

Repeated sampling of different individuals but the same clusters to
improve precision of difference-in-differences estimators:
the DISC design

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Abstract

We describe the DISC (Different Individuals, Same Clusters) design, a sampling scheme that can improve the precision of difference-in-differences (DID) estimators in settings involving repeated sampling of a population at multiple time points. Although cohort designs typically lead to more efficient DID estimators relative to repeated cross-sectional (RCS) designs, they are often impractical in practice due to high rates of loss-to-follow-up, individuals leaving the risk set, or other reasons. The DISC design represents a hybrid between a cohort sampling design and a RCS sampling design, an alternative strategy in which the researcher takes a single sample of clusters, but then takes different cross-sectional samples of individuals within each cluster at two or more time points. We show that the DISC design can yield DID estimators with much higher precision relative to a RCS design, particularly if random cluster effects are present in the data-generating mechanism. For example, for a design in which 40 clusters and 25 individuals per cluster are sampled (for a total sample size of $n=1,000$), the variance of a commonly-used DID treatment effect estimator is 2.3 times higher in the RCS design for an intraclass correlation coefficient (ICC) of 0.05, 3.8 times higher for an ICC of 0.1, and 7.3 times higher

for an ICC of 0.2.

Keywords: difference-in-differences, before and after survey, repeated cross-sectional sampling, cohort sampling

1 Introduction

Longitudinal studies that involve repeated sampling of a population at two or more time points are ubiquitous in many fields, including epidemiology, implementation science, global health, and economics ([Diggle et al., 2002](#)).

Sometimes these studies are purely observational, and interest lies in assessing changes over time within a population. Other studies may involve experimental or quasi-experimental designs, seeking to understand the impact of an intervention over a given time period.

Longitudinal studies are often characterized as either cohort designs (in which the same individuals are measured at multiple points in time) or repeated cross-sectional (RCS) designs (in which two or more independent samples are drawn from a population at different time points) ([Feldman and McKinlay, 1994](#); [Mann, 2003](#); [Hulley et al., 2013](#)).

It is generally accepted that if individual outcomes are correlated, cohort designs will generally lead to greater statistical efficiency relative to RCS designs ([Diehr et al., 1995](#)). However, cohort designs are often not possible for a variety of practical reasons. For example, it may be logistically difficult to follow up with the same individuals, resulting in high rates of loss-to-follow-up, which can lead to selection bias at subsequent time points if individuals who drop out of the study do not drop out at random. Another reason why cohort designs may not be possible is if the time period of the study is long (e.g., multiple years) and individuals of interest leave the risk set after a narrow window of time, such as in studies of neonatal or infant mortality.

A further complication with these studies, especially those that seek to learn about a population spread over a large geographic area, is that data often must be collected through complex survey designs, such as multistage cluster sample household surveys ([Lehtonen and Pahkinen, 2004](#); [Chaudhuri and Stenger, 2005](#)). These surveys may involve stratification, cluster sampling, unequal sample weights, and so on, all of which must be accounted for statistically in the data analysis.

These surveys are a fundamental source of population health data; for example, as part of the the Demographic and Health Survey (DHS) program, hundreds of nationally representative surveys have been done across over 80 countries in the last four decades (Fabic et al., 2012). These complex survey designs lead to dependent data units, and specialized methods need to be used to account for this in the analysis stage (Rao and Wu, 1988; Lumley, 2004; Rabe-Hesketh and Skrondal, 2006).

With clustered data, it is typically the case that two individuals within a cluster are more similar to one another than two individuals within different clusters. Furthermore, cluster-level factors (which may be measured or unmeasured) may be strongly associated with the outcome of interest. For example, the distance of a community to the nearest health facility is known to be strongly associated with a variety of health outcomes (Kenny et al., 2015). When cluster-level variables are associated with the outcome, estimators of change over time or intervention effects within a RCS design may have much higher variance relative to the same estimators resulting from cohort designs.

To address this issue, we propose a design in which the same clusters are sampled repeatedly, but within each cluster, different samples of individuals are collected at different time points. We refer to this as the DISC (different individuals, same clusters) design, and study its properties both mathematically and via statistical simulation.

This design is not unprecedented, and is actually quite common in the context of cluster randomized controlled trials (cRCT), where it is (confusingly) referred to as “cross-sectional sampling”. For example, Lakshminarayan et al. (2010) randomized hospitals (clusters) to receive either a performance feedback intervention or standard-of-care, examining the effects on care quality for stroke patients; the same set of hospitals were observed at multiple time points, but different sets of patients were observed at different time points. However, this sort of design is far less common in quasi-experimental longitudinal designs, and so it is useful to define terminology for this situation to enable researchers to speak more precisely about potential design choices and trade-offs.

The remainder of this paper is organized as follows. In section 2, we characterize the DISC design as compared to cohort and RCS designs. In section 3, we compare the variance analytically between the RCS and DISC methods for a difference-in-differences design and show that variance is higher for the RCS method than for the DISC method. In section 4, we describe methods and results from a simulation study comparing the RCS and DISC methods, and show that the analytical

variance for each method matches the simulated variance. In section 5, we discuss applications of the DISC design, as well as limitations and future extensions of the work.

2 Characterizing the DISC design

Figure 1 visually depicts the differences between cohort, RCS, and DISC sampling. In each panel, the rectangles represent clusters (with the green/solid rectangles representing clusters that were sampled) and the small circles represent individuals within those clusters (again with the green/solid circles representing individuals who were sampled). Panel (a) depicts a RCS sample, in which one sample of clusters and individuals is taken at time 1 and a different sample of clusters and individuals is taken at time 2. Panel (b) depicts a cohort sample, in which the same clusters and individuals are sampled at both time points. Panel (c) depicts a DISC sample, in which the same clusters are selected at both time points, while two different samples of individuals are taken within each cluster at the two time points. As depicted in Figure 1, it may be the case with the DISC design that a small proportion of individuals are selected at both time points, but this is typically not problematic from an analytic point of view since the samples corresponding to the two time points are independent.

Figure 1 visually describes the design in the simple situation of two time points and one level of clustering, but the same principle generalizes to higher dimensions. More than two levels of clustering is common in practice; for example, many household surveys involve first sampling a district (or other higher-level administrative unit) as the primary sampling unit, then sampling communities within districts, and finally sampling households within communities. In this scenario, a DISC design might involving selecting either the same communities or different communities at each time point. In a three-level cluster sampling structure, a convenient notation to represent different designs would be to write either “S-S-D” (where “S” stands for “same” and “D” stands for “different”) or “S-D-D” to distinguish between DISC designs in which the second level of clustering are the same between surveys or different between surveys. With this notation, “S-S-S” would represent a cohort study and “D-D-D” would represent a repeated cross-sectional study, and thus, this notation unifies all three sampling schemes. Similarly, the DISC design can be used when there are more than two time points, a situation sometimes referred to as a *generalized*

difference-in-differences design (Richardson et al., 2023).

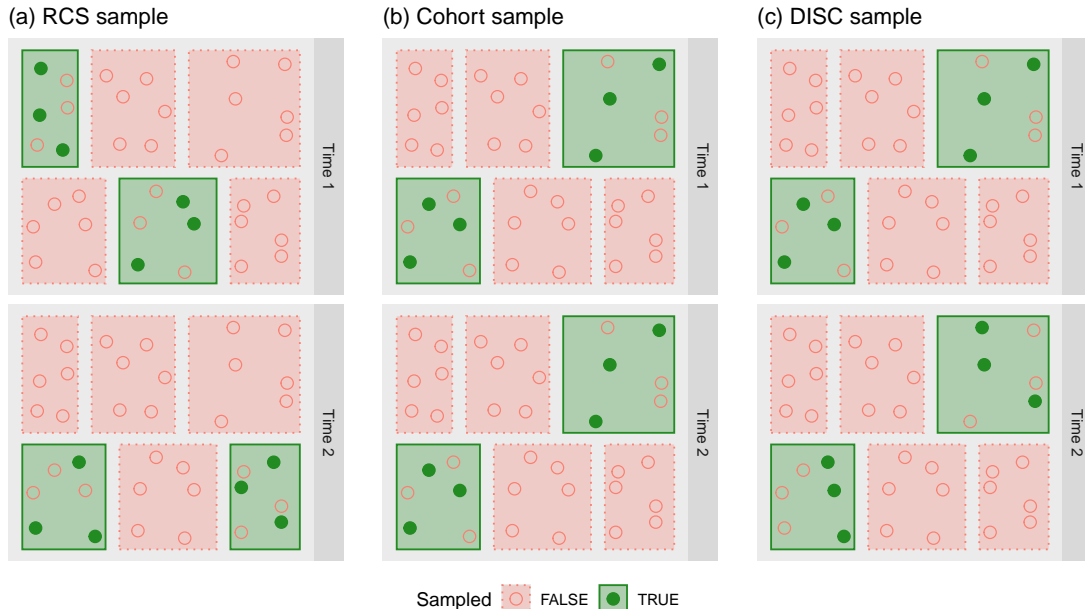


Figure 1: Visual representation of the DISC design (panel (c)), compared to the repeated cross sectional (RCS; panel (a)) and cohort (panel (b)) sample designs. Rectangles represent clusters and circles represent individuals. Rectangles with solid borders and green shading represent those that are sampled and rectangles with dotted borders and pink shading represent those that are not sampled. Circles with a solid green fill represent those that are sampled and circles with a pink outline and no fill represent those that are not sampled. For each panel, the upper set of rectangles represents selections at the first time point and the lower set represents selections at the second time point.

3 Analytic variance comparison between RCS and DISC designs

In this section, we describe a simple data generating mechanism and analytically show that the variance of a simple DID estimator can be much lower when using a DISC design relative to a RCS design.

Suppose that we are interested in a population containing C clusters, where cluster i contains N_i individuals. At each time point $j \in \{1, 2\}$, a sample of clusters is taken, and subsequently a sample of individuals is taken within each selected cluster. We assume that clusters are selected with probability-proportional-to-size (PPS) and that within each cluster, a sample of individuals of fixed size m is taken (Rosén, 1997). For simplicity, assume the same number of clusters is sampled at both time points and that there is no missingness or non-response. Let $I_1 \subset \{1, 2, \dots, C\}$ and

$I_2 \subset \{1, 2, \dots, C\}$ denote indexing sets corresponding to the clusters sampled at time points 1 and 2, respectively. For the DISC design $I_1 = I_2$, and for the RCS design $I_1 \neq I_2$. For each sampled cluster i and each time point j , let $K_{ij} \subset \{1, 2, \dots, N_i\}$ be an indexing set (of size m) for the sample of individuals. Also, let n be the total number of individuals sampled across all clusters at each time point.

Let Y_{ijk} denote the outcome of interest corresponding to individual $k \in K_{ij}$ within cluster $i \in I_j$ at time point j , and let X_i be an indicator variable that equals one if cluster i is exposed to some “treatment” condition of interest at time 2 and equals zero otherwise (note that in a traditional DID design, no one is exposed to the treatment at time 1). For simplicity, we do not consider other covariates and we assume that an equal number of clusters are sampled from the “treatment group” (those with $X_i = 1$) and the “control group” (those with $X_i = 0$). In this simple setting, the participant-level DID estimand is given by

$$\delta \equiv \{E(Y_{i2k} | X_i = 1) - E(Y_{i1k} | X_i = 1)\} - \{E(Y_{i2k} | X_i = 0) - E(Y_{i1k} | X_i = 0)\}. \quad (1)$$

That is, δ represents the difference between the change over time in the treatment group minus the change over time in the control group. At this stage, we intentionally do not consider whether δ corresponds to a treatment effect defined in terms of potential outcomes or other issues related to causal inference, as these issues are tangential to the present discussion. The expression given in (1) suggests the estimator

$$\hat{\delta} \equiv \left\{ \frac{2}{n} \sum_{i \in I_2} \sum_{k \in K_{i2}} X_i Y_{i2k} - \frac{2}{n} \sum_{i \in I_1} \sum_{k \in K_{i1}} X_i Y_{i1k} \right\} - \left\{ \frac{2}{n} \sum_{i \in I_2} \sum_{k \in K_{i2}} (1 - X_i) Y_{i2k} - \frac{2}{n} \sum_{i \in I_1} \sum_{k \in K_{i1}} (1 - X_i) Y_{i1k} \right\}, \quad (2)$$

which is equivalent to what one would obtain if, for example, a linear model including indicator variables for time 2, treatment group, and the interaction of treatment and time 2 (the common parameterization of a simple DID linear model) was fit using generalized estimating equations with an independence working correlation matrix. Although many other difference-in-differences estimators have been proposed (see, for example, [Callaway and Sant’Anna, 2021](#)), we focus on (2)

for simplicity. Note that this corresponds to a participant-average treatment effect, as opposed to a group-average treatment effect (Imai et al., 2009; Kahan et al., 2023), as all individuals are implicitly weighted equally (which is a consequence of PPS sampling; see, for example, Makela et al., 2018).

We are interested in comparing $\text{Var}(\hat{\delta})$ between the two designs. To do so, we assume that data at the population level were generated according to the following simple model:

$$Y_{ijk} = \mu_j + \delta X_{ij} + \alpha_i + \epsilon_{ijk},$$

where (μ_1, μ_2, δ) is a fixed vector, $X_{ij} \equiv X_i I(j = 2)$, and $\epsilon_{ijk} \stackrel{iid}{\sim} N(0, \sigma^2)$, $\alpha_i \stackrel{iid}{\sim} N(0, \tau^2)$, and $\epsilon_{ijk} \perp\!\!\!\perp \alpha_i$. μ_j is the mean outcome at time j , and so $\delta = \mu_2 - \mu_1$. We also denote $\hat{\delta}_{\text{RCS}}$ to equal $\hat{\delta}$ under the RCS design and denote $\hat{\delta}_{\text{DISC}}$ to equal $\hat{\delta}$ under the DISC design.

Under this model, it can be shown that under the RCS design, assuming the population of clusters is sufficiently large, the variance of $\hat{\delta}_{\text{RCS}}$ is given by

$$\text{Var}(\hat{\delta}_{\text{RCS}}) = \frac{8(m\tau^2 + \sigma^2)}{n}.$$

Under the DISC design, the variance of $\hat{\delta}_{\text{DISC}}$ is given by

$$\text{Var}(\hat{\delta}_{\text{DISC}}) = \frac{8\sigma^2}{n}.$$

See Appendix B for a derivation of these results.

Considering the ratio of variances between the two designs can be informative. For a fixed sample size n , the relative variance of the treatment effect estimator in the RCS design relative to the DISC design is given by $1 + m\tau^2/\sigma^2$. It can also be helpful to write this ratio as a function of the intraclass correlation coefficient (ICC), defined as $\rho \equiv \tau^2/(\tau^2 + \sigma^2)$, a measure commonly used to quantify the proportion of the total variance of an outcome variable of interest that is due to cluster effects. The ICC is a common input of power formulas for cluster randomized trials (Hemming et al., 2020) as well as observational designs; Korevaar et al. (2021) show that ICC values in the range of 0.02 to 0.1 are commonly encountered in cluster randomized trials, although this value is highly context-dependent. As a function of ρ , the ratio equals $1 + m\rho/(1 - \rho)$. In

Figure 2 we plot $\text{Var}(\hat{\delta}_{\text{RCS}})$ and $\text{Var}(\hat{\delta}_{\text{DISC}})$ as a function of ρ for a fixed value of n and several values of m ; the residual standard deviation σ^2 is scaled such that $\text{Var}(\hat{\delta}_{\text{DISC}}) = 1$, which implies that $\text{Var}(\hat{\delta}_{\text{RCS}})$ is equivalent to the ratio of variances between the two designs.

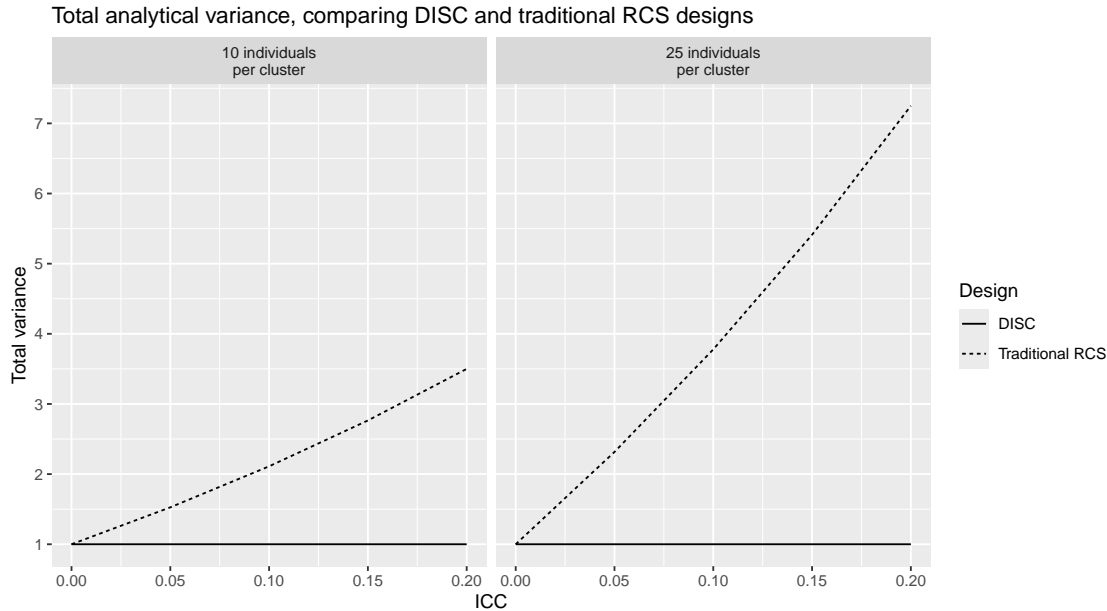


Figure 2: Total analytical variance comparing DISC and RCS designs as a function of the intraclass correlation coefficient (ICC), for a design involving a total of $n=1,000$ individuals. The panel on the left shows a design in which there are 100 clusters and 10 individuals sampled per cluster and the panel on the right shows a design in which there are 40 clusters and 25 individuals sampled per cluster.

From Figure 2, we see that, as expected, the variance in the DISC design does not depend on the ICC. Conversely, the variance in the RCS design can become extremely high relative to the variance in the DISC design for higher ICC values. For example, for a design in which 40 clusters and 25 individuals per cluster are sampled (for a total sample size of $n=1,000$), the variance of the treatment effect estimator is 2.3 times higher in the RCS design for an ICC of 0.05, 3.8 times higher for an ICC of 0.1, and 7.3 times higher for an ICC of 0.2.

4 Simulation study

Data were generated to mimic a two-stage sampling design, with clusters sampled first and individuals sampled second. A population of 1000 clusters was generated, with half assigned to the intervention group and half to the control group. Clusters were then sampled from this population

using two different procedures, one for the traditional RCS design and one for the DISC design. In the traditional RCS design, a random sample of half intervention and half control clusters was taken to represent the baseline, and another random sample of half intervention and half control clusters was taken to represent the endline (representing $I_1 \neq I_2$). In the DISC design, a random sample of half intervention and half control clusters was taken to represent the baseline, and the same sample of clusters was taken to represent the endline (representing $I_1 = I_2$). Next, a population of individuals was created to represent the sample of individuals taken within each cluster. Because clusters are sampled using probability proportional to size and the number of individuals sampled per cluster is constant, we did not generate a population of individuals to sample from within each cluster, but instead created only data for each individual sampled. Individual residuals were generated according to a normal distribution with a mean of 0 and standard deviation of 1. Outcome values were then generated for each individual in the sample using according to the simple model defined in section 3:

$$Y_{ijk} = \mu_j + \delta X_{ij} + \alpha_i + \epsilon_{ijk},$$

which represents the simplest version of a difference-in-differences equation, with no explanatory variables. For simplicity we assumed a mean outcome of 0 at baseline and endline among the control group, and a treatment effect of 1.

After generating the dataset, a linear model was fit to the data, with the generated outcome values as the dependent variable and an interaction term between intervention and time representing the difference-in-differences effect. Simulated estimator efficiency was evaluated by comparing total variance between the traditional RCS design and the DISC design for increasing total n . All simulations were conducted in R version 4.3.2 and structured using the **SimEngine** package (Kenny and Wolock, 2024). Results based on 1,000 simulation replicates are shown compared to analytical results in figure 3 for a selection of model parameters. Estimates are accurate overall as compared to empirical variance, and minor deviations from calculated values are likely due to Monte Carlo error.

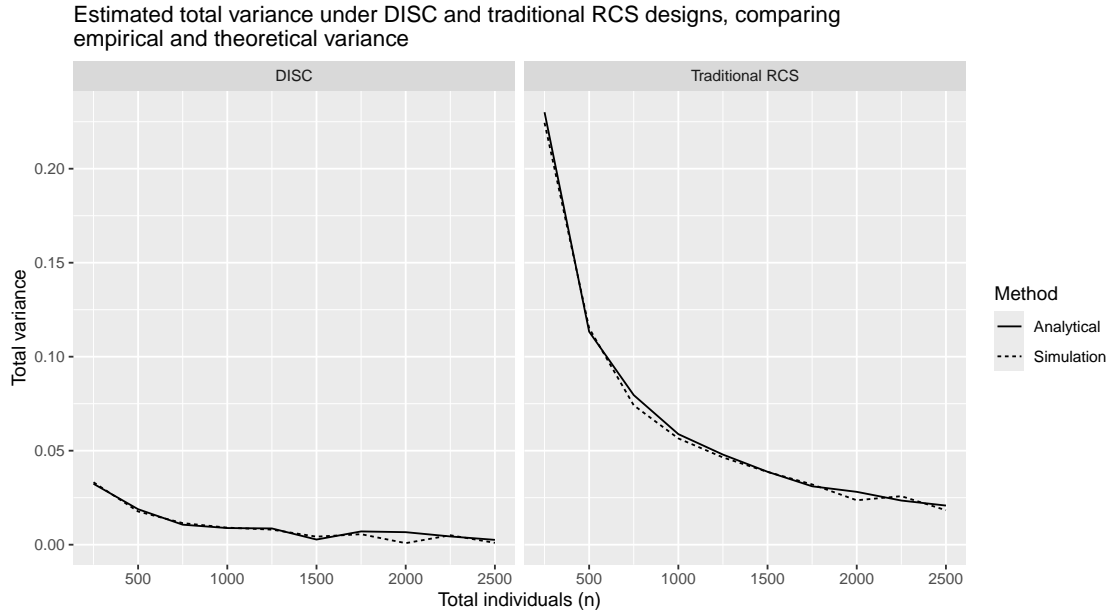


Figure 3: Estimated total variance under DISC and RCS designs, comparing empirical and theoretical variance, for different numbers of individuals sampled, for a design assuming 100 clusters sampled and an intraclass correlation coefficient of 0.2. Lines have been jittered using $h = 0.003$, so that both lines can be seen in the visualization. This illustrates that empirical and theoretical variance match, and that total variance is much higher for the traditional RCS design, especially when n is low.

5 Discussion

In this paper, we describe the DISC design (DISC = “Different Individuals, Same Clusters”), a hybrid between a repeated cross-sectional (RCS) design and a cohort design for settings in which cluster sampling is used. We show that the use of the DISC design can result in difference-in-differences (DID) treatment effect estimators that have substantially lower variance than the analogous estimator resulting from a repeated cross-sectional design. The variance ratio increases as a function of the ICC, and for a fixed total sample size (in terms of number of individuals), it increases as the number of clusters decreases.

Although this paper focused on settings where interest lies in difference-in-differences estimators, the DISC design is equally advantageous for studies in which interest lies in uncontrolled before-and-after comparisons (i.e., changes over time). A simple modification to the estimators and arguments given in section 3 can be done to show that the variance ratio is identical.

One limitation of the DISC design is that if there are any changes over the study period in terms

of the total number of clusters in the population or the sizes of the clusters, the sample at the second time point may no longer be representative of the population. Such changes may occur due to the establishment of new communities, people entering or leaving the eligibility set over time, migration between communities, or other reasons. Whether or not this property is undesirable depends on whether primary interest lies in assessing a (controlled or uncontrolled) change over time versus in estimates of an outcome of interest at each of the time points in the study. If a change in an outcome over time is observed in a setting where there are ongoing shifts in the underlying population, this change can be partitioned into the portion of the change resulting from changes in the outcome among the people who were in the population for the duration of the study versus the portion of the change resulting from people entering or leaving the population. If interest lies in the former, which will typically be the case when evaluating an intervention through a difference-in-differences estimator, the DISC design is advantageous. It also may be possible to use post-hoc weighting techniques (Royal, 2019) to remove bias if researchers are interested in estimating the population value of an outcome at points in the study other than the first time point.

Another extension would be to consider open cohort designs, in which individuals may enter or exit the cohort during the study period. One can imagine a DISC design in which certain clusters enter or exit the study at different time points, and this represents a promising direction for future research.

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B Variance calculations

The estimator given in (2) is defined as

$$\hat{\delta} \equiv \left\{ \frac{2}{n} \sum_{i \in I_2} \sum_{k \in K_{i2}} X_i Y_{i2k} - \frac{2}{n} \sum_{i \in I_1} \sum_{k \in K_{i1}} X_i Y_{i1k} \right\} \\ - \left\{ \frac{2}{n} \sum_{i \in I_2} \sum_{k \in K_{i2}} (1 - X_i) Y_{i2k} - \frac{2}{n} \sum_{i \in I_1} \sum_{k \in K_{i1}} (1 - X_i) Y_{i1k} \right\},$$

Assume that the population of clusters is sufficiently large such that the probability of selecting the same cluster at both time points is zero (a simplifying assumption to ease calculations). Then under the RCS design, labeling our estimator as $\hat{\delta}_{\text{RCS}}$, it holds that

$$\begin{aligned} \text{Var}(\hat{\delta}_{\text{RCS}}) &= \text{Var} \left[\left\{ \frac{2}{n} \sum_{i \in I_2} \sum_{k \in K_{i2}} X_i Y_{i2k} - \frac{2}{n} \sum_{i \in I_1} \sum_{k \in K_{i1}} X_i Y_{i1k} \right\} \right. \\ &\quad \left. - \left\{ \frac{2}{n} \sum_{i \in I_2} \sum_{k \in K_{i2}} (1 - X_i) Y_{i2k} - \frac{2}{n} \sum_{i \in I_1} \sum_{k \in K_{i1}} (1 - X_i) Y_{i1k} \right\} \right] \\ &= 2 \text{Var} \left\{ \frac{2}{n} \sum_{i \in I_2} \sum_{k \in K_{i2}} X_i Y_{i2k} - \frac{2}{n} \sum_{i \in I_2} \sum_{k \in K_{i2}} (1 - X_i) Y_{i2k} \right\} \\ &= 2 \text{Var} \left\{ \frac{2}{n} \sum_{i \in I_2} \sum_{k \in K_{i2}} (2X_i - 1) Y_{i2k} \right\} \\ &= \frac{8}{n^2} \left[\sum_{i \in I_2} \left\{ (2X_i - 1)^2 \text{Var} \sum_{k \in K_{i2}} Y_{i2k} \right\} \right] \\ &= \frac{8}{n^2} \left[\sum_{i \in I_2} \left\{ \text{Var} \sum_{k \in K_{i2}} (\mu_2 + \delta X_{ij} + \alpha_i + \epsilon_{ijk}) \right\} \right] \\ &= \frac{8}{n^2} \left[\sum_{i \in I_2} \left\{ \text{Var}(m\alpha_i) + \sum_{k \in K_{i2}} \text{Var}(\epsilon_{ijk}) \right\} \right] \\ &= \frac{8m}{n^2} \left[\sum_{i \in I_2} \left\{ m\tau^2 + \sigma^2 \right\} \right] \\ &= \frac{8(m\tau^2 + \sigma^2)}{n} \end{aligned}$$

Under the DISC design, we can label this estimator as $\hat{\delta}_{\text{DISC}}$, and making a similar simplifying assumption that the probability of sampling the same individual at both time points is zero, it holds that

$$\begin{aligned}
\text{Var}(\hat{\delta}_{\text{DISC}}) &= \text{Var} \left[\left\{ \frac{2}{n} \sum_{i \in I_2} \sum_{k \in K_{i_2}} X_i Y_{i2k} - \frac{2}{n} \sum_{i \in I_1} \sum_{k \in K_{i_1}} X_i Y_{i1k} \right\} \right. \\
&\quad \left. - \left\{ \frac{2}{n} \sum_{i \in I_2} \sum_{k \in K_{i_2}} (1 - X_i) Y_{i2k} - \frac{2}{n} \sum_{i \in I_1} \sum_{k \in K_{i_1}} (1 - X_i) Y_{i1k} \right\} \right] \\
&= \frac{4}{n^2} \text{Var} \left[\sum_{i \in I_1} X_i \left(\sum_{k \in K_{i_2}} Y_{i2k} - \sum_{k \in K_{i_1}} Y_{i1k} \right) \right. \\
&\quad \left. - \sum_{i \in I_1} (1 - X_i) \left(\sum_{k \in K_{i_2}} Y_{i2k} - \sum_{k \in K_{i_1}} Y_{i1k} \right) \right] \\
&= \frac{4}{n^2} \text{Var} \left[\sum_{i \in I_1} X_i \left(\sum_{k \in K_{i_2}} (\delta + \epsilon_{i2k}) - \sum_{k \in K_{i_1}} \epsilon_{i1k} \right) \right. \\
&\quad \left. - \sum_{i \in I_1} (1 - X_i) \left(\sum_{k \in K_{i_2}} \epsilon_{i2k} - \sum_{k \in K_{i_1}} \epsilon_{i1k} \right) \right] \\
&= \frac{4}{n^2} \text{Var} \sum_{i \in I_1} (2X_i - 1) \left(\sum_{k \in K_{i_2}} \epsilon_{i2k} - \sum_{k \in K_{i_1}} \epsilon_{i1k} \right) \\
&= \frac{4}{n^2} \sum_{i \in I_1} \left(\sum_{k \in K_{i_2}} \sigma^2 + \sum_{k \in K_{i_1}} \sigma^2 \right) \\
&= \frac{8\sigma^2}{n}
\end{aligned}$$