparison groups.

The first step in conducting the assessment is to create the analysis sample for a particular follow-up period of interest. As described earlier, this data set should initially contain those sample members who have valid assessment values for the follow-up period of interest. In addition, to show the baseline equivalence of that sample (that is, the sample in which you wish to compare outcomes), you should remove any sample members who do not have baseline assessments for the key variables described above. This will ensure that the ultimate analysis sample will have complete data for the outcome of interest, as well as all key baseline variables.⁶

The table shell below (Table 1) provides a template to use for your assessment. The final column indicates the statistical significance of the difference between the intervention and comparison group means for each baseline characteristic of interest. This is the key condition that the HHS evidence review team examines when assessing baseline equivalence.

As shown in Table 1, you should document the sample sizes of the two groups in the analysis sample, *average* values of

the continuous baseline measures (or the prevalence rates for dichotomous measures), and the standard deviations of the measures (if continuous). The intervention-comparison group difference in the average value of each measure should also be computed and tested to determine whether it is significantly different from zero, as this is the key criterion used to assess baseline equivalence in the HHS evidence review. Importantly, the approach for conducting these statistical tests should be consistent with the study's design, so it may require taking into account clustering or stratification of the sample. For example, if the study randomly assigned schools to a condition within districts, the statistical test of baseline equivalence should incorporate dummy variables for districts and a clustering adjustment, such as school random effects or Huber-White clustering corrections for schools (Williams, 2000).

Although not currently required by the HHS evidence review, we also recommend examining the magnitude of the intervention-comparison group difference to ensure that the groups are not "substantively different" even if they are not statistically significantly different from each other. For example, if the difference between the two groups on a key baseline variable is not statistically significant but equals 20 percentage points, from a face validity perspective, readers may consider the groups different and may question the validity of the impacts.

Table 1. Analysis Sample (N, =, N, =): Summary Statistics of Key Baseline Measures, by Study Group

	Intervention Group		Comparison Group		Baseline Differences	
Baseline Measure	Mean (or %)	Standard deviation ^a	Mean (or %)	Standard deviation ^a	Mean difference	<i>p</i> -value of difference
Age or Grade Level						
Gender						
Race/ethnicity						
Behavioral measure, such as sexual initiation (for studies with youth at least 14 years old)						

Table notes: [Describe the analytic procedure used to test the intervention-comparison group difference in baseline means] ^a Include if a continuous measure.

Best practices for continuous variables assessed at baseline

When assessing baseline equivalence of continuous measures, researchers should consider whether alternate specifications for those measures should be examined. This goes beyond the minimum mean difference requirements in the HHS standards but may capture important differences that could confound intervention impacts. For example, suppose a study that includes girls ages 12 through 18 looks at an outcome of teen pregnancy. HHS standards require that the average ages of the intervention and comparison groups are not significantly different from each other. However, teen pregnancy can vary markedly in particular age categories, such as those under 14, ages 14 to 16, and over 16. Examining only average ages of this hypothetical study's intervention and comparison groups could miss important differences between the two groups in their age *distributions* that could be confounded with intervention impacts. Given this possibility, it would be useful for researchers conducting this study to also compare the age distributions of the intervention and comparison groups, in addition to assessing differences in averages in key measures at baseline. This could be done by separately examining each age category as a dichotomous variable in the baseline equivalence assessment, and estimating a linear probability model to assess the difference in the prevalence rates of the age categories across intervention and comparison groups.

Best practices for binary and categorical variables assessed at baseline

When assessing baseline equivalence of binary and categorical measures, researchers should consider whether it is important to examine combinations of the measures in addition to examining them individually. Like the previous example, the HHS evidence standards do not require this type of analysis, but such an assessment might increase the face validity of the results. For example, suppose a study includes girls who are all 16 years old. HHS standards require that race/ethnicity and at least one behavioral measure, such as sexual initiation, of the intervention and comparison groups are not significantly different. However, examining intervention-comparison group differences in race/ethnicity separately from group differences in sexual initiation could miss important differences between the two groups in the combinations of these measures. Even if the sexual initiation rates and race/ethnicity profiles of participants look similar across the intervention and comparison groups, the prevalence of the various combinations of sexual initiation and race/ ethnicity may differ across the intervention and comparison groups. To ensure that intervention-comparison group differences in combinations of race/ethnicity and sexual initiation are not an issue, researchers conducting this hypothetical study could examine group differences among individuals with the various combinations of these measures. This could be done by conducting the baseline equivalence assessments for combinations of variables, as shown in the table shell below (Table 2) for sexual initiation and race/ethnicity.

Intervention Group	Comparison Group	Differences	
Percentage	Percentage	Percentage points	<i>p</i> -value of difference
	Intervention Group Percentage	Intervention Group Comparison Group Percentage Percentage Image: Comparison of the second se	Intervention Group Comparison Group Different Percentage Percentage Percentage points Image: State

Table 2. Analysis Sample (N₁ =, N₂ =): Summary Statistics of Combinations of Key Baseline Measures, by Study Group

Step 3. Improving baseline equivalence in the analysis sample to potentially meet HHS evidence standards

If the diagnostic procedure outlined above reveals evidence of inequivalence, it is necessary to revisit what is considered the analysis sample for estimating intervention impacts. Among various approaches for addressing baseline inequivalence, one technique in particular—matching methods—has been shown to be effective. In a nutshell, matching methods can be used to construct a comparison group that is similar to an intervention group on observed baseline characteristics.

Exact matching

A straightforward way to implement the matching approach is to select, for each intervention group member, a comparison group member who is *identical* on each characteristic of interest. For example, to identify groups that are equivalent in age, gender, and race/ethnicity, select for each intervention group member a comparison group member who has the same values for the characteristics. Because the initial comparison group was baseline inequivalent with the intervention group, this approach will yield a subset of the comparison group for inclusion in the impact analysis. Identifying an exact match for each intervention group member should ensure that the analysis sample produced by the matching procedure meets the HHS evidence review requirements for baseline equivalence-in fact, this exact matching will ensure that the two groups have identical characteristics. This approach can be especially useful if a handful of outliers produce large group differences, and removing those outliers makes the intervention and comparison groups largely identical.

A potential limitation of this approach is that the comparison group may not contain an exact match for every intervention group member on all the characteristics that must be equivalent at baseline. For example, if four dichotomous variables are used to select a comparison group (such as dummy variables for age, gender, race, and ethnicity), there are 16 possible combinations of values for those variables. The combination of characteristics for some intervention group members may not exist in the comparison group, and therefore, the number of exact matches might be a small subset of the original sample; this will limit power for the subsequent impact estimates.

Propensity score methods

Researchers who encounter problems using exact matching approaches should consider an alternate option: using propensity scores. This approach uses analytic methods to identify a subset of the original comparison group that is similar to participants, *on average*. The process generally involves two steps: (1) calculating a propensity score—a single number that can be used to assess the similarity between individuals on multiple measures—for each intervention and comparison group member; and (2) selecting the subset of comparison group members whose propensity scores are similar to those of intervention participants. This approach does not necessarily identify for each participant an exact match from the comparison group (as the first approach does), but it can identify a subset of comparison group members who are similar to participants *on average*. The Technical Appendix provides more details about using propensity scores to identify a comparison group that is, on average, similar to the intervention group along all key variables examined in the evidence review.

In most situations, the Evaluation Technical Assistance team suggests first trying to do exact matching to improve the baseline equivalence of the analysis sample, since this approach is easily understandable and is likely to produce an analytic sample that will meet the baseline equivalence standard. However, if there is a sizeable proportion of intervention participants for whom an exact match cannot be obtained, we suggest trying a propensity score approach. If using the propensity score approach also results in a sizeable proportion of intervention participants who do not match comparison group sample members, then we suggest using the matching approach (exact or propensity) that minimizes the number of intervention participants who are deleted in the analysis, to maximize the power of the final impact analysis.

Step 4. Estimating impacts based on a matched sample

To estimate impacts from a matched sample, researchers should take certain steps to ensure that the impact estimation is likely to meet HHS evidence standards.

As stated above, before estimating intervention impacts, the baseline equivalence of the matched sample should be demonstrated and shown, using a format such as the one shown in Table 1. By demonstrating that this analysis sample is equivalent at baseline, the study will have the potential to meet HHS evidence standards (provided that the impact analysis is conducted appropriately).

To ensure that impact estimates are credible and likely to meet HHS evidence standards, researchers should:

- **1.** Estimate impacts using the sample of intervention and comparison group members who are baseline equivalent along the pre-intervention measures mentioned above.
- Adjust the impacts for the pre-intervention measures used in the matching analysis. Specifically, include all the pre-intervention variables used in the matching analysis as covariates in the impact regression model. We also suggest adjusting

impacts for any other pre-intervention measures that are correlated with outcomes. (This will improve precision of the impact estimate and adjust for any other differences between conditions).

- **3.** Conduct a statistical test of the significance of the impact estimates that reflects the study's design:
 - For clustered designs—such as those that randomly assigned centers to intervention or comparison status but analyzed outcomes of individuals—ensure that the statistical tests account for the clustering of individuals in the groups.
 - For designs that conducted intervention-comparison assignment within strata or blocks, account for the number of strata created when conducting the statistical tests (for example by including dummy indicators for each stratum as a covariate in the impact analysis).
- **4.** If propensity scores were used to identify the ultimate analysis sample, test whether the impacts are sensitive to alternate approaches used to generate the baseline equivalent sample. See the Technical Appendix for details on the types of robustness and sensitivity assessments that should be examined in this situation.

To present results from these analyses, consider showing impact results in a table, such as Table 3 below.

Step 5. Documenting matching results in a paper or final report to align with best practices

In TPP final evaluation reports, the approach for presenting impact estimates based on matching to improve baseline equivalence will depend on the study design (RCT or QED), level of sample attrition (for RCTs), and the degree to which the analysis sample groups are equivalent on key variables at baseline.

The following flow chart (Figure 1) illustrates the logic that should inform your approach. There are two scenarios that will require a matching analysis in order to be eligible for a moderate evidence rating (rather than a low rating):

1. RCTs with high levels of sample attrition at the unit of assignment and a lack of equivalence on a key characteristic at baseline for the analysis sample.

2. QEDs with a lack of equivalence on a key characteristic at baseline for the analysis sample.

In all other scenarios, the study will not be perceived to have a baseline equivalence issue, and therefore, a matching analysis is not necessary.

Figure 1: Decision rules to inform if matching analysis is necessary



While the HHS evidence standards will allow a study with low levels of cluster attrition and high levels of subcluster attrition to meet standards, we strongly encourage study researchers in this situation to also include impacts based on a matching analysis in an appendix if there are significant differences in the analytic samples at baseline. This additional, supplementary analysis may allow the study to be able to provide compelling evidence of program impact if the attrition standards change in the future.

Comparison Group Intervention Group Estimated Effects Outcome Mean Standard Mean Standard Mean p-value of Measures (or proportion) **Deviation**^a (or proportion) deviation^a difference difference Measure 1 Measure n

Note: [Describe the analytic approach used here, to align with the design and with the analytic approach used to demonstrate equivalence.] ^a Include if a continuous measure.

Table 3. Post-Intervention Outcomes and Effects for the Analysis Sample (N_i =, N_c =)

Endnotes

¹This is known as the "selection" internal validity threat, as defined by Campbell and Stanley (1963).

²Nonresponse in the context of an RCT includes the loss of any sample members who were initially randomized but were not included in the ultimate impact analysis. Common sources of nonresponse in TPP Evaluations include non-consent (after random assignment), program dropout, and nonresponse at the focal follow-up period used to estimate intervention impacts.

³ In studies with more than two conditions (e.g. three groups were randomly assigned to intervention 1, intervention 2, or no services), the steps laid out in this brief should be conducted separately for each contrast between groups analyzed in a final report.

⁴ A brief on **sample attrition** provides more information on how studies can assess this threat and determine whether a matching analysis is necessary to meet HHS evidence standards.

⁵ Studies can meet HHS evidence standards if they meet these and other conditions laid out in the evidence standards **protocol**.

⁶ The TPP Evaluation Technical Assistance team described several missing data approaches in the **Missing Data Brief**, that are appropriate for only RCTs with low attrition. For high-attrition RCTs and QEDs, the HHS evidence review will require a demonstration of baseline equivalence of the analytic sample *without imputation*, and therefore, the analysis sample must include cases with complete records on all key baseline and outcome variables.

References

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TECHNICAL APPENDIX: Estimating and Using Propensity Scores to Obtain a Baseline-Equivalent Sample

A propensity score $\lambda(x)$ represents the probability of receiving the intervention (T = 1), given a set of characteristics *x* (Rosenbaum and Rubin 1983; Rosenbaum 2002). More formally,

$\lambda(x) = \Pr\left(T = 1|x\right),$

where x includes key baseline characteristics that are expected to be related to intervention status and outcomes.

In the intervention evaluation literature, this propensity score can be used to produce an unbiased impact estimate, under the assumption that all important covariates are observed in *x*. Specifically, Rosenbaum and Rubin showed that statistical matching using propensity scores can be used to select a subset of the comparison group that is similar, on *average*, to intervention participants along those characteristics, which can facilitate the generation of an internally valid impact estimate.

The following general steps outline how to use propensity scores to identify a subset of the comparison group that is similar to intervention participants for the estimation of an internally valid impact. These steps are described in additional detail below. First, use intervention participants and all potential comparison group members to determine how each baseline characteristic that affects outcomes also affects intervention participant status. Then, using this information, assign to each intervention participant and each potential comparison group member a propensity score that summarizes how each individual's baseline characteristics collectively influence intervention participant status. Finally, select a subset of the comparison group whose propensity scores are similar to those of intervention participants. This subset of comparison group members with propensity scores similar to those of the intervention group will allow for a more credible, internally valid estimate of intervention impacts than one based on a larger sample of comparison group members that is baseline inequivalent.

More specifically, the following steps can be used to assign a propensity score to each intervention participant and potential comparison group member:

- 1. Code an indicator variable equal to one for each intervention participant and zero for each individual in the pool of potential comparison group members. Call this indicator variable P.
- 2. Define indicator and continuous variables that represent the demographics and preintervention outcomes of intervention participants and potential comparison group members. For the purposes of producing an internally valid comparison that can meet HHS evidence standards, these variables should include demographics (gender, race/ethnicity, age), behavioral assessments of the outcomes of interest measured at baseline (if applicable), as well as other variables measured

at baseline that are expected to influence intervention assignment as well as follow-up outcomes of interest. Call this collection of variables X.

- 3. Using intervention participants and potential comparison group members, estimate a probability model—such as a logit or probit—where the dependent variable is P and the independent variables are X. Although some might argue that it is necessary for the probability model to align with the study design, we advocate for using a simple approach that does not take into account clustering or stratification, regardless of design:
 - **Clustered design.** Since the purpose of the propensity modeling approach is to obtain the correct parameter estimates for producing propensity scores, and not adjusting the standard errors of the parameter estimates, we do not feel that it is necessary to move away from a standard logit or probit regression approach in order to obtain plausible parameter estimates. As such, we suggest ignoring clustering in the estimation of the propensity scores.
 - Stratified design. Since the HHS evidence review focuses only on the demonstration of baseline equivalence on a subset of variables (which we have suggested including in the propensity model), it is unnecessarily restrictive to conduct propensity modeling separately by strata, since the end result of the modeling and matching procedure (described below) can produce groups that are equivalent on the key characteristics of interest. As such, we suggest ignoring strata in the estimation of the propensity scores to increase the ease of estimation and likelihood of identifying matches for each participant.

Results from the probability model will include parameter estimates, or a collection of values that indicate how each respective X affects P. Call this collection of values BETA.

4. For each participant and potential comparison group member, define a variable that equals the predicted probability of treatment (this will be the transformation of the sum of each BETA value times each respective X value and can be requested as an output in standard statistical packages). Call this variable P*. P* equals each individual's propensity score.

- 5. Select the subset of the comparison group for analysis using $P^{*,1}$ First, identify the subset of comparison group members whose propensity score falls within the minimum and maximum values of intervention participants (known as, the region of common support). Then, for each intervention group member, select a single comparison group member to serve as a potential match. The general approach for matching is to identify comparison group sample members with propensity scores that are very close to the propensity scores of each intervention group member. There are a number of ways of identifying matches (for example, see Austin 2011 for a comprehensive listing of methods). Matching can be performed to minimize the total difference in propensity scores across all intervention members and their matched comparison group (optimal matching), or it can be performed to only allow matches of a certain quality to occur (caliper matching-in which matches are only considered if the propensity scores differ by less than a certain level, known as the caliper). Matching can be conducted with or without replacement (so that a comparison group member may be matched to multiple members of the intervention group). Selecting with replacement is particularly important if there are few comparison group members who are similar to intervention participants.²
- 6. Assess baseline equivalence of intervention participants and the subset of comparison group members who are matched. That is, complete Table 1 in the main brief text and check for any intervention-comparison group differences on the pre-intervention measures.
- 7. If the two groups differ on a pre-intervention measure of interest, revise the propensity model (the logit or probit) used in step 3 above to include higher-order terms for continuous measures and/or interactions for binary/categorical measures that are significantly different from each other. That is, if variable X₁ is significantly different across groups, then re-estimate the propensity model to include higher-order versions of X₁ or interact X₁ with other variables that are strongly related to intervention status.
- Stop when you have identified a subset of the comparison group that is baseline equivalent with intervention participants.

Rosenbaum and Rubin (1983) showed that a comparison group selected using propensity scores can produce unbiased impact estimates if two conditions are satisfied: (1) all the characteristics that are related to participant status and outcomes are observed, and (2) intervention and comparison group members with similar propensity scores are similar on individual characteristics. It is not possible to know for certain whether condition 1 is verified. However, adhering to the HHS standards will ensure that several characteristics that the literature indicates are related to the outcomes of interest are included in the analytic model, and researchers can use additional data appropriate for their own populations to supplement the analysis to further support this claim. Condition 2 can be verified through the iterative process of estimating a propensity model, identifying matches, assessing equivalence, and re-specifying the model as necessary.

As the process for using propensity scores above demonstrates, at certain points in the process researchers may need to make a subjective decision. For example, researchers will need to decide what types of matching techniques they will use, and make additional decisions within each technique. In addition, if intervention participants and the subset of comparison group members selected with propensity scores differ on a pre-intervention measure, the propensity model will need to be revised until a balanced comparison group is identified. It is possible that more than one way of revising the probability model will produce a comparison group that is baseline equivalent with intervention participants.

Given that using propensity scores to obtain baseline-equivalent groups requires making a number of decisions, researchers should calculate impacts based on at least two versions of the analysis (using different matching approaches or using different specifications of the propensity model) to assess whether impacts are sensitive to the subjective decisions made by the researcher. If the impacts are sensitive, this should be mentioned when reporting the results. If the impacts are not sensitive to the researcher's decisions, then it is sufficient to provide a footnote in the results about the additional analyses that were conducted, and indicate that the results were substantively the same.

¹There are a number of options for identifying a subset of the comparison group that may be baseline equivalent to intervention participants. This brief focuses on the use of propensity matching approaches for obtaining equivalence of the analytic sample because matching approaches are straightforward, understandable to a broad audience, and will achieve the goal of improving the equivalence of the analytic sample. For information on alternate approaches (such as inverse weighting or stratification of the propensity score), see Rosenbaum, 1987, or Rosenbaum and Rubin, 1983.

 $^{^{2}}$ We recommend that matching occur with replacement, so that each intervention member can be matched to the comparison group member with the closest P* value – that is, each participant's optimal match, which ultimately produces the optimal match for the entire intervention group. That said, we are not advocating for the duplication of comparison group members in the ultimate impact analysis. Rather, a comparison group member who ends up matching to multiple intervention group members should only contribute a single observation (with weight equal to the other sample members in the analysis sample).