Power and Sample Size Calculations for Rerandomized Experiments

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Abstract

Power is an important aspect of experimental design, because it allows researchers to understand the chance of detecting causal effects if they exist. It is common to specify a desired level of power, and then compute the sample size necessary to obtain that level of power; thus, power calculations help determine how experiments are conducted in practice. Power and sample size calculations are readily available for completely randomized experiments; however, there can be many benefits to using other experimental designs. For example, in recent years it has been established that rerandomized designs, where subjects are randomized until a prespecified level of covariate balance is obtained, increase the precision of causal effect estimators. This work establishes the statistical power of rerandomized treatment-control experiments, thereby allowing for sample size calculators. Our theoretical results also clarify how power and sample size are affected by treatment effect heterogeneity, a quantity that is often ignored in power analyses. Via simulation, we confirm our theoretical results and find that rerandomization can lead to substantial sample size reductions; e.g., in many realistic scenarios, rerandomization can lead to a 25\% or even 50\% reduction in sample size for a fixed level of power, compared to complete randomization. Power and sample size calculators based on our results are in the R package \texttt{rerandPower} on CRAN.
1 Introduction

Here we consider conducting a randomized experiment where subjects are divided into two groups, with the aim of estimating causal effects between the two groups. Randomized experiments are frequently considered the gold standard of scientific inquiry because even simple causal effect estimators, such as the average difference in outcomes between the two groups (Splawa-Neyman et al., 1990; Rubin, 2008; Imbens & Rubin, 2015). However, there can be large benefits to using covariate information when randomizing subjects. For example, causal effect estimators can be substantially more precise if subjects are first grouped into blocks with similar covariate values, and then randomized within those blocks (Fisher, 1935; Box et al., 1978; Imai, 2008; Miratrix et al., 2013; Pashley & Miratrix, 2021). More generally, one can use rerandomization (Cox, 2009; Morgan & Rubin, 2012), where subjects are randomized until a prespecified level of covariate balance is obtained. Block randomization is a special case of rerandomization, where subjects are randomized until there is balance across all blocks.

Since Morgan & Rubin (2012), there has been a surge in works that establish the benefits of rerandomization; this includes experiments with tiers of covariates (Morgan & Rubin, 2015), sequential experiments (Zhou et al., 2018), factorial experiments (Branson et al., 2016; Li et al., 2020), stratified experiments (Wang et al., 2021), and experiments with high-dimensional covariates (Branson & Shao, 2021; Zhang et al., 2021). A common theme of these works is that causal effect estimators are more precise under rerandomization than under complete randomization, especially if covariates are highly associated with the outcomes of the experiment. This was formalized in Li et al. (2018), who found that the mean-difference estimator under the rerandomization scheme of Morgan & Rubin (2012) asymptotically follows a non-Normal distribution with narrower quantile ranges than the corresponding Normal distribution under complete randomization. This non-Normal distribution can be used to conduct inference for causal effects, thereby leading to more precise confidence intervals than under complete randomization.

Intuitively, because rerandomization increases estimation precision, it should also increase testing power, in the sense that we should be more likely to detect causal effects if they exist. While this has been alluded to in the literature (Morgan & Rubin, 2012), the power of rerandomized experiments has not been established. Establishing the power of rerandomized experiments has important consequences for how these experiments should be conducted in practice. In particular, for completely randomized experiments, it is common to specify a desired level of power, and then compute the sample size necessary to obtain that level of
power (Lenth, 2001; Maxwell et al., 2008; Chow et al., 2017). As a result, there are many publicly available sample size calculators for completely randomized experiments.

This work establishes the statistical power of rerandomized experiments, thereby allowing for sample size calculators for rerandomized experiments. For simplicity we focus on the mean-difference estimator; by doing so, we can leverage results from Li et al. (2018) to derive the power of the mean-difference estimator under rerandomization, and then relate power to sample size. We find that rerandomization can lead to substantial sample size reductions; e.g., in many realistic scenarios, rerandomization can lead to a 25% or even 50% reduction in sample size for a fixed level of power. This has important practical implications, because it quantifies how rerandomized experiments can reduce the amount of resources necessary to detect causal effects if they are present. Our results also clarify previous works on power analysis and sample size. In particular, our results quantify how power and sample size are affected by treatment effect heterogeneity, a quantity that is often ignored in power analyses. More generally, this work adds to the literature on power calculations for complex experimental designs, such as two-stage randomized experiments (Jiang & Imai, 2020), regression discontinuity designs (Schochet, 2009), and difference-in-difference designs (Schochet, 2021). Power and sample size calculators based on our results are in the R package rerandPower on CRAN.

2 Notation

Consider designing a randomized experiment with \(N\) subjects indexed by \(i = 1, \ldots, N\) that will be divided into two groups, e.g., treatment and control. Let \(Z = (Z_1, \ldots, Z_N)\) denote the binary group indicator, where \(Z_i = 1\) denotes treatment and \(Z_i = 0\) denotes control. We assume that before treatment is assigned, there is a \(K\)-length vector of covariates \(X_i\) available for each subject; define \(X \equiv (X_1, \ldots, X_N)^T\) as the \(N \times K\) covariate matrix. Finally, let \(Y_i(1)\) and \(Y_i(0)\) denote the potential outcomes for subject \(i\), where \(Y_i(1)\) denotes the outcome that subject \(i\) will yield if they are assigned to \(Z_i = 1\), and \(Y_i(0)\) is analogously defined. Throughout, we assume \(Y_i(1)\) and \(Y_i(0)\) are fixed; the outcome that subject \(i\) yields during the experiment is only random to the extent that \(Z_i\) is random.

Let \(\tau_i = Y_i(1) - Y_i(0)\) denote the treatment effect for subject \(i\). Because only \(Y_i(1)\) or \(Y_i(0)\) are observed for any given subject, \(\tau_i\) is not fully observed for any subject. Nonetheless, average treatment effects, and other causal estimands, can still be estimated. We assume
that the goal of the experiment is to well-estimate the average treatment effect, defined as

\[ \tau = N^{-1} \sum_{i=1}^{N} \tau_i = \bar{Y}(1) - \bar{Y}(0). \]  

(1)

There are many possible estimators for \( \tau \) in a randomized experiment; for simplicity, we focus on the mean-difference estimator, defined as:

\[ \hat{\tau} = \frac{\sum_{i=1}^{N} Z_i Y_i(1)}{\sum_{i=1}^{N} Z_i} - \frac{\sum_{i=1}^{N} (1 - Z_i) Y_i(0)}{\sum_{i=1}^{N} (1 - Z_i)}. \]  

(2)

In this work, we will discuss the statistical power of different experimental designs when using the mean-difference estimator \( \hat{\tau} \) to estimate \( \tau \). By focusing on a single, simple estimator, we will be able to pinpoint how different experimental designs affect the statistical power of the same estimator.

The power will depend on the magnitude of \( \tau \) and the experimental design used to assign treatment to the \( N \) subjects, as well as the variance of the potential outcomes and the variance of the individual treatment effects, which are respectively defined as:

\[ S_z^2 = (N - 1)^{-1} \sum_{i=1}^{N} \left( Y_i(z) - \bar{Y}(z) \right)^2, \quad \text{for } z \in \{0, 1\}, \]  

(3)

\[ S_\tau^2 = (N - 1)^{-1} \sum_{i=1}^{N} (\tau_i - \tau)^2. \]  

(4)

We focus on completely randomized in Section 3 and rerandomized experiments in Section 4.

3 Completely Randomized Experiments

3.1 Defining the Experimental Design

An experimental design is defined by the probability distribution it places on different treatment allocations \( Z \). We write an experimental design as \( P(Z \mid X) \), signifying that it may depend on the covariates \( X \). Completely randomized experiments do not use \( X \) when allocating treatment; instead, a fixed number of \( N_1 \) subjects are assigned to treatment and a fixed number of \( N_0 \) subjects are assigned to control, completely at random. A completely
randomized experimental design is defined as (Imbens & Rubin 2015, Chapter 4):

\[
P(Z = z \mid X) = \begin{cases} 
  \left(\frac{N}{N_1}\right)^{-1} & \text{if } \sum_{i=1}^{N} z_i = N_1 \\
  0 & \text{otherwise.}
\end{cases}
\] (5)

The completely randomized experimental design (5) is equivalent to random permutations of a vector with \(N_1\) 1s and \(N_0\) 0s. Let \(p_1 = N_1/N\) and \(p_0 = N_0/N\) denote the proportions of subjects under treatment and control, respectively. Under complete randomization, \(p_1\) and \(p_0\) are fixed.

3.2 Inference and Power

It is well-known that under complete randomization, the mean-difference estimator \(\hat{\tau}\) is unbiased and asymptotically Normally distributed (Splawa-Neyman et al., 1990; Li & Ding, 2017):

\[
V^{-1/2}N^{1/2}(\hat{\tau} - \tau) \sim N(0, 1), \quad \text{where} \quad V = p_1^{-1}S_1^2 + p_0^{-1}S_0^2 - S_\tau^2.
\] (6)

To avoid technical complexity, we state the Normality instead of asymptotic Normality of \(\hat{\tau}\) in (6). The variance \(V\) depends on the proportion of treatment and control subjects \(p_1\) and \(p_0\), the variance of the potential outcomes \(S_1^2\) and \(S_0^2\), and the variance of the individual treatment effects \(S_\tau^2\). The proportions are prespecified as part of the experimental design; meanwhile, \(S_1^2\) and \(S_0^2\) can be estimated but \(S_\tau^2\) cannot without additional assumptions, because \(\tau_i\) is not fully observed for any subject.

In practice, we can estimate \(V\) conservatively. Splawa-Neyman et al. (1990) proposed \(\hat{V}_N = p_1^{-1}s_1^2 + p_0^{-1}s_0^2\), where \(s_1^2\) and \(s_0^2\) are sample versions of \(S_1^2\) and \(S_0^2\). The estimator \(\hat{V}_N\) implicitly estimates treatment effect heterogeneity as \(\hat{S}_\tau^2 = 0\) and is thus conservative, in the sense that \(E(\hat{V}_N - V) = S_\tau^2 \geq 0\). Recently, Ding et al. (2019) noted that \(S_\tau^2 \geq S_{\tau|X}^2\), where \(S_{\tau|X}^2\) is the variance of the linear projection of the individual effects on \(X\), which can be consistently estimated by a sample analogue \(s_{\tau|X}^2\). Based on this, they proposed an improved variance estimator \(\hat{V}_{\text{dfm}} = \hat{V}_N - s_{\tau|X}^2\). Throughout, we will consider both variance estimators and use the generic notation \(\hat{V}\) for descriptive convenience. As demonstrated in Li & Ding (2017) and Ding et al. (2019), \(\hat{V}\) has a probability limit \(\tilde{V}\) no less than the true variance \(V\), i.e., \(\tilde{V} = \hat{V} + o_P(1) \geq V + o_P(1)\). The probability limits of \(\hat{V}_N\) and \(\hat{V}_{\text{dfm}}\) are, respectively,

\[
\tilde{V}_N = p_1^{-1}S_1^2 + p_0^{-1}S_0^2, \quad \tilde{V}_{\text{dfm}} = p_1^{-1}S_1^2 + p_0^{-1}S_0^2 - S_{\tau|X}^2.
\] (7)
Thus, the variance estimator $\hat{V}_N$ becomes consistent when $S_\tau^2 = 0$, and $\hat{V}_{dfm}$ becomes consistent more broadly when the individual effects can be linearly explained by the covariates.

From (6), the two-sided $(1 - \alpha)$-level confidence interval for the average treatment effect $\tau$ is:

$$\hat{\tau} \pm z_{1-\alpha/2} \hat{V}^{1/2} N^{-1/2},$$

where $z_{1-\alpha/2}$ denotes the $(1 - \alpha/2)$-quantile of a standard Normal distribution. Consider testing the null $H_0: \tau = 0$ against the alternative $H_A: \tau \neq 0$. The confidence interval (8) implies the following test:

$$\begin{cases}
\text{Reject } H_0: \tau = 0 & \text{if } |\hat{\tau}| > z_{1-\alpha/2} \hat{V}^{1/2} N^{-1/2} \\
\text{Fail to Reject } H_0: \tau = 0 & \text{otherwise.}
\end{cases}$$

We have the following theorem, which establishes the power of the above test.

**Theorem 1.** Under complete randomization, the power of the test (9) is asymptotically:

$$\Phi \left( \frac{z_{1-\alpha/2} \hat{V}^{1/2} - \tau N^{1/2}}{\hat{V}^{1/2}} \right) + \Phi \left( \frac{z_{\alpha/2} \hat{V}^{1/2} - \tau N^{1/2}}{\hat{V}^{1/2}} \right) \geq \Phi \left( \frac{z_{1-\alpha/2} \hat{V}^{1/2} - \tau N^{1/2}}{\hat{V}^{1/2}} \right),$$

where $\Phi(\cdot)$ and $\Phi(\cdot)$ denote the distribution and survival functions of a standard Normal distribution, respectively, $V$ denotes the variance in (6), and $\hat{V}$ denotes the probability limit of the corresponding variance estimator, for example, $\hat{V}_N$ or $\hat{V}_{dfm}$ in (7).

Theorem 1 is quite similar to classical results for statistical power in randomized experiments (e.g., Lachin 1981), with two caveats. First, and most importantly: Almost all power results implicitly assume $S_\tau^2 = 0$ (Lachin 1981; Cohen, 1992; Lerman, 1996; Wittes, 2002); indeed, because $S_\tau^2$ cannot directly be estimated, it is common to assume $S_\tau^2 = 0$ and use the variance estimator $\hat{V}_N$. Furthermore, if a super-population is assumed, $S_\tau^2$ is not involved in the asymptotic variance of the mean-difference estimator (Imbens & Rubin 2015, Chapter 6; Ding et al. 2017). However, under a finite-population framework, even when one uses the estimator $\hat{V}_N$, $S_\tau^2$ is still involved in the true variance of $\hat{\tau}$, and thus is also involved in the power of a completely randomized experiment. In other words, most power results assume $\hat{V}_N$ is consistent for the true variance $V$, when really it is conservative, unless truly $S_\tau^2 = 0$. Theorem 1 emphasizes this point, as well as allows for less conservative estimators for $V$, such as $\hat{V}_{dfm}$. We have the following corollary, which is the more typical power result found in the literature.
Corollary 1. If $S^2_\tau = 0$, such that $\bar{V} = V$ in (6), then the bound in Theorem 1 simplifies to

$$\Phi\left(z_{1-\alpha/2} - \frac{\tau N^{1/2}}{\sqrt{V}}\right).$$

The second caveat of Theorem 1 is: Almost all power results state that power is equal to the right-hand side in Theorem 1 (Lachin, 1981; Lerman, 1996; Wittes, 2002), when really it is bounded by the right-hand side. However, the second quantity on the left-hand side of Theorem 1 is the area of the left-tail of a Normal distribution, which will typically be quite small when $\tau$ is positive. Furthermore, the right-hand side of Theorem 1 is actually the power for the alternative hypothesis $H_A : \tau > 0$ at significance level $\alpha/2$. The reason that much of the literature either focuses on one-sided tests or states that power is equal to the right-hand side of Theorem 1 is that it simplifies sample size calculations, as we will see next. For this reason, and ease of exposition, when making sample size calculations, we assume the power of the test (9) is equal to, rather than bounded by, the right-hand side of Theorem 1. In other words, we assume $\tau > 0$ and focus on one-sided tests when making sample size calculations.

3.3 Sample Size Calculations

The following theorem establishes the relationship between the sample size $N$ and a prespecified degree of power $\gamma$ when we use the test (9) to conduct inference for a completely randomized experiment.

**Theorem 2.** Let $\gamma \geq \alpha/2$ denote a prespecified degree of power, where $\gamma$ is the probability we correctly reject the null hypothesis $H_0 : \tau = 0$ using the test (9) under complete randomization. Then, we have the following relationship between $N$ and $\gamma$:

$$N = \left(\frac{z_{1-\alpha/2} \bar{V}^{1/2} - z_{1-\gamma} V^{1/2}}{\tau}\right)^2,$$

where $V$ denotes the variance in (6) and $\bar{V}$ denotes the probability limit of the corresponding variance estimator, for example, $\bar{V}_n$ or $\bar{V}_{DFM}$ in (7).

We need $\gamma \geq \alpha/2$ because otherwise $z_{1-\alpha/2} \bar{V}^{1/2} - z_{1-\gamma} V^{1/2}$ may be negative, which would imply $N^{1/2} < 0$. We have the following corollary when $S^2_\tau = 0$.

**Corollary 2.** If $S^2_\tau = 0$, such that $\bar{V} = V$ in (6), then the sample size in Theorem 2 simplifies
to

\[ N = (p^{-1} S_1^2 + p_0^{-1} S_0^2) \left( z_{1-\alpha/2} - z_{1-\gamma} \right)^2. \]  

(10)

Theorem 2 shows that the sample size is (a) increasing in the power \( \gamma \in (\alpha/2, 1) \), (b) decreasing in the average treatment effect \( \tau \), (c) increasing in the potential outcome variances \( S_1^2 \) and \( S_0^2 \) if \( \gamma \geq 0.5 \), and (d) decreasing in the treatment effect heterogeneity \( S_\tau^2 \) if \( \gamma \geq 0.5 \). The first three observations are well-known in the literature, but, to our knowledge, the fourth observation has remained largely unacknowledged. However, it is intuitive: If treatment effect heterogeneity is large, then the variance of the mean-difference estimator is small, as shown in (6). This additional precision is propagated into the sample size necessary to achieve a certain degree of power. Furthermore, this demonstrates that assuming \( S_\tau^2 = 0 \) is a conservative assumption, not only in terms of the width of confidence intervals, which is well-known, but also in terms of the presumed sample size needed to achieve a certain degree of power. If one has a priori knowledge about the degree of treatment effect heterogeneity that will result in an experiment, then as long as the desired power is greater than 0.5, one could use Theorem 2 to argue that the required sample size for that experiment can be less than what is recommended in classic power calculations, which assume \( S_\tau^2 = 0 \) and thus use Corollary 2 to calculate sample size. However, this argument should be proceeded with caution, because typically there is no knowledge about the degree of treatment effect heterogeneity that will result from a given experiment.

Remark 1. Technically, the sample size \( N \) is also on the right-hand side of the equality in Theorem 2, in the sense that \( N \) is involved in the definitions of \( S_1^2 \), \( S_0^2 \), and \( S_\tau^2 \), as shown in Section 2. This is a by-product of adopting a finite-population framework, where these quantities are defined for a population of \( N \) subjects specifically. Nonetheless, we write \( N \) in terms of \( S_1^2 \), \( S_0^2 \), and \( S_\tau^2 \), because it is quite common to specify these quantities when making sample size calculations. Indeed, nearly all power and sample size calculators require users to specify super-population versions of \( S_1^2 \) and \( S_0^2 \) (e.g., Lachin 1981; Wittes 2002), even though the experiment will involve a finite population of subjects and not a super population. Thus, with a slight abuse of notation, we can view \( S_1^2 \), \( S_0^2 \), and \( S_\tau^2 \) in Theorem 2 as limits of potential outcome variances and treatment effect heterogeneity, thereby allowing for sample size calculators under a finite-population framework.
4 Rerandomized Experiments

4.1 Defining the Experimental Design

In the previous section we considered a two-group completely randomized experiment with \( N \) subjects. Within that experimental design, we derived the power of the mean-difference estimator in Theorem 1 and the sample size required to achieve a certain degree of power in Theorem 2. In this section we will consider a two-group rerandomized experiment with \( N \) subjects, where subjects are randomized to treatment or control until a certain degree of covariate balance is achieved. We will derive the power of the mean-difference estimator and the corresponding sample size for this experimental design, which constitutes the main contributions of this paper.

We assume the rerandomized experimental design of Morgan & Rubin (2012), where \( N_1 = Np_1 \) subjects are completely randomized to treatment and \( N_0 = Np_0 \) subjects to control for fixed proportions \( p_1 \) and \( p_0 \) until \( M \leq a \) for a prespecified threshold \( a \), where \( M \) is the Mahalanobis distance, defined as:

\[
M = \frac{N_1N_0}{N}(\bar{X}_1 - \bar{X}_0)^T(S_X^2)^{-1}(\bar{X}_1 - \bar{X}_0), \tag{11}
\]

where \( \bar{X}_1 \) is the \( K \)-length vector of covariate means in the treatment group, and \( \bar{X}_0 \) is analogously defined for the control group. Meanwhile, \( S^2_{z|X} \equiv (N-1)^{-1}\sum_{i=1}^{N}(X_i - \bar{X})(X_i - \bar{X})^T \) denotes the covariance matrix of \( X \), which is fixed across randomizations.

4.2 Inference and Power

Under rerandomization, the asymptotic distribution of \( \hat{\tau} | M \leq a \) is not Normally distributed. This distribution depends on the extent to which covariates are correlated with potential outcomes; thus, it is helpful to define the covariance between covariates and potential outcomes, as well as the variance of the linear projection of potential outcomes on covariates:

\[
S_{z,X} = S_{X,z}^T = (N-1)^{-1}\sum_{i=1}^{N}Y_i(z) - Y(z) \{X_i - \bar{X}\}^T, \quad S^2_{z|X} = S_{z,X}(S_X^2)^{-1}S_{X,z},
\]

for \( z \in \{0, 1\} \). Similarly, let \( S^2_{\tau|X} \) be the variance of the linear projection of \( \tau \) on covariates. Li et al. (2018, Theorem 1) found that the asymptotic distribution of \( \hat{\tau} \) under rerandomization...
is:

$$V^{-1/2} N^{1/2} (\hat{\tau} - \tau) \mid M \leq a \sim (1 - R^2)^{1/2} \epsilon_0 + RL_{K,a}, \tag{12}$$

where \(V\) is defined as in (6), \(\epsilon_0 \sim N(0,1), R^2\) is the squared multiple correlation between \(X\) and the potential outcomes:

$$R^2 = \frac{p_1^{-1} S_{i|X}^2 + p_0^{-1} S_{0|X}^2 - S_{\tau|X}^2}{p_1^{-1} S_1^2 + p_0^{-1} S_0^2 - S_{\tau}^2}, \tag{13}$$

and \(L_{K,a} \sim \chi_{K,a} \beta_{K}^{1/2}\) where

$$\chi_{K,a}^2 \sim \chi_K^2 \leq a, \quad S \sim -1 + 2 \text{Bern}(1/2), \quad \beta_K \sim \text{Beta}{1/2, (K - 1)/2}. \tag{14}$$

The rerandomization distribution (12) and the complete randomization distribution (6) are identical only if \(R^2 = 0\) or \(a = \infty\). Otherwise, (12) will be a non-Normal distribution that has less variance than a standard Normal distribution (Li et al., 2018).

Because \(\hat{\tau} \mid M \leq a\) has a non-Normal distribution, quantiles of a non-Normal distribution should be used for inference. The asymptotic distribution (12) is complex, thereby making its quantiles difficult to compute in closed-form, but the representation (14) makes it simple to approximate (12) with simple Monte Carlo after specifying \(S_1^2, S_0^2, S_{\tau}^2, \text{ and } R^2\). Li et al. (2018) found that the analogous conservative Neymanian confidence interval for the mean-difference estimator for rerandomized experiments is:

$$\hat{\tau} \pm \nu_{1-\alpha/2}(\hat{R}^2) \hat{V}^{1/2} N^{-1/2}, \tag{15}$$

where \(\nu_{1-\alpha/2}(\rho^2)\) is the \((1 - \alpha/2)\)-quantile of the distribution \((1 - \rho^2)^{1/2} \epsilon_0 + \rho L_{K,a} \). In (15), \(\hat{V}\) is defined the same as that for completely randomized experiments, i.e., \(\hat{V} = \hat{V}_N\) or \(\hat{V}_{DFM}\), and \(\hat{R}^2 = (p_1^{-1} s_{1|X}^2 + p_0^{-1} s_{0|X}^2 - s_{\tau|X}^2) / \hat{V}, \) where \(s_{1|X}^2\) and \(s_{0|X}^2\) are sample analogues of \(S_{1|X}^2\) and \(S_{0|X}^2\), and \(s_{\tau|X}^2\) is a consistent estimator for \(S_{\tau|X}^2\), as defined in (Li et al., 2018). As demonstrated in (Li et al., 2018), \(\hat{V}_N\) and \(\hat{V}_{DFM}\) have the same probability limits under rerandomization as that under complete randomization, i.e., \(\hat{V}_N = \hat{V}_N + o_P(1)\) and \(\hat{V}_{DFM} = \hat{V}_{DFM} + o_P(1)\) with \(\hat{V}_N\) and \(\hat{V}_{DFM}\) defined in (7), and \(\hat{R}^2\) has probability limit \(\hat{R}^2 = VR^2 / \hat{V} \leq R^2\), i.e., \(\hat{R}^2 = \hat{R}^2 + o_P(1)\). Thus, \(\hat{R}^2\) is a conservative estimator to the extent that \(\hat{V}\) is conservative. Furthermore, \(\nu_{1-\alpha/2}(R^2) \leq z_{1-\alpha/2}\) for all \(\alpha \in (0,1)\), with equality only if \(R^2 = 0\) or \(a = \infty\). As a result, the confidence interval for a rerandomized experiment (15) will be strictly narrower than the confidence interval for a completely randomized experiment (8) as long as the covariates have any linear association with the outcomes (Li et al., 2018, Theorem 2).
The rerandomization confidence interval (15) implies the following two-sided test:

\[
\begin{align*}
\text{Reject } H_0 : \tau = 0 & \quad \text{if } |\hat{\tau}| > \nu_{1-\alpha/2}(\hat{R}^2)\hat{V}^{1/2}N^{-1/2} \\
\text{Fail to Reject } H_0 : \tau = 0 & \quad \text{otherwise.}
\end{align*}
\]  

We then have the following theorem.

**Theorem 3.** Under rerandomization, the power of the test (16) is asymptotically:

\[
\bar{V}_{R^2} \left\{ \frac{\nu_{1-\alpha/2}(\hat{R}^2)\hat{V}^{1/2} - \tau N^{1/2}}{V^{1/2}} \right\} + V_{R^2} \left\{ \frac{\nu_{\alpha/2}(\hat{R}^2)\hat{V}^{1/2} - \tau N^{1/2}}{V^{1/2}} \right\} \geq \bar{V}_{R^2} \left\{ \frac{\nu_{1-\alpha/2}(\hat{R}^2)\hat{V}^{1/2} - \tau N^{1/2}}{V^{1/2}} \right\},
\]

where \( V_{R^2}(\cdot) \) and \( V_{R^2}(\cdot) \) denote the distribution and survival functions of \( (1 - R^2)^{1/2}e_0 + RL_{K,a} \), respectively, \( V \) denotes the variance in (6), and \( \tilde{V} \) denotes the probability limit of the corresponding variance estimator, for example, \( \tilde{V}_N \) or \( \tilde{V}_{DFM} \) in (7).

Theorem 3 and its proof are the same as Theorem 1, except Theorem 1 relies on the Normal quantile \( z_{1-\alpha/2} \) and distribution function \( \Phi(\cdot) \), whereas Theorem 3 relies on the non-Normal quantile \( \nu_{1-\alpha/2}(\hat{R}^2) \) and distribution function \( V_{R^2}(\cdot) \). As noted earlier, \( \nu_{1-\alpha/2}(\hat{R}^2) \) and \( V_{R^2}(\cdot) \) cannot be computed exactly, but they can be easily approximated via Monte Carlo.

Theorem 1 establishes testing power under complete randomization, and Theorem 3 establishes testing power under rerandomization. Intuitively, power under rerandomization will be greater than power under complete randomization, because the rerandomization confidence interval (15) is narrower than the randomization confidence interval (8). Thus, we have the following theorem.

**Theorem 4.** If \( \tilde{V} = V \), then for any \( \tau \geq 0 \),

\[
\bar{V}_{R^2} \left\{ \frac{\nu_{1-\alpha/2}(\hat{R}^2)\hat{V}^{1/2} - \tau N^{1/2}}{V^{1/2}} \right\} \geq \Phi \left( \frac{z_{1-\alpha/2}\hat{V}^{1/2} - \tau N^{1/2}}{V^{1/2}} \right). \tag{17}
\]

When \( \tilde{V} > V \), (17) still holds when \( \tau \geq \nu_{1-\alpha/2}(\hat{R}^2)\hat{V}^{1/2}N^{-1/2} \); otherwise, (17) may be violated.

From Theorem 4 as long as we can conduct asymptotically exact inference, in the sense that \( \tilde{V} = V \), rerandomized experiments provide greater power than completely randomized experiments. However, in the general scenario where we perform conservative inference, in the sense that \( \tilde{V} > V \), it is possible that power under rerandomization is strictly less
than power under complete randomization. The main reason is that inference for both completely randomized and rerandomized experiments is conservative by the same amount (e.g., the variance estimator for $N^{1/2}(\hat{\tau} - \tau)$ is asymptotically conservative by an amount of $\tilde{V} - V$ under both designs), rendering inference for rerandomized experiments relatively more conservative, because the distribution of $N^{1/2}(\hat{\tau} - \tau)$ has smaller variability. This additional conservativeness has an adverse effect on power, but the additional precision from rerandomization has a beneficial effect on power; Theorem 4 establishes that the beneficial effect outweights the adverse effect as long as the true treatment effect isn’t very small. To illustrate this trade-off, we consider a simple numerical example.

**Example 1.** Suppose that $\tilde{V} = 1$ and $R^2 = 0.5$. We consider two cases, which correspond to $\tilde{V} = V$ and $\tilde{V} > V$, as in Theorem 4. In Case (i), the probability limits of our estimators are the same as the corresponding truth, i.e., $\tilde{V} = V$ and $\tilde{R}^2 = R^2$. Meanwhile, in Case (ii), our inference is asymptotically conservative, in the sense that $\tilde{V} = 1.1 > V$ and $\tilde{R}^2 = VR^2/\tilde{V} \approx 0.455$. Figure 1 shows the lower bound of the power (as in Theorems 2 and 3) for the 0.05-level two-sided test for the mean-difference estimator under complete randomization and rerandomization, with the true average treatment effect $\tau$ ranging from 0 to 0.5. From Fig. 1(a), when we can conduct asymptotically exact inference, the power at $\tau = 0$ equals the nominal level 0.025 under both designs, and rerandomization provides better power than complete randomization. From Fig. 1(b), when we can only conduct conservative inference, the power at $\tau = 0$ is less than the nominal 0.025 under both designs, and moreover, the test is more conservative under rerandomization. However, the power of rerandomization quickly passes that of complete randomization when $N^{1/2}\tau$ is not too small, and the cutoff for $N^{1/2}\tau$ is much smaller than the theoretical cutoff $\nu_{1-\alpha/2}(\tilde{R}^2)\tilde{V}^{1/2} \approx 1.52$ in Theorem 4. In addition, in Fig. 1(c) we also consider Case (iii), which is the same as Case (ii), except that our inference is much more conservative with $\tilde{V} = 10$. In this case, the power of rerandomization also passes that of complete randomization when $N^{1/2}\tau$ is not too small, and the cutoff becomes closer to the theoretical cutoff $\nu_{1-\alpha/2}(\tilde{R}^2)\tilde{V}^{1/2} \approx 6.04$.

### 4.3 Sample Size Calculations

Theorem 3 establishes the testing power of a rerandomized experiment. As in Section 3, to simplify sample size calculations, we assume that power is equal to the right-hand side of Theorem 3 rather than bounded by it; again, this is a reasonable assumption as long as the treatment effect $\tau$ is positive. The following theorem establishes the relationship between the sample size $N$ and a prespecified degree of power $\gamma$ when we use the test (16) to conduct inference for a rerandomized experiment.
Figure 1: Lower bound of the power for the 0.05-level two-sided test using the mean-difference estimator under complete randomization (solid line) and rerandomization (dashed line). The dotted horizontal line denotes 0.025. The dotdash vertical line in (c) refers to the threshold \( \nu_1 - \alpha/2 (\tilde{R}^2) \tilde{V}^{1/2} \) as in Theorem 4.

**Theorem 5.** Let \( \gamma \geq \alpha/2 \) denote a prespecified degree of power, where \( \gamma \) is the probability we correctly reject the null hypothesis \( H_0 : \tau = 0 \) using the test (16) under rerandomization. Then, we have the following relationship between \( N \) and \( \gamma \):

\[
N = \left\{ \frac{\nu_1 - \alpha/2 (\tilde{R}^2) \tilde{V}^{1/2} - \nu_1 - \gamma (R^2) V^{1/2}}{\tau} \right\}^2,
\]

where \( \nu_\alpha(R^2) \) denotes the \( \alpha \)-quantile of the distribution \((1 - R^2)^{1/2} \epsilon_0 + RL_{K,\alpha}, V \) denotes the variance in (6), \( \tilde{V} \) denotes the probability limit of the corresponding variance estimator, \( R^2 \) denotes the squared multiple correlation between covariates and potential outcomes in (13), and \( \tilde{R}^2 \) denotes the probability limit of the corresponding estimator for \( R^2 \).

Theorem 5 and its proof are the same as Theorem 2 except Theorem 2 relies on the standard Normal quantiles \( z_{1-\alpha/2} \) and \( z_{1-\gamma} \), whereas Theorem 5 relies on the non-Normal quantiles \( \nu_1 - \alpha/2 (\tilde{R}^2) \) and \( \nu_1 - \gamma (R^2) \).

Intuitively, because rerandomization provides more precise confidence intervals, and thus more power, as established by Theorem 4, rerandomization should require a smaller sample size than complete randomization to achieve the same degree of power. In other words, for a fixed power level, we would expect the sample size in Theorem 5 to be smaller than the sample size in Theorem 2. The relationship between the complete randomization sample size in Theorem 2 and the rerandomization sample size in Theorem 5 is communicated in the following theorem.
Theorem 6. Let \( \gamma \geq \alpha/2 \) denote the probability we correctly reject the null hypothesis \( H_0: \tau = 0 \). Let \( N_{cr} \) denote the sample size required to achieve power \( \gamma \) under complete randomization, and let \( N_{rr} \) denote the sample size required to achieve power \( \gamma \) under rerandomization. Then:

\[
\frac{N_{rr}}{N_{cr}} = \left( \frac{\nu_{1-\alpha/2}(\tilde{R}^2)\tilde{V}^{1/2} - \nu_{1-\gamma}(R^2)V^{1/2}}{z_{1-\alpha/2}V^{1/2} - z_{1-\gamma}V^{1/2}} \right)^2,
\]  

(18)

where \( V \) denotes the variance in (6), \( \tilde{V} \) denotes the probability limit of the corresponding variance estimator, \( R^2 \) denotes the squared multiple correlation between covariates and potential outcomes in (13), and \( \tilde{R}^2 \) denotes the probability limit of the corresponding estimator for \( R^2 \). Furthermore, if \( \tilde{V} = V \), then the ratio in (18) is less than or equal to 1. Also, if \( \gamma \geq 0.5 \), then the ratio in (18) is (a) less than or equal to 1, (b) increasing in the number of covariates \( K \) and the rerandomization threshold \( a \), and (c) decreasing in \( R^2 \). Otherwise, if \( \gamma < 0.5 \), then the ratio in (18) may be greater than 1.

This result greatly simplifies when \( S_r^2 = 0 \).

Corollary 3. When \( S_r^2 = 0 \) and \( \gamma \geq \alpha/2 \), the ratio between \( N_{rr} \) and \( N_{cr} \) simplifies to:

\[
\frac{N_{rr}}{N_{cr}} = \left( \frac{\nu_{1-\alpha/2}(R^2) - \nu_{1-\gamma}(R^2)}{z_{1-\alpha/2} - z_{1-\gamma}} \right)^2 \leq 1.
\]

(19)

Moreover, if \( \gamma \geq 0.5 \), then the ratio in (19) is increasing in the number of covariates \( K \) and the rerandomization threshold \( a \), and is decreasing in \( R^2 \).

Theorem 6 confirms that a smaller sample size is needed under rerandomization to achieve the same amount of statistical power, compared to complete randomization, at least when \( \gamma \geq 0.5 \). The smaller the ratio \( N_{rr}/N_{cr} \), the larger the benefit of rerandomization over complete randomization in terms of sample size. This begs the question: How large are the sample size gains for rerandomization? This depends on the degree of separation between the standard Normal quantiles and the quantiles of \( (1 - R^2)^{1/2} \epsilon_0 + RL_{K,a} \), which in turn depend on \( R^2, K, \) and \( a \). In what follows, we conduct a simulation study to assess the ratio \( N_{rr}/N_{cr} \) for different \( K, R^2, a \), thereby allowing us to understand the sample size gains of rerandomization over complete randomization.
5 Numerical Examples

5.1 Setup and Parameters

Theorem 6 establishes, for any significance level $\alpha$ and power $\gamma$, the ratio between the sample size needed under rerandomization to achieve power $\gamma$ and the sample size needed under complete randomization. This ratio, $N_{rr}/N_{cr}$, depends on the number of covariates $K$, the correlation $R^2$, and the rerandomization threshold $a$. In this section, we present a simulation study to better understand how $N_{rr}/N_{cr}$ behaves for different $K$, $R^2$, and $a$, as well as varying levels of treatment effect heterogeneity. The smaller the ratio, the larger the benefits of rerandomization over complete randomization in terms of sample size.

We will consider covariates $K \in \{1, 10, 20, \ldots, 100\}$, correlation $R^2 \in \{0, 0.1, \ldots, 0.9\}$, and acceptance probabilities $p_a \in \{0.001, 0.01, 0.1\}$, where $p_a$ is defined as $p_a = P(M \leq a)$, i.e., the probability that a given randomization fulfills the rerandomization criterion. For simplicity, we focus on significance level $\alpha = 0.05$ and power $\gamma = 0.8$, both of which are common values in the power analysis literature. We found that results were consistent across other values of $\alpha$ and $\gamma$. The sample size ratio $N_{rr}/N_{cr}$ in Theorem 6 also depends on the quantiles of the non-Normal distribution $(1 - R^2)^{1/2}c_0 + RL_{K,a}$ defined in (12), which only depends on $K$, $R^2$, and $p_a$. For each $K$, $R^2$, and $p_a$, we will simulate $10^6$ draws from this distribution, thereby approximating the quantiles $\nu_{1-\alpha/2}$ and $\nu_{1-\gamma}$.

We will first consider the case where there is no treatment effect heterogeneity, such that $S_2^2 = 0$. As a result, the sample size ratio does not depend on the potential outcome variances $S_1^2$ and $S_0^2$, as shown in Corollary 3. Then we will consider the case where there is treatment effect heterogeneity, and thus $S_1^2$, $S_0^2$, and $S_2^2$ will affect the sample size ratio.

5.2 No Treatment Effect Heterogeneity

Figure 2 displays $N_{rr}/N_{cr}$ for different combinations of $K$, $R^2$, and $p_a$. There are several observations that can be made from Fig. 2, all of which validate the statements made in Theorem 6. First, the ratio is always below 1. This confirms that there are always sample size benefits when running a rerandomized experiment, compared to a completely randomized experiment. Furthermore, the ratio is decreasing in $R^2$ and increasing in $K$ and $p_a$. This demonstrates that the sample size benefits of rerandomization are large when a stringent criterion is used to balance a few covariates that are strongly related with experimental outcomes. More generally, Fig. 2 shows that rerandomization can lead to substantial sample size gains: For example, if $p_a = 0.001$, the median of the ratios in Fig. 2 is 0.75, and if further $R^2 \geq 0.3$ and $K \leq 50$, the ratio ranges from 0.1 to 0.84 with a median of 0.58. Thus,
rerandomization appears to reduce the sample size by 25% or even 50% for many realistic scenarios, compared to complete randomization.

Because there is no treatment effect heterogeneity, the results in Fig. 2 hold for any degree of potential outcome variation $S_1^2$ and $S_0^2$, as established by Corollary 3 and any average treatment effect $\tau$. According to Theorem 2, the sample size needed to achieve power $\gamma$ under complete randomization is increasing in $S_1^2$, $S_0^2$ and decreasing in $\tau$. Thus, as $S_1^2$, $S_0^2$ increase and as $\tau$ decreases, the nominal sample size gains from rerandomization can be arbitrarily large. For example, consider conducting an experiment where we desire 80% power and $S_1 = S_0 = 4$. When $\tau = 2$, i.e. half a standard deviation, which is a medium effect according to a commonly used effect size rule-of-thumb by Cohen (2013), the necessary sample size under complete randomization is $N_{cr} \approx 126$. In this case, one may view the results in Fig. 2 as modest: If the covariates are modestly related to the outcomes ($R^2 = 0.3$), there are a moderate amount of covariates ($K = 50$), and we use a somewhat stringent rerandomization criterion ($p_a = 0.01$), we would expect only an approximately 14% reduction in sample size under rerandomization, or 18 fewer subjects. However, when we consider a small effect $\tau = 0.8$, or one-fifth of a standard deviation, $N_{cr} \approx 785$. In this scenario, a 14% sample size reduction, or approximately 110 fewer subjects, may be considered quite large.
5.3 Treatment Effect Heterogeneity

Now we consider the case where $S^2_\tau > 0$, and thus power and sample size will depend on the potential outcome variances $S^2_1$ and $S^2_0$ in addition to $S^2_\tau$. As discussed in Section 3, to our knowledge the literature has not discussed how treatment effect heterogeneity affects the power of completely randomized experiments, let alone rerandomized experiments. First we will discuss how treatment effect heterogeneity affects power and sample size for complete randomization and rerandomization, and then we will discuss how heterogeneity affects the sample size ratio $N_{cr}/N_{rr}$.

The asymptotic power for completely randomized experiments is characterized by Theorem 1; for fixed values of $S^2_1$, $S^2_0$, and $\tau$, the power is increasing in $S^2_\tau$ as long as $\tau > z_{1-\alpha/2}V^{1/2}N^{-1/2}$, where $V$ is the probability limit of the variance estimator, defined in (6); otherwise, it is decreasing in $S^2_\tau$. From Theorem 3, a similar result holds for rerandomized experiments, where power is increasing in $S^2_\tau$ as long as $\tau > \nu_{1-\alpha/2}(\tilde{R}^2)\tilde{V}^{1/2}N^{-1/2}$. Thus, treatment effect heterogeneity has a beneficial effect on power for relatively large effect sizes but an adverse effect for relatively small effect sizes. Furthermore, because $\nu_{1-\alpha/2}(\tilde{R}^2) \leq z_{1-\alpha/2}$ for all $\alpha \in (0, 1)$, power is increasing in $S^2_\tau$ for a wider range of effect sizes under rerandomization than under complete randomization. In other words, treatment effect heterogeneity is less likely to adversely affect power under rerandomization than under complete randomization. We illustrate this point further via simulation in the supplementary material.

However, the results in the previous paragraph only hold when the variances $S^2_1$ and $S^2_0$ are fixed, and it’s difficult to imagine a scenario where an increase in $S^2_\tau$ does not also increase $S^2_1$, which adversely affects power. For example, previous works studying treatment effect heterogeneity have considered data-generating models like $Y_i(1) = Y_i(0) + \tau + \sigma_\tau Y_i(0)$ for some heterogeneity parameter $\sigma_\tau$ (Ding et al., 2016; Branson & Dasgupta, 2020). In this case, $S^2_1 = (1 + \sigma_\tau)^2S^2_0$ and $S^2_\tau = \sigma_\tau^2S^2_0$, and thus more heterogeneity increases both $S^2_1$ and $S^2_\tau$. Because power tends to be decreasing in $S^2_1$ and $S^2_\tau$ for large $S^2_1$, this suggests that treatment effect heterogeneity generally has an adverse effect on power.

Meanwhile, from Theorems 2 and 5, the sample size necessary to achieve power $\gamma \geq 0.5$ is decreasing in $S^2_\tau$ as long as $\gamma \geq 0.5$. Thus, for a fixed $\tau$ and power $\gamma \geq 0.5$, treatment effect heterogeneity has a beneficial effect on sample size for both completely randomized and rerandomized experiments. Indeed, this is analogous to the aforementioned results on power, because $\gamma > 0.5$ when $\tau > z_{1-\alpha/2}V^{1/2}N^{-1/2}$ for completely randomized experiments and when $\tau > \nu_{1-\alpha/2}(\tilde{R}^2)\tilde{V}^{1/2}N^{-1/2}$ for rerandomized experiments. However, if increased heterogeneity results in increased potential outcome variation, this may have an adverse affect on sample size, in the sense that increased $S^2_1$ will in turn increase sample size when $\gamma \geq 0.5$, as communicated in Theorems 2 and 5. These results are also illustrated via simulation.
in the supplementary material. We found that potential outcome variation tends to have a larger impact on power and sample size than treatment effect heterogeneity, validating common power analyses that focus on potential outcome variation rather than treatment effect heterogeneity.

Finally, we consider how treatment effect heterogeneity affects the sample size ratio $N_{rr}/N_{cr}$. As communicated in Theorem 6, when $S_1 > 0$, the sample size ratio depends on two conservative estimators: $\hat{V}$, which impacts inference for complete randomization and rerandomization, and $\hat{R}^2 = VR^2/\hat{V}$, which only impacts inference for rerandomization. As a result, the sample size under rerandomization $N_{rr}$ is doubly-impacted by the conservative estimator $\hat{V}$, thereby diminishing the sample size benefits of rerandomization when there is treatment effect heterogeneity. To demonstrate, let’s consider an experiment where $p_1 = p_0 = 0.5$ and $S_1 = S_0 = 4$, the significance level is $\alpha = 0.05$, the desired power is $\gamma = 0.8$, and acceptance probability is $p_a = 0.001$. Figure 3 shows the resulting $N_{rr}/N_{cr}$ for treatment effect heterogeneity $S_\tau \in \{2, 4, 6\}$ for different $K$ and $R^2$. Many of the results from Fig. 2 still hold: $N_{rr}/N_{cr}$ is decreasing in $R^2$, increasing in $K$, and always below 1, as established by Theorem 6. However, we see that this ratio is increasing in the treatment effect heterogeneity $S_1^2$; thus, rerandomization has less ability to reduce sample sizes when there is large treatment effect heterogeneity. However, $S_\tau = 6$ denotes unusually large effect heterogeneity, because it is larger than $S_1$ and $S_0$. Furthermore, it’s important to remember that the ratio result in Theorem 6 holds for any $\tau$; thus, as discussed in Section 5.2, when $\tau$ is small, $N_{cr}$ will be large, making even small multiplicative sample size reductions possibly worthwhile.

Furthermore, because the potential outcome variances $S_1^2$ and $S_0^2$ also impact power and sample size, they may also impact the ratio $N_{rr}/N_{cr}$. Let us consider the same example in Fig. 3 but where we fix $K = 10$ and vary $S_1, S_0, S_\tau$, and $R^2$. Figure 4 shows the ratio for different values of $S_1, S_0, S_\tau$, and $R^2$; in Fig. 4 we restricted the color scale to $[0.25, 1.0]$ to more easily see trends for this plot. We see that as $S_1$ and $S_0$ increase, $N_{rr}/N_{cr}$ somewhat decreases, signaling that rerandomization can lead to larger sample size reductions when potential outcome variances are high. However, it appears that treatment effect heterogeneity has a relatively larger adverse impact on these sample size reductions; in other words, there is more variation with respect to the vertical axis in Fig. 4 than the horizontal axis. Thus, if higher treatment effect heterogeneity in turn induces higher potential outcome variation, the adverse effects of heterogeneity will likely outweigh the beneficial effects of higher variation, thereby limiting the amount of sample size reductions we can expect from rerandomization.
Figure 3: The sample size ratio $N_{tr}/N_{cr}$ when running an experiment with $p_1 = p_0 = 0.5$ and $S_1 = S_0 = 4$, where $\alpha = 0.05$, $\gamma = 0.8$, and $p_a = 0.001$. The three panels correspond to heterogeneity $S_\tau \in \{2, 4, 6\}$.

Figure 4: The sample size ratio $N_{tr}/N_{cr}$ when running an experiment with $p_1 = p_0 = 0.5$ and $S_1 = S_0 = 4$, where $\alpha = 0.05$, $\gamma = 0.8$, $K = 10$, and $p_a = 0.001$. The three panels correspond to $R^2 \in \{0.2, 0.5, 0.8\}$. 


6 Discussion and Conclusion

Our results focus on the power of rerandomized experiments with two groups, where the mean-difference estimator is used for inference. One can also consider the power of rerandomized experiments with more than two groups. Rerandomization theory can be readily extended to more than two groups (Branson et al., 2016; Li et al., 2020), and thus we posit that our results will also hold for rerandomized experiments with more than two groups. However, because multiple causal estimands arise in this setting, power analyses become much more complex. The power of these experiments will depend on the potential outcome variance in each group, the effect heterogeneity for each estimand, and the rerandomization criterion for each estimand. Thus, power analysis results for these experiments will be notationally complex, but deriving such results can rely on the same conceptual framework developed in this paper.

Our results also assume that the Mahalanobis distance on the covariate means is used as the rerandomization criterion, but other criteria could be used. For example, Morgan & Rubin (2015) proposed using several Mahalanobis distance criteria, where criteria corresponding to more important tiers of covariates are more stringent. The supplementary material of Li et al. (2018) derives the asymptotic distribution of the mean-difference estimator under such a rerandomization scheme, which could then be used to study testing power. Again the power analysis results will be notationally complex, because one would have to consider the Mahalanobis distance for each tier of covariates. Furthermore, an interesting direction for future work is exploring the power of rerandomized experiments that do not use the Mahalanobis distance. For example, Branson & Shao (2021) proposed using a modified Mahalanobis distance that incorporates a ridge penalty, such that precision is increased in high-dimensional or high-collinearity settings. Thus, we suspect that testing power may increase as well, compared to standard rerandomization.

Finally, one could consider using an estimator other than the mean-difference estimator after rerandomization. Our results rely on knowing the asymptotic distribution of the mean-difference estimator under rerandomization. Thus, in order to consider the power of other estimators under rerandomization, one must first establish the asymptotic distribution of such an estimator, and this is largely an open problem. For example, the asymptotic distribution of the linear regression estimator after rerandomization has only recently been established (Li & Ding, 2020). Thus, studying the asymptotic distribution of other estimators after rerandomization is an important line of future work, because it will allow for a better understanding of the precision and power benefits of rerandomization.
A Proof of Theorem 1

We aim to compute the asymptotic power of the test (9), where we reject the null hypothesis if $|\hat{\tau}| > z_{1-\alpha/2}\tilde{V}^{1/2}N^{-1/2}$, where $\tilde{V}$ is the estimator for the variance in (6). Asymptotically, the test (9) rejects the null hypothesis if $|\hat{\tau}| > z_{1-\alpha/2}V^{1/2}N^{-1/2}$, where $V$ is the probability limit of $\tilde{V}$. First, we have:

$$P\left(\hat{\tau} > z_{1-\alpha/2}V^{1/2}N^{-1/2}\right) = P\left(\frac{\hat{\tau} - \tau}{V'^{1/2}N^{-1/2}} > \frac{z_{1-\alpha/2}V^{1/2}N^{-1/2} - \tau}{V'^{1/2}N^{-1/2}}\right)$$

$$= \Phi\left(\frac{z_{1-\alpha/2}V^{1/2}N^{-1/2} - \tau}{V'^{1/2}N^{-1/2}}\right)$$

$$= \Phi\left(\frac{z_{1-\alpha/2}V^{1/2} - \tau N^{1/2}}{V^{1/2}}\right)$$

where $\Phi(\cdot)$ is the survival function of the standard Normal distribution, which follows from the asymptotic distribution of $\hat{\tau}$ under complete randomization in (6). Similarly,

$$P\left(\hat{\tau} < -z_{1-\alpha/2}V^{1/2}N^{-1/2}\right) = P\left(\hat{\tau} < z_{\alpha/2}V^{1/2}N^{-1/2}\right)$$

$$= P\left(\frac{\hat{\tau} - \tau}{V'^{1/2}N^{-1/2}} < \frac{z_{\alpha/2}V^{1/2}N^{-1/2} - \tau}{V'^{1/2}N^{-1/2}}\right)$$

$$= \Phi\left(\frac{z_{\alpha/2}V^{1/2}N^{-1/2} - \tau}{V'^{1/2}N^{-1/2}}\right)$$

$$= \Phi\left(\frac{z_{\alpha/2}V^{1/2} - \tau N^{1/2}}{V^{1/2}}\right)$$

where $\Phi(\cdot)$ is the distribution function of the standard Normal distribution. Adding (20) and (21) gives us $P(|\hat{\tau}| > z_{1-\alpha/2}V^{1/2}N^{-1/2})$ and thus Theorem 1.

B Proof of Theorem 2

Let $\gamma$ denote a prespecified degree of power desired for a completely randomized experiment, where $\gamma$ is the probability we reject the null hypothesis using the test (9). Then, according to Theorem 1, we have:

$$\gamma = 1 - \Phi\left(\frac{z_{1-\alpha/2}V^{1/2} - \tau N^{1/2}}{V^{1/2}}\right)$$
As we discussed at the end of Section 3.2, the above assumes for simplicity that the power
is equal to, rather than bounded by, the right-hand side in Theorem 1. Then, solving for
$N$,
we have:
$$
\frac{z_{1-\alpha/2} \tilde{V}^{1/2} - \tau N^{1/2}}{V^{1/2}} = z_{1-\gamma}
\rightarrow z_{1-\alpha/2} \tilde{V}^{1/2} - \tau N^{1/2} = z_{1-\gamma} V^{1/2}
\rightarrow N = \left( \frac{z_{1-\alpha/2} \tilde{V}^{1/2} - z_{1-\gamma} V^{1/2}}{\tau} \right)^2
$$
which is the result in Theorem 2.

C  Dispersive ordering of the Normal and non-Normal distributions

The following theorem establishes the dispersive ordering of the Normal and non-Normal
distributions involved in the asymptotic approximations for complete randomization and
rerandomization, which is important for proving Theorem 4 and Corollary 3. For two random
variables $X$ and $Y$ with distribution functions $F$ and $G$ and quantile functions $F^{-1}$ and $G^{-1}$,
$X$ is said to be less dispersed than $Y$ (or $F$ is less dispersed than $G$) if $F^{-1}(\beta) - F^{-1}(\alpha) \leq G^{-1}(\beta) - G^{-1}(\alpha)$ for any $0 < \alpha < \beta < 1$.

**Theorem 7.** For any $a \in [0, \infty]$, integer $K \geq 1$ and $\rho \in [0, 1]$, $\sqrt{1 - \rho^2} \varepsilon_0 + \rho L_{K,a}$ is less
dispersed than $\varepsilon_0$, where $\varepsilon_0$ and $L_{K,a}$ are mutually independent.

To prove Theorem 7, we need the following five lemmas.

**Lemma 1.** For any integer $K \geq 1$ and threshold $a \in (0, \infty)$, the probability density function
of $L_{K,a}$ is
$$
g_{K,a}(x) = \phi(x) \frac{F_{K-1}(a - x^2)}{F_K(a)},
$$
where $\phi$ is the density of $\mathcal{N}(0, 1)$, $F_K$ is the distribution function of $\chi^2_K$, and $F_0(x) = \mathbb{1}(x \geq 0)$
is the distribution function of point mass at 0.

Theorem 7 follows immediately from Li et al. (2018, Proof of Proposition 2). For completeness, we give a proof below. Let $D = (D_1, \ldots, D_K) \sim \mathcal{N}(0, I_K)$. For $x \in \mathbb{R}$,
\[-\sqrt{a}, \sqrt{a},\]

\[
\Pr(L_{K,a} \leq x) = \Pr(D_1 \leq x \mid D^\top D \leq a) = \frac{\Pr(D_1 \leq x, D^\top D \leq a)}{\Pr(D^\top D \leq a)}
= \frac{1}{F_K(a)} \int_{-\infty}^{\infty} \Pr(t \leq x, t^2 + \sum_{j=2}^{K} D_j^2 \leq a) \phi(t)dt = \frac{1}{F_K(a)} \int_{-\infty}^{x} F_{K-1}(a - t^2)\phi(t)dt,
\]

which implies that

\[
g_{K,a}(x) = \frac{d}{dx} \Pr(L_{K,a} \leq x) = \frac{1}{F_K(a)} F_{K-1}(a - x^2)\phi(x) = \phi(x) \frac{F_{K-1}(a - x^2)}{F_K(a)}.
\]

Note that \(F_{K-1}(a - x^2)\) is zero when \(|x| > \sqrt{a}\), and \(L_{K,a}\) has support \([-\sqrt{a}, \sqrt{a}].\) We can then derive Lemma 1.

**Lemma 2.** For any \(a \in (0, \infty),\) \(K \geq 1\) and \(c \in \mathbb{R},\) define

\[
h_{K,a,c}(x) = \log g_{K,a}(x) - \log \phi(x + c), \quad (-\sqrt{a} \leq x \leq \sqrt{a}).
\]

Then \(d^2h_{K,a,c}(x)/dx^2 \leq 0\) for \(x \in (-\sqrt{a}, \sqrt{a}).\)

of Lemma 1. From Lemma 1

\[
h_{K,a,c}(x) = \log g_{K,a}(x) - \log \phi(x + c) = \log \phi(x) + \log F_{K-1}(a - x^2) - \log F_K(a) - \log \phi(x + c)
= \log F_{K-1}(a - x^2) + cx + c^2/2 - \log F_K(a).
\]

When \(K = 1,\) \(h_{1,a,c}(x)\) reduces to \(cx + c^2/2 - \log F_1(a),\) i.e., a linear function of \(x.\) Consequently, \(d^2h_{1,a,c}(x)/dx^2\) is zero for all \(x \in (-\sqrt{a}, \sqrt{a}),\) i.e., Lemma 2 for \(K = 1.\) Below we consider only the case with \(K > 1.\)

Let \(f_K(x)\) be the density of \(\chi^2_K,\) and \(\dot{f}_K(x) = df_K(x)/dx\) be its derivative over \(x.\) By the property of chi-square distribution,

\[
\dot{f}_K(x) = f_K(x) \cdot \left(\frac{K/2 - 1}{x} - \frac{1}{2}\right) = f_K(x) \cdot \frac{K - 2 - x}{2x}.
\]
Consequently, for $K > 1$, the second derivative of $h_{K,a,c}$ has the following equivalent forms:

\[
\frac{d^2}{dx^2} h_{K,a,c}(x) = \frac{d^2}{dx^2} \log F_{K-1}(a - x^2) = \frac{d}{dx} \left\{ \frac{f_{K-1}(a - x^2) \cdot (-2x)}{F_{K-1}(a - x^2)} \right\}
\]

\[
= \frac{K - 1 - 2a}{K - 2 - (a - x^2)} \cdot \frac{F_{K-1}(a - x^2)}{2(a - x^2)} \cdot \frac{\Delta_{K-1}(a - x^2)}{\{F_{K-1}(a - x^2)\}^2}
\]

\[
= \frac{4x^2 \cdot f_{K-1}(a - x^2)}{\{F_{K-1}(a - x^2)\}^2} \cdot \Delta_{K-1}(a - x^2),
\]

where

\[
\Delta_{K}(x) = \frac{K - 2 - x}{2x} \cdot F_{K}(x) - f_{K}(x).
\]

Thus, to prove Lemma 2, it suffices to prove $\Delta_{K}(x) \leq 0$ for all $K > 1$ and $x \in (0, \infty)$. Note that $\Delta_{K}(x) \leq -f_{K}(x) \leq 0$ when $x \geq K - 2$. It suffices to show $\Delta_{K}(x) \leq 0$ all $K > 2$ and $x \in (0, K - 2)$.

For $K > 2$ and $x \in (0, K - 2)$, define

\[
\tilde{\Delta}_{K}(x) = \frac{2x}{K - 2 - x} \Delta_{K}(x) = F_{K}(x) - \frac{2x}{K - 2 - x} f_{K}(x).
\]

It then suffices to show $\tilde{\Delta}_{K}(x) \leq 0$ all $K > 2$ and $x \in (0, K - 2)$. By some algebra and from (22), the derivative of $\tilde{\Delta}_{K}(x)$ has the following equivalent forms:

\[
\frac{d}{dx} \tilde{\Delta}_{K}(x) = f_{K}(x) - \frac{2(K - 2)}{(K - 2 - x)^2} f_{K}(x) = \frac{2x}{K - 2 - x} f_{K}(x) = -\frac{2(K - 2)}{(K - 2 - x)^2} f_{K}(x) \leq 0.
\]

We can verify that $\lim_{x \to 0^+} \tilde{\Delta}_{K}(x) = 0$. Thus, we must have $\tilde{\Delta}_{K}(x) \leq 0$ for all $x \in (0, K - 2)$.

From the above, Lemma 2 holds.

For a real function $\psi$ defined on $\mathcal{I} \subset \mathbb{R}$, the number of sign changes of $\psi$ in $\mathcal{I}$ is defined by

\[
S^-_{\mathcal{I}}(\psi) = S^-_{\mathcal{I}}(\psi(x)) = \sup S^-_{\mathcal{I}}[\psi(x_1), \psi(x_2), \ldots, \psi(x_m)]
\]

(23)

where $S^-_{\mathcal{I}}(y_1, y_2, \ldots, y_m)$ is the number of sign changes of the indicated sequence, zero terms being discarded, and the supremum in (23) is over all sets $x_1 < x_2 < \ldots < x_m$ with $x_i \in \mathcal{I}$ and $m < \infty$. For any $c \in \mathbb{R}$ and function $\psi$, define $\psi_c(x) = f(x - c)$.
Lemma 3. Let $F$ and $G$ be two absolutely continuous distributions, having intervals as their support, and let $f$ and $g$ be the corresponding densities. If $S_R^- (f_c - g) \leq 2$ for every $c \in \mathbb{R}$, with the sign sequence being $- , + , -$ in case of equality, then $F$ is less dispersed than $G$.

*Proof.* Lemma 3 follows from Shaked (1982, Theorem 2.5). \hfill \Box

Lemma 4. For any $a \in [0, \infty]$ and integer $K \geq 1$, $L_{K,a}$ is less dispersed than $\varepsilon_0$.

*Proof.* Lemma 4 holds obviously when $a$ equals zero or infinity. Below we consider only the case where $a \in (0, \infty)$. Let $g_{K,a}$ and $\phi$ be the densities of $L_{K,a}$ and $\varepsilon_0$, and $I = [-\sqrt{a}, \sqrt{a}]$. For any $c \in \mathbb{R}$, define $g_{K,a,c}(x) = g_{K,a}(x - c)$, $I_c = [-\sqrt{a} + c, \sqrt{a} + c]$, $h_{K,a,c}$ the same as in Lemma 2. We then have, for any $x \in I_c$,

$$\text{sign} \{ g_{K,a,c}(x) - \phi(x) \} = \text{sign} \{ g_{K,a}(x - c) - \phi(x - c + c) \} = \text{sign} \{ h_{K,a,c}(x - c) \} .$$

Consequently, $S_{I_c}^- (g_{K,a,c} - \phi) = S_{I_c}^- (h_{K,a,c})$. From Lemma 2, $h_{K,a,c}$ is a concave function on $I$. This then implies that

$$S_{I_c}^- (g_{K,a,c} - \phi) = S_{I_c}^- (h_{K,a,c}) = \begin{cases} 0, & \text{with sign being + or -}, \\ 1, & \text{with sign sequence being (-, +) or (+, -)}, \\ 2, & \text{with sign sequence being (-, +, -)}. \end{cases}$$

Note that $g_{K,a,c}(x) = 0 < \phi(x)$ for $x \notin I_c$. We can then verify that $S_R^- (g_{K,a,c} - \phi)$ must have the following forms:

$$S_R^- (g_{K,a,c} - \phi) = \begin{cases} 0, & \text{with sign being -}, \\ 2, & \text{with sign sequence being (-, +, -)}. \end{cases}$$

From Lemma 3, we can know that $L_{K,a}$ is less dispersed than $\varepsilon_0$. Therefore, Lemma 4 holds. \hfill \Box

Lemma 5. Let $W$ be a random variable independent of $X$ and $Y$, where $X$ is less dispersed than $Y$. Let $f(w)$ be the density of $W$. If $f(w) > 0$ for all $w$ and $d^2/dw^2 (\log f(w))$ exists and is non-positive for all $w$, then $X + W$ is less dispersed than $Y + W$.

*Proof.* Lemma 5 follows from Lewis & Thompson (1981, Theorem 7). \hfill \Box

*Proof.* Let $\varepsilon_1 \sim \mathcal{N}(0,1)$ be independent of $(\varepsilon_0, L_{K,a})$. From Lemma 4, $L_{K,a}$ is less dispersed than $\varepsilon_0$, which immediately implies that $\rho L_{K,a}$ is less dispersed than $\rho \varepsilon_0$. Thus, Theorem 7 holds obviously when $\rho = 1$. Below we consider only the case where $0 \leq \rho < 1$. 

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By some algebra, the second derivative of the log-density of $\sqrt{1 - \rho^2 \varepsilon_0} \sim \mathcal{N}(0, 1 - \rho^2)$ is a constant $-(1 - \rho^2)^{-1} < 0$. Thus, from Lemma 3, we can know that $\sqrt{1 - \rho^2 \varepsilon_0 + \rho L_{K, a}}$ is less dispersed than $\sqrt{1 - \rho^2 \varepsilon_0} \sim \mathcal{N}(0, 1) \sim \varepsilon_0$.

From the above, Theorem 7 holds.

\[ \text{D \ Proof of Theorem 4} \]

We first consider the case where $\tilde{V} = V$, under which we also have $\tilde{R}^2 = R^2$. Let $\beta_{rr}$ and $\beta_{cr}$ denote the left and right hand sides of (17), respectively. We can then verify that

$$\nu_{1-\alpha/2}(R^2) - \nu_{1-\beta_{rr}}(R^2) = V^{-1/2}N^{1/2} = z_{1-\alpha/2} - z_{1-\beta_{cr}}.$$ 

Because $\tau \geq 0$, $1 - \alpha/2 \geq 1 - \beta_{rr}$. From Theorem 7, $\nu_{1-\alpha/2}(R^2) - \nu_{1-\beta_{rr}}(R^2) \leq z_{1-\alpha/2} - z_{1-\beta_{rr}}$. This then implies that $z_{1-\alpha/2} - z_{1-\beta_{cr}} \leq z_{1-\alpha/2} - z_{1-\beta_{rr}}$. Consequently, we must have $\beta_{rr} \geq \beta_{cr}$, i.e., the inequality in (17) holds.

We then consider the case where $\tau \geq \nu_{1-\alpha/2}(\tilde{R}^2)\tilde{V}^{1/2}N^{-1/2}$. Again, we use $\beta_{rr}$ and $\beta_{cr}$ to denote the left and right hand sides of (17), respectively. We can then verify that

$$\nu_{1-\alpha/2}(\tilde{R}^2)\tilde{V}^{1/2} - \nu_{1-\beta_{rr}}(\tilde{R}^2)\tilde{V}^{1/2} = N^{1/2} = z_{1-\alpha/2}\tilde{V}^{1/2} - z_{1-\beta_{cr}}V^{1/2}.$$ 

Because $\tau \geq \nu_{1-\alpha/2}(\tilde{R}^2)\tilde{V}^{1/2}N^{-1/2}$, $\beta_{rr} \geq 1/2$. Note that the distribution $(1 - R^2)^{1/2}\varepsilon_0 + RL_{K, a}$ is symmetric around zero. From Li et al. (2018, Theorem 2), we can verify that $-\nu_{1-\beta_{rr}}(R^2) = \nu_{1-\beta_{rr}}(R^2) = z_{1-\beta_{rr}} - z_{1-\beta_{cr}}$ and $\nu_{1-\alpha/2}(R^2) \leq z_{1-\alpha/2}$. These imply that

$$z_{1-\alpha/2}\tilde{V}^{1/2} - z_{1-\beta_{cr}}V^{1/2} = \nu_{1-\alpha/2}(\tilde{R}^2)\tilde{V}^{1/2} - \nu_{1-\beta_{rr}}(\tilde{R}^2)\tilde{V}^{1/2} \leq z_{1-\alpha/2}\tilde{V}^{1/2} - z_{1-\beta_{cr}}V^{1/2}.$$ 

Consequently, we must have $\beta_{rr} \geq \beta_{cr}$, i.e., the inequality in (17) holds.

From the above, Theorem 4 holds.

\[ \text{E \ Proof of Theorem 6} \]

Define $N_{cr}$ as the complete randomization sample size provided by Theorem 2 and define $N_{rr}$ as the rerandomization sample size provided by Theorem 5. We immediately have:

$$\frac{N_{rr}}{N_{cr}} = \left( \frac{\nu_{1-\alpha/2}(\tilde{R}^2)\tilde{V}^{1/2} - \nu_{1-\beta}(R^2)V^{1/2}}{z_{1-\alpha/2}\tilde{V}^{1/2} - z_{1-\beta}V^{1/2}} \right)^2.$$
We first consider the case where $\tilde{V} = V$, under which $\tilde{R}^2 = R^2$ and the ratio in (18) simplifies to

$$\frac{N_{tr}}{N_{cr}} = \left( \frac{\nu_{1-\alpha/2}(R^2)V^{1/2} - \nu_{1-\gamma}(R^2)V^{1/2}}{z_{1-\alpha/2}V^{1/2} - z_{1-\gamma}V^{1/2}} \right)^2 = \left( \frac{\nu_{1-\alpha/2}(R^2) - \nu_{1-\gamma}(R^2)}{z_{1-\alpha/2} - z_{1-\gamma}} \right)^2.$$  

From Theorem 7, when $\gamma \geq \alpha/2$, we have $\nu_{1-\alpha/2}(R^2) - \nu_{1-\gamma}(R^2) \leq z_{1-\alpha/2} - z_{1-\gamma}$. This immediately implies that the ratio in (18) is less than or equal to 1.

We then consider the case where $\gamma \geq 0.5$. From [Li et al. (2018, Theorem 2)], both $\nu_{1-\alpha/2}(R^2)$ and $\nu_{1-\gamma}(R^2)$ are decreasing in $R^2$ and increasing in $K$ and $a$, and they are less than or equal to $z_{1-\alpha/2}$ and $z_{1-\gamma}$, respectively. Consequently,

$$\nu_{1-\alpha/2}(\tilde{R}^2)\tilde{V}^{1/2} - \nu_{1-\gamma}(R^2)V^{1/2} = \nu_{1-\alpha/2}(\tilde{R}^2)\tilde{V}^{1/2} + \nu_{1-\gamma}(R^2)V^{1/2} \leq z_{1-\alpha/2}\tilde{V}^{1/2} + z_{1-\gamma}V^{1/2} = z_{1-\alpha/2}\tilde{V}^{1/2} - z_{1-\gamma}V^{1/2},$$

which immediately implies that the ratio in (18) is less than or equal to 1. Moreover, $\nu_{1-\alpha/2}(\tilde{R}^2)\tilde{V}^{1/2} - \nu_{1-\gamma}(R^2)V^{1/2} = \nu_{1-\alpha/2}(\tilde{R}^2)\tilde{V}^{1/2} + \nu_{1-\gamma}(R^2)V^{1/2}$ is decreasing in $R^2$ and increasing in $K$ and $a$. This then implies that the ratio in (18) is decreasing in $R^2$ and increasing in $K$ and $a$.

From the above, Theorem 6 holds.

**F  Proof of Corollary 3**

First, when $S_2^2 = 0$, $\tilde{V} = V$. The equivalent form of $N_{tr}/N_{cr}$ as well as the inequality in (19) then follows immediately from the proof of Theorem 6. Second, when $\gamma \geq 0.5$, Theorem 6 immediately implies that the ratio in (19) is decreasing in $R^2$ and increasing in $K$ and $a$. From the above, Corollary 3 holds.

**G  Additional Numerical Examples: How Treatment Effect Heterogeneity Affects Power and Sample Size in Randomized and Rerandomized Experiments**

As discussed in Section 5.3, the asymptotic power for completely randomized experiments is characterized by Theorem 1 for fixed values of $S_1^2$, $S_0^2$, and average treatment effect $\tau$, the power is increasing in $S_2^2$ as long as $\tau > z_{1-\alpha/2}\tilde{V}^{1/2}N^{-1/2}$, where $\tilde{V}$ is the probability limit of the estimator for $V$, defined in (6). As a toy example, consider the case where we
run a balanced \((p_1 = p_0 = 0.5)\) completely randomized experiment with \(N = 100\) subjects, where \(S_1 = S_0 = 4\), and we use the ubiquitous variance estimator \(\hat{V}_n = p_1^{-1}s_1^2 + p_0^{-1}s_0^2\) and thus \(\hat{V}_n = p_1^{-1}S_1^2 + p_0^{-1}S_0^2\). Thus, power is increasing in \(S_\tau^2\) as long as \(\tau > z_{1-\alpha/2} \cdot 8 \cdot 0.1 \approx 1.6\) for \(\alpha = 0.05\). Figure 5a shows power for this toy example when we vary \(S_\tau\) for \(\tau = 2\) and \(\tau = 0.8\); we see that power is monotonically increasing in \(S_\tau\) for the former but monotonically decreasing for the latter. This suggests that treatment effect heterogeneity has a beneficial effect on power for large effect sizes but an adverse effect for small effect sizes; thus, if we incorrectly assume \(S_\tau^2 = 0\) (a common assumption in power analyses), we may underestimate power for large effect sizes but overestimate power for small effect sizes. Note that, in Fig. 5a, \(S_\tau = 8\) is very extreme; in this case, \(V = 0\) (i.e., the true variance of the mean-difference estimator is 0), and thus power is either 0 or 1, depending on whether \(\tau > z_{1-\alpha/2} \cdot \sqrt{\text{Var}} \cdot N^{-1/2}\).

Alternatively, we can consider a fixed average treatment effect \(\tau\) and study the power of a completely randomized experiment when we vary \(S_1^2\) and \(S_0^2\) in addition to \(S_\tau^2\). Figures 5b and 5c show the power for the aforementioned toy example for \(\tau = 2\) and \(\tau = 0.8\), respectively, for different values of \(S_1, S_0, S_\tau\). When \(\tau = 2\), power is monotonically increasing in \(S_\tau\) (as we saw in Fig. 5a), but only for small values of \(S_1\) and \(S_0\); otherwise, it is monotonically decreasing. Meanwhile, we see that power is always monotonically decreasing in \(S_\tau\) when \(\tau = 0.8\). Furthermore, we see in Fig. 5b and 5c that power is monotonically decreasing in \(S_1\) and \(S_0\), which is already a well-known phenomenon in power analyses. Taking all of Fig. 5 together, it appears that treatment effect heterogeneity can have an adverse effect on power if \(\tau\) is small and/or the potential outcome variances are large. However, it also appears that the potential outcome variances tend to have a more consequential effect on power than treatment effect variation.

However, it is important to note that when \(\tau > z_{1-\alpha/2} \cdot \sqrt{\text{Var}} \cdot N^{-1/2}\), the asymptotic power of a completely randomized experiment will always be greater than or equal to 50%, as a consequence of Theorem 1. Thus, for a fixed \(\tau\) and a desired level of power \(\gamma \geq 0.5\), treatment effect heterogeneity actually has a beneficial effect on the required sample size to achieve power \(\gamma\), in the sense that larger \(S_\tau^2\) leads to a smaller required sample size, as a consequence of Theorem 2. To demonstrate, let us again consider our toy example where \(p_1 = p_0 = 0.5, S_1 = S_0 = 4,\) and \(\tau = 2\). Figure 6a displays the sample size \(N_{cr}\) to achieve power \(\gamma = 0.8\) and \(\gamma = 0.4\) under complete randomization for increasing values of \(S_\tau\). We see that for \(\gamma = 0.8\), sample size is increasing in \(S_\tau\), but it is decreasing in \(S_\tau\) when \(\gamma = 0.4\); this is analogous to our previous finding that power is increasing in \(S_\tau\) only for treatment effects above a certain magnitude. Furthermore, note that in the extreme case when \(S_\tau = 8, V = 0\), and thus \(N_{cr}\) is no longer a function of \(\gamma\) (as shown in Theorem 2).

Again we can also consider varying \(S_1^2\) and \(S_0^2\), in addition to \(S_\tau^2\); the resulting sample
(a) Power when varying $S_\tau$ for $S_1 = S_0 = 4$, when $\tau = 2$ (solid line) and $\tau = 0.8$ (dotted line).

(b) Power when varying $S_\tau$ as well as $S_1$ and $S_0$ for $\tau = 2$. Power ranges from 20.6% to 100.0%.

(c) Power when varying $S_\tau$ as well as $S_1$ and $S_0$ for $\tau = 0.8$. Power ranges from 0.0% to 16.9%.

Figure 5: Power of a completely randomized experiment under several scenarios when $p_1 = p_0 = 0.5$ and $N = 100$.

size $N_{cr}$ required to achieve power $\gamma = 0.8$ is shown in Figures 6b and 6c for $\tau = 2$ and $\tau = 0.8$, respectively. For both of these scenarios, the sample size is decreasing in $S_\tau^2$ (because $\gamma > 0.5$), again suggesting that larger treatment effect heterogeneity can have a beneficial effect on the sample size $N_{cr}$. However, Fig. 6b and 6c also suggest that the potential outcome variances have a larger effect on the sample size $N_{cr}$ than treatment effect heterogeneity, validating common power analyses that focus on these quantities rather than treatment effect heterogeneity for completely randomized experiments. In particular, if increased treatment effect heterogeneity in turn increases potential outcome variances, then in general heterogeneity may have an adverse affect on sample size.

Finally, we can also consider how treatment effect heterogeneity affects power and sample size for rerandomized experiments. The asymptotic power for rerandomized experiments is characterized by Theorem 3 for fixed values of $S_1^2$, $S_0^2$, and average treatment effect $\tau$, the power is increasing in $S_\tau^2$ as long as $\tau > \nu_{1-\alpha/2}(\bar{R}^2)\sqrt{1/2}N^{-1/2}$, where $\nu_{1-\alpha/2}(\bar{R}^2)$ denotes the $(1-\alpha/2)$-quantile of the distribution $\sqrt{1-\bar{R}^2}\epsilon_0 + \sqrt{\bar{R}^2}L_{K,a}$ and $\bar{R}^2 = VR^2/V$. Note that $\nu_{1-\alpha/2}(\bar{R}^2) \leq z_{1-\alpha/2}$ for all $\alpha \in (0,1)$, with equality only if $\bar{R}^2 = 0$. Thus, the same conclusions made in this section for completely randomized experiments also hold for rerandomized experiments, but for smaller effect sizes. In other words, under rerandomization, a smaller $\tau$ is required in order for power to be increasing in $S_\tau^2$; or conversely, a smaller sample size $N_{rr}$ is required to achieve a certain level of power $\gamma \geq 0.5$, as established Theorem 6.
(a) $N_{cr}$ when varying $S_{\tau}$ for $S_1 = S_0 = 4$ and $\tau = 2$, when $\gamma = 0.8$ (solid line) and $\gamma = 0.4$ (dotted line).

(b) $N_{cr}$ when varying $S_{\tau}, S_1, S_0$ for $\tau = 2$. $N_{cr}$ ranges from approximately 62 to approximately 503.

(c) $N_{cr}$ when varying $S_{\tau}, S_1, S_0$ for $\tau = 0.8$. $N_{cr}$ ranges from approximately 385 to approximately 3140.

Figure 6: Sample size $N_{cr}$ required to achieve power $\gamma$ when running a completely randomized experiment with $p_1 = p_0 = 0.5$ under different scenarios. In (b) and (c), $\gamma = 0.8$.

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