

# Updates to the User's Manual and Statistical Theory Appendix for *RCT-YES* Versions 1.3 and 1.4

Peter Z. Schochet:	Project Lead, Author of Manua
Carlo Caci:	Interface Developer
Mason DeCamillis:	R Software Developer
Matthew Jacobus:	Stata Software Developer

Mathematica Policy Research, Inc.

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This manual discusses updates to the *RCT-YES* software for Versions 1.3 and 1.4. It serves as a supplement to the more detailed May 2016 and January 2018 *RCT-YES* User's Manuals and Statistical Theory Appendixes (all found at <u>www.rct-yes.com</u>).

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# Introduction

The free *RCT-YES* software (<u>www.rct-yes.com</u>) estimates and reports average treatment effects for evaluations of interventions, programs, and policies using randomized controlled trial designs (RCTs) or quasi-experimental designs (QEDs) with comparison groups. The software is applicable to a wide range of evaluation designs used in social policy and related research. The methods underlying the software are based on a new design-based statistical theory that has important advantages over traditional model-based methods used in social policy research (Schochet, 2016; 2018). The software is user friendly with no knowledge of computer programming required. The software reports study findings in formatted tables and graphs that meet industry standards, and conform to What Works Clearinghouse evidence reviews (Scher and Cole, 2017).

*RCT-YES* Version 1.0 was released in May 2016 with associated documentation available at <u>www.rct-yes.com</u>. Version 1.1 was released in June 2016 to fix minor program bugs. Version 1.2 was released in January 2018 with important new features implemented in response to user feedback. The key new feature was that the software can now accommodate designs with more than two research groups (multi-armed designs). Version 1.3 was released in mid-2020 and provides a slightly updated variance estimator for random (super-population) block designs where the study blocks (such as sites) are assumed to be sampled from a broader block population. Version 1.4 was released in November 2020 and fixes a bug in Version 1.3 so that the program now automatically checks for software updates on the *RCT-YES* website.

This brief note discusses the statistical theory updates in Versions 1.3 and 1.4. The new versions do not involve any changes to the program inputs or data dictionary, but involve a slight change to the variance estimators for random block designs for the super-population model.

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# Versions 1.3 and 1.4 Updates: February 2019 and October 2020

RCT-YES Version 1.4 was released in November 2020 and fixes a bug in Version 1.3 so that the program now automatically checks for software updates on the RCT-YES website. RCT-YES Version 1.3 was released in February 2019 and updates Version 1.2 which was released in January 2018.

#### A. Updates to Program Inputs

Versions 1.3 and 1.4 do not involve any changes to the program inputs or the data dictionary.

#### **B.** Updates to Running the Program

Versions 1.3 and 1.4 involve no updates on the process for running the program and generating the output files and graphs.

### C. Updates to Statistical Theory

# 1. Variance estimators have been slightly adjusted for random block designs (Designs 2 and 4) for the super-population model

In random block designs, the study blocks (such as sites) are assumed to be randomly sampled from a super-population of blocks, so that the study results are assumed to generalize to this broader population. For non-clustered designs, random block designs essentially involve three stages of sampling: (1) blocks, (2) individuals within blocks, and (3) randomization of individuals to the treatment and control groups. For clustered designs, random block designs involve an additional stage of sampling of clusters within blocks.

In previous software versions, *RCT-YES* estimated variances for random block designs (specified using the options SUPER\_POP=1 and CATE\_UATE=0 or 2) using the following variance formula where, for illustration, we assume a simple differences-in-means estimator and a non-clustered design (see Equation (6.25) on page 83 of the Statistical Theory Appendix [Schochet, 2016]):

(1) 
$$As\hat{y}Var(\hat{b}_{PATE}) = \frac{1}{(h-1)h\overline{w}^2} \overset{h}{a}_{b=1}^{h} (w_b \hat{b}_{b,PATE} - \overline{w} \hat{b}_{PATE})^2$$
.

In this expression,  $\hat{b}_{PATE} = \mathbf{a}_{b=1}^{h} w_b \hat{b}_{b,PATE} / \mathbf{a}_{b=1}^{h} w_b$  is the pooled impact estimate across the *h* blocks,  $\hat{b}_{b,PATE}$  is the impact estimate in block  $b, w_b$  is the block-specific weight, and  $\overline{w} = \mathbf{a}_{b=1}^{h} w_b / h$  is the average block weight.

As shown in Lemma 6.2 in Schochet (2016), conditional on the weights, the variance estimator in Equation (1) is consistent for the true asymptotic variance of  $\hat{b}_{PATE}$ :

(2) 
$$AsyVar_{RIB}(\hat{\beta}_{PATE}) = \frac{1}{hE_B(w_b)^2} \left[ E_B[w_b^2(\frac{\sigma_{Tb}^2}{n_{Tb}} + \frac{\sigma_{Cb}^2}{n_{Cb}})] + Var_B(w_b(\mu_{Tb} - \mu_{Cb})) \right],$$

where expectations are sequentially taken over the randomization distribution (R) in each block, the super-population of students (I) in each block, and finally over the super-population of blocks (B). In this expression,  $n_{Tb}$  is the number of treatment individuals,  $n_{Cb}$  is the number of controls,  $m_{Tb}$  and  $m_{Cb}$  are mean potential outcomes in I, and  $s_{Tb}^2$  and  $s_{Cb}^2$  are corresponding super-population variances.

The variance estimator in Equation (1) assumes that the block weights and impacts are independent. However, an *RCT-YES* user pointed out that this assumption might not realistic in some real-world applications, where the block weights and impacts could be correlated. For example, in a multi-site trial, site-level impacts might be larger (or smaller) in more populous sites with larger weights than in less populous sites.

To adjust for these potential correlations, RCT-YES now uses the following variance estimator:

(3) 
$$As\hat{y}Var(\hat{b}_{PATE}) = \frac{1}{(h-1)h\overline{w}^2} \hat{a}_{b=1}^h w_b^2 (\hat{b}_{b,PATE} - \hat{b}_{PATE})^2,$$

which treats the weights slightly differently than in Equation (1) by replacing  $\overline{w}$  with  $w_b$  in the parentheses in the numerator. Thus, the weights now appear outside the parentheses as squared terms rather than inside the parentheses.

The consistency of the variance estimator in Equation (3) for the asymptotic PATE variance in Equation (2) can be established using results in Cochran (1977; Theorem 11.2 and pages 300-305) on the variance of ratio estimators for population means (and totals) for two-stage clustered designs (see Schochet and Kautz, 2018 for a formal proof of this result). To provide intuition on this result, note that Cochran considers variance estimation for ratio estimators of the form  $\hat{y}_{CR} = \mathbf{a}_{b=1}^{h} w_b \bar{y}_{Cb} / \mathbf{a}_{b=1}^{h} w_b$ , where  $\bar{y}_{Cb}$  is the observed mean outcome, say for the control group, for cluster *b*. Cochran considers designs with sampling from finite universes, but we can extend his results to consider sampling from infinite populations at both stages. In this context, Cochran's results (Equation 11.30) imply that the variance estimator,

(4) 
$$As\hat{y}Var(\hat{y}_{CR}) = \frac{1}{(h-1)h\bar{w}^2} \overset{h}{\overset{h}{a}}_{b=1} w_b^2 (\bar{y}_{Cb} - \hat{y}_{CR})^2,$$

is a consistent estimator for the true asymptotic variance of  $\hat{y}_{CR}$ :

(5) 
$$AsyVar_{IB}(\hat{y}_{CR}) = \frac{1}{hE_B(w_b)^2} \stackrel{\acute{e}}{\underset{}{\otimes}} E_B[w_b^2(\frac{s_{Cb}^2}{n_{Cb}})] + Var_B(w_b m_{Cb}) \stackrel{\acute{u}}{\underset{}{\otimes}} \stackrel{\acute{u}}{\underset{}{\underset{}{\otimes}}} \stackrel{\acute{u}}{\underset{}{\otimes}} \stackrel{\acute{u}}{\underset{}{\otimes}} \stackrel{\acute{u}}{\underset{}{\underset{}{\otimes}}} \stackrel{\acute{u}}{\underset{}{\underset{}{\otimes}}} \stackrel{\acute{u}}{\underset{}{\underset{}{\otimes}}} \stackrel{\acute{u}}{\underset{}{\underset{}{\otimes}}} \stackrel{\acute{u}}{\underset{}{\underset{}{\otimes}}} \stackrel{\acute{u}}{\underset{}{\underset{}{\otimes}}} \stackrel{\acute{u}}{\underset{}{\underset{}{\underset{}{\otimes}}}} \stackrel{\acute{u}}{\underset{}{\underset{}{\underset{}{\otimes}}}} \stackrel{\acute{u}}{\underset{}{\underset{}{\underset{}{\underset{}{\underset{}}{\underset{}}{\underset{}}}}} \stackrel{\acute{u}}{\underset{}{\underset{}}{\underset{}}} \stackrel{\acute{u}}{\underset{}} \stackrel{\acute{u}}{\underset{}} \stackrel{\acute{u}}{\underset{}}} \stackrel{\acute{u}}{\underset{}} \stackrel{\acute{u}}{\underset{}}} \stackrel{\acute{u}}{\underset{}} \stackrel{i}}{\underset{}} \stackrel{\acute{u}}{\underset{}} \stackrel{\acute{u}}{\underset{}}$$

In this expression, the first term pertains to the variation of individual outcomes within clusters while the second term pertains to the variation of mean outcomes between clusters in the superpopulation.

We can now extend these results to random block designs by viewing blocks as clusters, and viewing the treatment and control group samples as separate random samples from common superpopulations in each block. The outcomes of the treatment and control groups might be correlated within a block due to a common block effect (which can improve precision), but the two samples are drawn independently. Thus, we can establish the consistency of Equation (3) by replacing  $\overline{y}_{Cb}$ with  $\hat{b}_{b,PATE}$  and  $\hat{\overline{y}}_{CR}$  with  $\hat{b}_{PATE}$  in Equations (4) and (5). Intuitively, for multi-stage clustered designs, parallel variance formulas apply for estimating means and estimating the difference between two correlated means measured from the same clusters.

The same adjustments to the variance formulas for parallel random block designs were made in *RCT*-YES for models with covariates, clustered designs, subgroup analyses, and baseline equivalency analyses. (This page left intentionally blank for double-sided copying)

## References

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