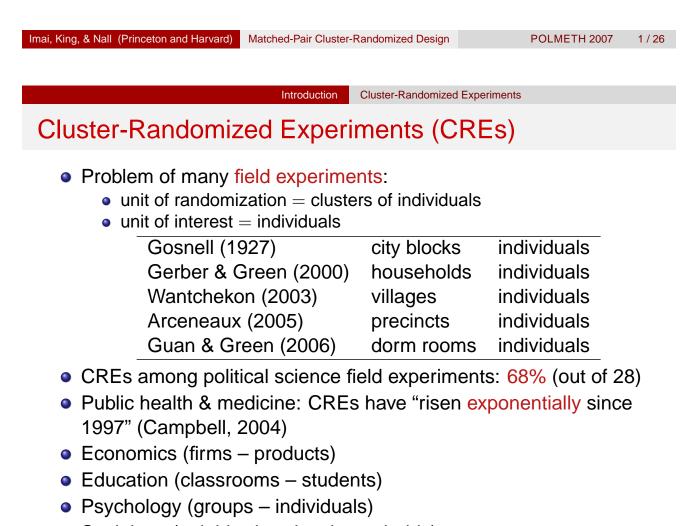
The Essential Role of Pair Matching in Cluster-Randomized Experiments, with Application to the Mexican Universal Health Insurance Evaluation

> Kosuke Imai Princeton University Gary King Clayton Nall Harvard University

> > July 19, 2007



Sociology (neighborhoods – households)

Design and Analysis of CREs

- Cluster randomization \rightarrow loss of efficiency & specialized methods
- Prop. of polisci CREs which completely ignore the design: $\approx 50\%$
- Prop. of polisci CREs which use design-based analysis: 0%
- Prop. of polisci CREs which make more assumptions than necessary: 100%
- Matched-Pair Designs (MPDs) to improve efficiency:
 - Pair clusters based on the similarity of background characteristics
 Within each pair, randomly assign one cluster to the treatment group and the other to the control group
- Use of MPDs in CREs:
 - Prop. of public health CREs: $\approx 50\%$ (Varnell *et al.*, 2004)
 - Prop. of polisci CREs: 0%

Imai, King, & Nall (Princeton and Harvard)	Matched-Pair Cluster-Randomized Design	POLMETH 2007	3 / 26

Methodological Recommendations Against MPDs

Introduction

- "Analytical limitations" of MPDs (Klar and Donner, 1997):
 - restriction of prediction models to cluster-level baseline risk factors

Design and Analysis in Practice

- inability to test for homogeneity of causal effects across clusters
- difficulties in estimating the intracluster correlation coefficient
- In 10 or fewer pairs, MPDs can lose power (Martin et al. 1993)
- Echoed by other researchers and clinical standard organizations
- These claims are all unfounded!
- No formal definition of causal effects to be estimated
- No formal evaluation of the existing estimators for MPDs

Contributions of Our Paper

• Conclusion: pair-matching should be used whenever feasible

- MPDs improve bias, efficiency, and power
- Not pairing = throwing away one's data!
- Show that "analytical limitations" do not exist or are irrelevant
- Show that power calculations rely on unrealistic assumptions
- Existing estimator is based on a highly restrictive model
- Formally define causal quantities of interest
- Propose new simple design-based estimators and s.e.'s
- Offer power and sample size calculations
- Extend the estimator to CREs with unit-level noncompliance
- Clarify the assumptions about interference

Imai, King, & Nall (Princeton and Harvard)	Matched-Pair Cluster-Randomized Design	POLMETH 2007	5 / 26

Evaluation of the Mexican Universal Health Insurance Program

Running Example: Seguro Popular de Salud (SPS)

- Evaluation of the Mexican universal health insurance program
- Aim: "provide social protection in health to the 50 million uninsured Mexicans" (Frenk *et al.*, 2003)
- A key goal: reduce out-of-pocket health expenditures
- Sounds obvious but not easy to achieve in developing countries
- Individuals must affiliate in order to receive SPS services
- 12,824 "health clusters"
- 100 clusters nonrandomly chosen for randomized evaluation
- Pairing based on population, socio-demographics, poverty, education, health infrastructure etc. (King *et al.*, 2007)
- "Treatment clusters": encouragement for people to affiliate
- Data: aggregate characteristics, surveys of 32,000 individuals

Causal Quantities of Interest

			Units within	
Qua	antities	Clusters	Clusters	Inferential Target
ψ_{S}	SATE	Observed	Observed	Observed sample
$\psi_{m{C}}$	CATE	Observed	Sampled	Population within observed clusters
$\psi_{\mathcal{U}}$	UATE	Sampled	Observed	Observable units within pop. of clusters
ψ_{P}	PATE	Sampled	Sampled	Population

- Sample Average Treatment Effect (SATE): $\psi_{S} \equiv \mathbb{E}_{S}(Y(1) - Y(0)) = \frac{1}{n} \sum_{k=1}^{m} \sum_{j=1}^{2} \sum_{i=1}^{n_{jk}} (Y_{ijk}(1) - Y_{ijk}(0))$
- Cluster Average Treatment Effect (CATE): $\psi_{C} \equiv \mathbb{E}_{\mathcal{C}}(Y(1) - (0)) = \frac{1}{N} \sum_{k=1}^{m} \sum_{j=1}^{2} \sum_{i=1}^{N_{jk}} (Y_{ijk}(1) - Y_{ijk}(0))$
- Unit Average Treatment Effect (UATE): $\psi_U \equiv \mathbb{E}_{\mathcal{U}}(Y(1) Y(0))$
- Population Average Treatment Effect (PATE): $\psi_P \equiv \mathbb{E}_{\mathcal{P}}(Y(1) Y(0))$

Imai, King, & Nall (Princeton and Harvard)	Matched-Pair Cluster-Randomized Design	POLMETH 2007	7 / 26

Matched-Pair, Cluster-Randomized Experiments Quantities of Interest

Interference in CREs under MPDs

- What is *interference*?: one's (potential) outcome depends on treatment assignment of others as well as her own
- Disease contagion, social pressure, help from families and friends
- Among individuals in the same cluster
- Between clusters in different pairs
- Between treatment and control clusters in the same pair
- (1) is allowed in CREs as a consequence of treatment
- (1) is not allowed in individual randomized trials
- (2) is not allowed in CREs under MPDs
- (3) is allowed:
 - with-interference causal effects
 - no-interference causal effects

Design-based Analysis of CREs under MPDs

- Existing Model-based approach: assume DGP for observed data
- Randomness comes from the assumed model
- If the model is correct, inference is valid
- If the model is incorrect, inference is invalid
- Our Design-based approach (Fisher and Neyman)
- Randomness comes from:
 - randomization of treatment assignment
 - random sampling of clusters and units within clusters
- Avoids modeling assumptions

Imai, King, & Nall (Princeton and Harvard)	Matched-Pair Cluster	-Randomized Design	POLMETH 2007	9 / 26	
	Estimators	Definitions			
Definition of Estimators					

- "A good estimator for one ATE is automatically a good estimator for the other" (Imbens, 2004)
- Does not apply to CREs
- Our estimator:

$$\hat{\psi}(w_k) \equiv \frac{1}{\sum_{k=1}^{m} w_k} \sum_{k=1}^{m} w_k \left\{ Z_k \left(\frac{\sum_{i=1}^{n_{1k}} Y_{i1k}}{n_{1k}} - \frac{\sum_{i=1}^{n_{2k}} Y_{i2k}}{n_{2k}} \right) + (1 - Z_k) \left(\frac{\sum_{i=1}^{n_{2k}} Y_{i2k}}{n_{2k}} - \frac{\sum_{i=1}^{n_{1k}} Y_{i1k}}{n_{1k}} \right) \right\}$$

	SATE	CATE	UATE	PATE
Point estimator	$\hat{\psi}(n_{1k}+n_{2k})$	$\hat{\psi}(N_{1k}+N_{2k})$	$\hat{\psi}(n_{1k}+n_{2k})$	$\hat{\psi}(N_{1k}+N_{2k})$
Variance	$\operatorname{Var}_{\boldsymbol{a}}(\hat{\psi})$	$\operatorname{Var}_{au}(\hat{\psi})$	$\operatorname{Var}_{ap}(\hat{\psi})$	$\operatorname{Var}_{aup}(\hat{\psi})$
Identified	no	no	YES	YES

Bias

• Bias expression for SATE ($E_a{\{\hat{\psi}(n_{1k} + n_{2k})\}} - \psi_S$):

$$\frac{1}{n}\sum_{k=1}^{m}\sum_{j=1}^{2}\left\{\left(\frac{n_{1k}+n_{2k}}{2}-n_{jk}\right)\sum_{i=1}^{n_{jk}}\frac{Y_{ijk}(1)-Y_{ijk}(0)}{n_{jk}}\right\}$$

Conditions for unbiasedness:

- **(1)** Exact match on sample cluster sizes: $n_{1k} = n_{2k}$ for all k
- 2 Exact match on within-cluster SATEs:

$$\sum_{i=1}^{n_{1k}} (Y_{i1k}(1) - Y_{i1k}(0)) / n_{1k} = \sum_{i=1}^{n_{2k}} (Y_{i2k}(1) - Y_{i2k}(0)) / n_{2k}$$
 for all k

- Match on cluster sizes and important covariates!
- Bias for CATE $(E_{au}(\hat{\psi}(N_{1k} + N_{2k})) \psi_C)$:

$$\frac{1}{N}\sum_{k=1}^{m}\sum_{j=1}^{2}\left\{\left(\frac{N_{1k}+N_{2k}}{2}-N_{jk}\right)E_{u}(Y_{ijk}(1)-Y_{ijk}(0))\right\}$$

● Additional condition for UATE & PATE: cluster sizes ⊥ ATEs

Estimators

Imai, King, & Nall (Princeton and Harvard)	Matched-Pair Cluster-Randomized Design	POLMETH 2007	11 / 26
--	--	--------------	---------

Bias

Existing Estimator

- Estimator based on harmonic mean weights and associated variance estimator (Donner, 1987): $w_k = n_{1k}n_{2k}/(n_{1k} + n_{2k})$
- No formal justification in the literature (weighted one-sample *t*-test)
- Assumed unrealistic unit-level model: for t = 0, 1,

$$\mathsf{Y}_{ijk}(t) \stackrel{\mathrm{i.i.d.}}{\sim} \mathsf{N}(\mu_t, \sigma)$$

Normality

- I.I.D. across units within each cluster, and across clusters & pairs
- Equal variances for potential outcomes
- Under the model, the estimator is UMVUE
- The model assumes there is no point of matching to begin with!
- Unless these assumptions are met, the estimator is invalid

Estimators Variance

Variance Identification and Estimation

• Our general unbiased variance estimator for $\hat{\psi}(\tilde{w}_k)$:

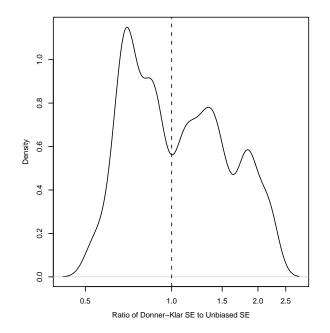
$$\hat{\sigma}(\tilde{w}_{k}) \equiv \frac{m}{(m-1)n^{2}} \sum_{k=1}^{m} \left[\tilde{w}_{k} \left\{ Z_{k} \left(\frac{\sum_{i=1}^{n_{1k}} Y_{i1k}}{n_{1k}} - \frac{\sum_{i=1}^{n_{2k}} Y_{i2k}}{n_{2k}} \right) + (1 - Z_{k}) \left(\frac{\sum_{i=1}^{n_{2k}} Y_{i2k}}{n_{2k}} - \frac{\sum_{i=1}^{n_{1k}} Y_{i1k}}{n_{1k}} \right) \right\} - \frac{n\hat{\psi}(\tilde{w}_{k})}{m} \right]^{2}$$

where \tilde{w}_k is the normalized weights, $\tilde{w}_k \equiv nw_k / \sum_{k=1}^m w_k$

- $E_a(\hat{\sigma}(\tilde{w}_k))$ is the sharp upper bound of SATE variance
- $E_{au}(\hat{\sigma}(\tilde{w}_k))$ is the sharp upper bound of CATE variance
- $E_{ap}(\hat{\sigma}(\tilde{w}_k))$ is UATE variance
- $E_{apu}(\hat{\sigma}(\tilde{w}_k))$ is PATE variance

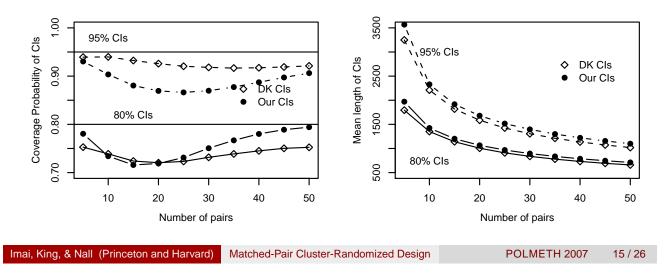
Imai, King, & Nall (Princeton and Harvard)	Matched-Pair Cluster	-Randomized Design	POLMETH 2007	13 / 26	
	Estimators	SPS Evaluation			
Illustration using SPS Data					

• The direction of bias for DK's s.e. is indeterminate: from 3 times larger to 3 times smaller.



Monte Carlo Evidence

- Setup:
 - Use population cluster sizes
 - Out-of-pocket health expenditure variable (peso)
 - Use cluster-specific sample mean and variances as truth
- CATE: ours (bias=0, RMSE=6), DK (bias=21, RMSE=22)
- PATE: confidence interval comparison



Comparing Matched-Pair and Other Designs Efficiency

Relative Efficiency of MPDs

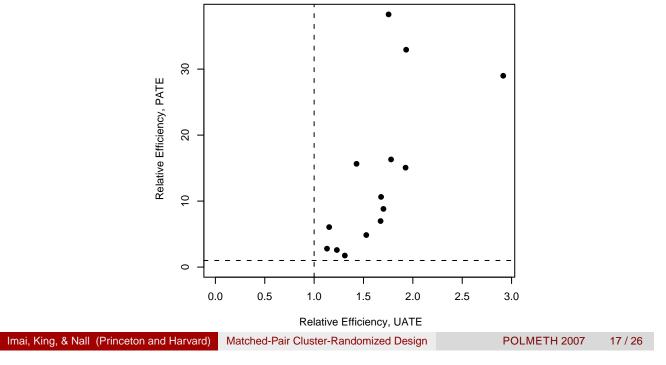
- Compare with Completely-Randomized Designs (CRDs)
- Relative efficiency of MPDs over CRDs:

$$\frac{\operatorname{Var}_{ac}(\hat{\tau}(\tilde{w}_{j}))}{\operatorname{Var}_{ap}(\hat{\psi}(\tilde{w}_{k}))} = \left\{ 1 - \frac{2\operatorname{Cov}_{p}(\tilde{w}_{k}\overline{Y_{jk}(1)}, \tilde{w}_{k}\overline{Y_{j'k}(0)})}{\sum_{t=0}^{1}\operatorname{Var}_{p}(\tilde{w}_{k}\overline{Y_{jk}(t)})} \right\}^{-1}$$

- Greater (positive) correlation within pair \rightarrow greater efficiency
- MPDs vs. Stratified Designs (CRDs within pre-defined strata)
- MPDs can improve efficiency within strata

Illustration Using SPS Data

- UATE: MPDs are between 1.1 and 2.9 times more efficient
- PATE: MPDs are between 1.8 and 38.3 times more efficient!



Comparing Matched-Pair and Other Designs Power

Power and Sample Size Calculations under MPDs

- Statistical power: prob. of rejecting the null when the null is false
- Assume equal cluster size for planning purposes
- UATE $(H_0: \psi_U = 0 \text{ and } H_A: \psi_U = \psi)$:

$$1 + \mathcal{T}_{m-1}(-t_{m-1,\alpha/2} \mid d_U\sqrt{m}) - \mathcal{T}_{m-1}(t_{m-1,\alpha/2} \mid d_U\sqrt{m}),$$

where $d_U \equiv \psi / \sqrt{\operatorname{Var}(D_k)}$.

• PATE ($H_0: \psi_P = 0$ and $H_A: \psi_U = \psi$):

$$1 + \mathcal{T}_{m-1}\left(-t_{m-1,\alpha/2} \mid \frac{d_P\sqrt{m}}{\sqrt{1+\pi/\bar{n}}}\right) - \mathcal{T}_{m-1}\left(t_{m-1,\alpha/2} \mid \frac{d_P\sqrt{m}}{\sqrt{1+\pi/\bar{n}}}\right)$$

where $d_P \equiv \psi / \sqrt{\operatorname{Var}_p \{E_u(D_k)\}}$ and π is the ratio of between-cluster and within-cluster variances.

• Sample size calculation: what sample size do I need in order to achieve a certain level of power under a particular H_A ?

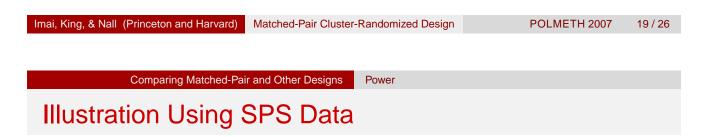
Power

Relative Power of MPDs

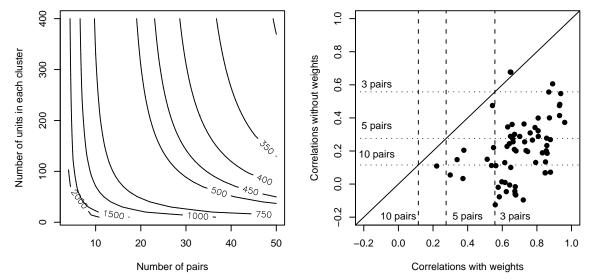
- When the number of pairs is fewer than 10, "the matched design will probably have less power than the unmatched design due to the loss of degrees of freedom" (Martin *et al.* 1993).
- Critical assumption: equal cluster sizes across all clusters
- In typical CREs, cluster sizes are different and observed
- Can match on cluster sizes:

 $\operatorname{Corr}_{\rho}(\tilde{w}_{k} \overline{Y_{jk}(1)}, \tilde{w}_{k} \overline{Y_{j'k}(0)}) \geq \operatorname{Corr}_{\rho}(\overline{Y_{jk}(1)}, \overline{Y_{j'k}(0)})$

- Efficiency gain of MPDs is greater in CREs than in individual randomized experiments
- Thus, power of MPDs is also greater



- power=0.8 and size=0.95
- Sample size calculation using out-of-pocket health care expenditure
- Comparison of within-pair correlations with and without weights



Unit-Level Noncompliance in CREs

- No interference between units within (and across) clusters
 - one's decision to comply doesn't depend on others' treatment assignment
 - one's potential outcomes don't depend on others' treatment assignment and receipt
- Always-takers, compliers, and never-takers (Angrist *et al.* 1996)
- In SPS evaluation, the wealthy are never-takers (56%)
- Always-takers are those who travel and sign up for SPS (7%)
- No defier (monotonicity)
- Zero ITT effect on non-compliers (exclusion restriction)
- Qol: Complier Average Causal Effect or CACE (for SATE, CATE, UATE or PATE)
- We offer a consistent estimator and its valid s.e.

Imai, King, & Nall (Princeton and Harvard)	Matched-Pair Cluster-Randomized Design	POLMETH 2007	21 / 26

SPS Evaluation

Empirical Analysis of SPS Data

- Average causal effects of SPS on the prob. of a household suffering from catastrophic health expenditures
- More than 30% of annual post-subsistence income (10% of all households)
- Its reduction is a major aim of SPS
- Predictions based on cluster-level baseline risk are straightforward
- Testing homogeneity of causal effects across pairs is also easy
- Loss of a cluster in follow-up results in loss of only one pair

		SATE	CATE	UATE	PATE
All	ITT	014 (≤ .007)	<i>−.</i> 023 (≤ .015)	014 (.007)	023 (.015)
	CACE	038 (≤ .018)	$064~(\le .024)$	038 (.018)	064 (.024)
Male-	ITT	016 (≤ .008)	−.025 (≤ .018)	016 (.008)	025 (.018)
Headed	CACE	<i>−</i> .042 (≤ .020)	$070~(\le .031)$	042 (.020)	070 (.031)

Concluding Remarks

Concluding Remarks

- Field experiments often require cluster randomization
- Our recommendations: MPDs for CREs
 - Select quantities of interest
 - Identify pre-treatment covariates for matching
 - Pair clusters based on the covariates and cluster sizes
 - Randomize treatment within each pair
 - Use design-based methods to analyze the data
- MPDs are preferred from perspectives of bias, efficiency, & power
- May affect CONSORT, Cochrane Collaboration, Council guidelines, etc.
- Our proposed estimators are design-based and avoid modeling assumptions
- Simple and require no simulation or numerical optimization
- R package experiment available at CRAN

Imai, King, & Nall (Princeton and Harvard)	Matched-Pair Cluster-Randomized Design	POLMETH 2007	23 / 26

Extra Slides Formal Design Definition, Notation, and Assumptions

Definition and Notation of MPDs

- Observed clusters: 2m
- Number of pairs: m
- Number of observed units within the *j*th cluster in the *k*th pair: n_{jk}
- Population size of cluster: N_{ik}
- Total number of observed units: $n = \sum_{k=1}^{m} (n_{1k} + n_{2k})$
- Two clusters within each pair are randomly ordered
- Simple randomization of an indicator variable: Z_k
- $Z_k = 1$ ($Z_k = 0$): first (second) cluster gets treated
- Treatment variables: $T_{1k} = Z_k$ and $T_{2k} = 1 Z_k$
- Potential outcomes for each individual: $Y_{ijk}(T_{ik})$
- Observed outcome: $Y_{ijk} = T_{jk} Y_{ijk}(1) + (1 T_{jk}) Y_{ijk}(0)$
- Cluster randomization: $(Y_{ijk}(1), Y_{ijk}(0)) \perp Z_k$
- For now, consider the intention-to-treat (ITT) analysis

Alternative Estimators

- Unbiased estimator for SATE & UATE (but not for CATE & PATE)
- Problem: not invariant to constant shift
- Variance estimator is also not invariant
- Invariant Estimator with smaller bias
- Exact calculation of variance is impossible
- Standard variance estimator is not invariant

Imai, King, & Nall (Princeton and Harvard)	Matched-Pair Cluster	-Randomized Design	POLMETH 2007	25 / 26		
	Extra Slides	Inference				
Inference under MPDs						

- Many pairs:
 - No additional assumption: central limit theorem
 - $(1 \alpha) \operatorname{Cl}: [\hat{\psi}(\tilde{w}_k) z_{\alpha/2}\sqrt{\hat{\sigma}(\tilde{w}_k)}, \hat{\psi}(\tilde{w}_k) + z_{\alpha/2}\sqrt{\hat{\sigma}(\tilde{w}_k)}]$
- Few pairs, many units:
 - CATE: $\tilde{w}_k D_k$ is normally distributed
 - SATE, UATE, & PATE: $\tilde{w}_k D_k$ is assumed to be normally distributed
 - $(1 \alpha) \operatorname{Cl}: \left[\hat{\psi}(\tilde{w}_k) t_{m-1,\alpha/2}\sqrt{\hat{\sigma}(\tilde{w}_k)}, \ \hat{\psi}(\tilde{w}_k) + t_{m-1,\alpha/2}\sqrt{\hat{\sigma}(\tilde{w}_k)}\right]$
- Few pairs, few units:
 - For all quantities: $\tilde{w}_k D_k$ is assumed to be normally distributed
- No "Behrens-Fisher" problem unlike CREs under completely-randomized designs
- Irrelevance of intracluster correlation coefficient (ICC): "an estimate of ρ [ICC] is required to compute appropriate standard errors for the analyses in question" (Donner 1998).