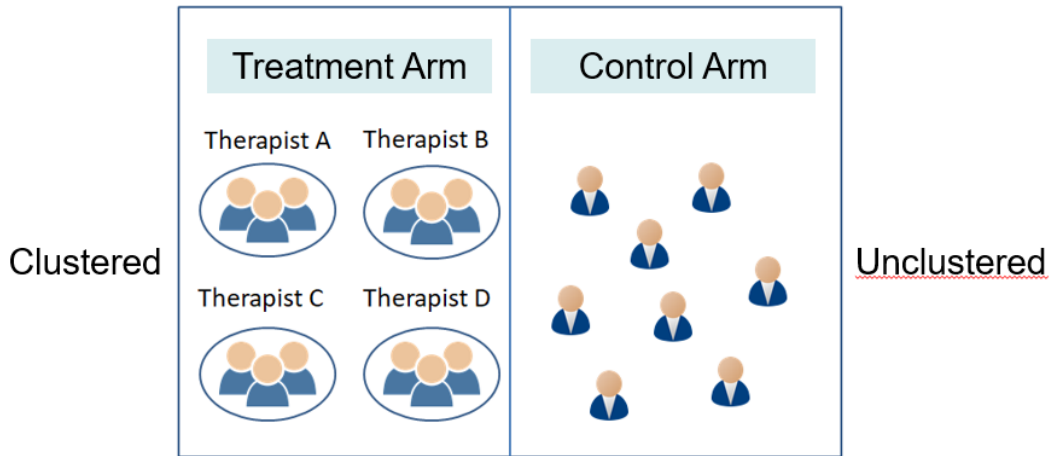


# Estimating Treatment Effects in Partially Clustered Randomized Controlled Trials with Missing Data: Challenges and Solutions

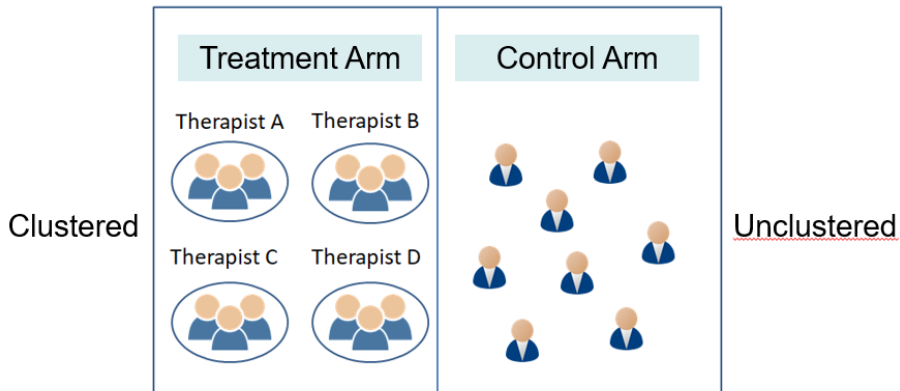
Manshu Yang

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The 2023 M3 Conference  
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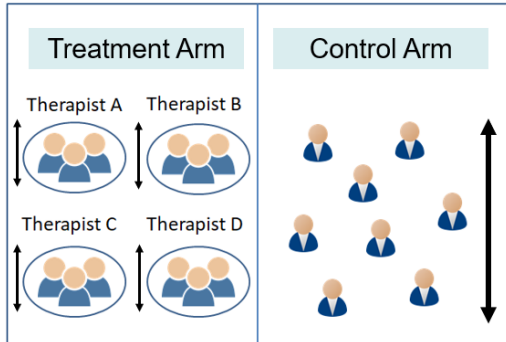
- **Feature 1: Partially Clustered Structure**



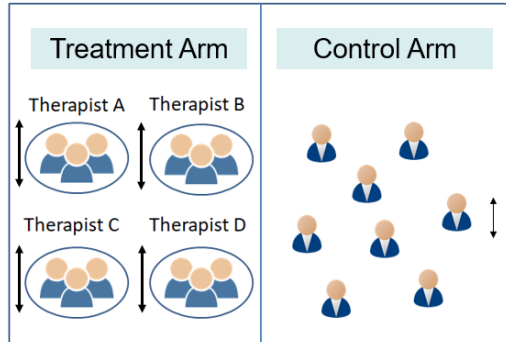
# Three Key Features of Partially Clustered RCTs

- Feature 1: Partially Clustered Structure
- **Feature 2: Heteroscedastic Residual Variances**

Treatment Variance < Control Variance

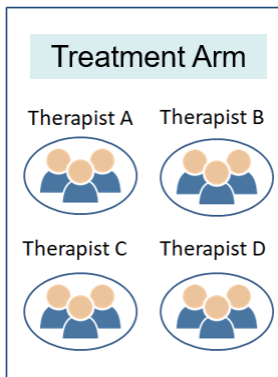


Treatment Variance > Control Variance



# Three Key Features of Partially Clustered RCTs

- Feature 1: Partially Clustered Structure
- Feature 2: Heteroscedastic Residual Variances
- **Feature 3: Small Sample Sizes**
  - fewer than 20 clusters, fewer than 30 persons per cluster



- Methods exist to analyze partially clustered data
  - Baldwin et al., 2011; Bauer et al., 2008; Candlish et al., 2018; Kelcey et al., 2020; Lai and Kwok, 2014; Lee and Thompson, 2005; Lohr et al., 2014; Moerbeek and Wong, 2008; Roberts and Roberts, 2005; Lachowicz et al., 2015; Sterba, 2017; Sterba et al., 2014

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- Missing data are inevitable in partially clustered RCTs
- However... little is known on how to handle missing data in partially clustered RCTs



- Three missing data mechanisms (Rubin, 1976)
  - Missing Completely At Random (MCAR)
  - Missing At Random (MAR)
  - Missing Not At Random (MNAR)
- Current study focuses on: **auxiliary-variable-dependent MAR (A-MAR)**
  - auxiliary variable (AV): not of primary research interest but drives missingness
- Both **outcome** and **covariates** could be incomplete
  - person-level covariates (e.g., age, pretest score)
  - cluster-level covariates (e.g., intervention fidelity)

- Issue 1: How to handle **missing covariates** involving random slopes?
  - maximum likelihood estimation (MLE) may not work
  - standard multiple imputation (joint modeling or chained equations) may not work
  - Recommended: **substantive-model-compatible sequential modeling imputation**
    - **sequential modeling multiple imputation (MI-SM)** (Carpenter and Kenward, 2013; Goldstein et al., 2014; Bartlett et al., 2015; Enders et al., 2020; Lüdtke et al., 2020)
    - **sequential fully Bayesian estimation (SFB)** (Erler et al., 2016; Zhang and Wang, 2017)

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- Issue 2: How to handle **heteroscedastic residual variances**?
  - Recommended: **arm-specific imputation**
    - separate imputations for treatment and control arms (Carpenter and Kenward, 2013; Enders and Gottschall, 2011; Yamaguchi et al., 2020)

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- Issue 3: Do standard missing data handling methods work with **small sample sizes**?

## Key Research Question: Which method performs the best?

- ① **MI-JM-SIM**: simultaneous MI via joint modeling
  - ② **MI-JM-AS**: arm-specific MI via joint modeling
  - ③ **MI-SM-AS**: arm-specific MI via sequential modeling
  - ④ **SFB-NON**: sequential fully Bayesian estimation using non-informative priors
  - ⑤ **SFB-WEAK**: sequential fully Bayesian estimation using weakly-informative priors
- In each Bayesian iteration step:
    - Joint modeling (JM): impute **outcome and covariates together**
      - assuming multivariate normality
    - Sequential modeling (SM): impute **covariates first** then impute outcome
      - imputation model compatible with analysis model

- Level-1 (Within Cluster) Model:

- ANCOVA model with heteroscedastic residual variances

$$Y_{ij} = \beta_{0j} + \beta_{1j}TREAT_{ij} + \beta_{2j}X1_{ij} + e_{ij} \quad (1)$$

$$e_{ij}|(TREAT = 0) \sim N(0, \sigma_{e_0}^2) \quad (2)$$

$$e_{ij}|(TREAT = 1) \sim N(0, \sigma_{e_1}^2) \quad (3)$$

- Level-2 (Between Cluster) Model:

- fixed intercept ( $\beta_{0j}$ ) indicates unclustered control arm
- random slope of  $TREAT$  ( $\beta_{1j}$ ) indicates clustered treatment arm
- effect of  $X1$  on  $Y$  ( $\beta_{2j}$ ) could be fixed or random

$$\beta_{0j} = \gamma_{00} \quad (4)$$

$$\beta_{1j} = \gamma_{10} + \gamma_{11}X2_j + u_{1j} \quad (5)$$

$$\beta_{2j} = \gamma_{20} + u_{2j} \quad or \quad \beta_{2j} = \gamma_{20} \quad (6)$$

- **Primary interest: average treatment effect**  $\gamma_{10}$

- Two auxiliary variables: person-level  $A_1$  and cluster-level  $A_2$
- Missingness in person-level covariate  $X_1$  depends on  $A_1$
- Missingness in cluster-level covariate  $X_2$  depends on  $A_2$
- Missingness in outcome  $Y$  depends on  $A_1 + A_2$

- Factors manipulated:
  - average treatment effect: 0 or 0.8
  - missing data scenario: incomplete  $Y$  and  $X_1$  vs. incomplete  $Y$  and  $X_2$
  - **No. of clusters:**  $c = 4, 8, 16$
  - **cluster size:**  $m = 5, 15, 30$
  - ratio of person-level residual variances between arms:  $\theta = 0.3, 1, 3$
  - % missing: 10% or 30%
  - $X_1$  effect: fixed or random
- 1,000 Replications
- Compared 5 missing data analysis methods:
  - MI-JM-SIM, MI-JM-AS, MI-SM-AS
  - SFB-NON, SFB-WEAK



## Results: Estimating Average Treatment Effect

Fixed X1 effect,  $ATE = 0.8$ , 30% missing

Incomplete Variables	Method	% Relative Bias		
		$\theta = 0.3$	$\theta = 1$	$\theta = 3$
Y and X1	MI-JM-SIM	-6.8	-1.5	7.8
	MI-JM-AS	-0.5	-0.8	-0.7
	MI-SM-AS	0.2	-0.1	-0.1
	SFB-NON	-5.1	0.6	<b>11.2</b>
	SFB-WEAK	-5.9	-0.2	<b>10.6</b>
Y and X2	MI-JM-SIM	-9.6	-4.5	4.7
	MI-JM-AS	-2.7	-1.8	-1.7
	MI-SM-AS	-3.5	-2.4	-2.4
	SFB-NON	-7.7	-0.7	9.6
	SFB-WEAK	-8.5	-1.7	8.7

- $\theta$  = ratio of person-level residual variances between arms

## Results: Estimating Cluster-Level Residual Variance

ATE = 0.8, 30% missing

Incomplete Variables	Method	% Relative Bias					
		Fixed X1, $c = 4$			Fixed X1, $c = 8$		
		$m=5$	15	30	$m=5$	15	30
Y and X1	MI-JM-SIM	<b>24.8</b>	8.4	6.4	<b>14.3</b>	1	-0.8
	MI-JM-AS	<b>24.7</b>	8.9	6.9	<b>14.9</b>	1.8	-0.4
	MI-SM-AS	<b>204.8</b>	<b>27.6</b>	<b>12.8</b>	<b>74.8</b>	9.9	1.7
	SFB-NON	<b>545.4</b>	<b>477.8</b>	<b>461.8</b>	<b>216.9</b>	<b>166.8</b>	<b>154.5</b>
	SFB-WEAK	<b>161.1</b>	<b>146.6</b>	<b>153.1</b>	<b>31</b>	<b>29</b>	<b>31.3</b>
Y and X2	MI-JM-SIM	<b>17.4</b>	2.8	5.3	8	0.2	0.9
	MI-JM-AS	<b>24.3</b>	7.5	9	<b>11.6</b>	5.1	5.2
	MI-SM-AS	<b>185</b>	<b>28.6</b>	<b>18.9</b>	<b>123.6</b>	<b>20.5</b>	<b>12.8</b>
	SFB-NON	<b>536.1</b>	<b>473.2</b>	<b>460.3</b>	<b>212.4</b>	<b>168.4</b>	<b>159.1</b>
	SFB-WEAK	<b>132.4</b>	<b>109.6</b>	<b>116.6</b>	<b>19.6</b>	<b>20.8</b>	<b>25.3</b>

- $c$  = No. of clusters
- $m$  = cluster size

## Results: Estimating Cluster-Level Residual Variance (Cont.)

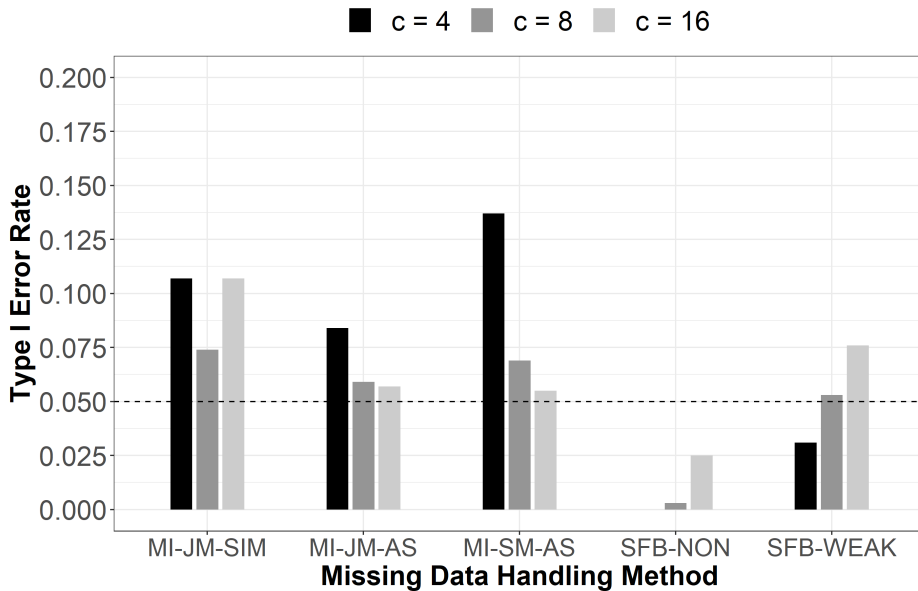
$ATE = 0.8$ , 30% missing

Incomplete Variables	Method	% Relative Bias					
		Fixed X1, $c = 16$			Random X1, $c = 16$		
		m=5	15	30	m=5	15	30
Y and X1	MI-JM-SIM	8.5	1.7	0.6	<b>-58.1</b>	<b>-70.7</b>	<b>-70.5</b>
	MI-JM-AS	8	2.6	1	<b>-51.9</b>	<b>-68.9</b>	<b>-69.6</b>
	MI-SM-AS	<b>21.3</b>	6.3	1.8	<b>39.8</b>	7.4	-0.3
	SFB-NON	<b>106.2</b>	<b>75.7</b>	<b>67.4</b>	<b>170.9</b>	<b>91.1</b>	<b>70.4</b>
	SFB-WEAK	3.5	<b>10</b>	<b>10.8</b>	<b>37.2</b>	8.9	7.9
Y and X2	MI-JM-SIM	0.8	-1.3	0.1	<b>-46.4</b>	<b>-56.8</b>	<b>-56.9</b>
	MI-JM-AS	4.5	2.9	4.1	<b>-43</b>	<b>-56</b>	<b>-56.4</b>
	MI-SM-AS	<b>22.4</b>	9.4	7.9	<b>32.8</b>	3.8	-3
	SFB-NON	<b>102.4</b>	<b>75.4</b>	<b>69.2</b>	<b>169.3</b>	<b>95</b>	<b>76.3</b>
	SFB-WEAK	-5.4	4.3	7.6	<b>38.5</b>	<b>17.7</b>	<b>16.1</b>

- $c$  = No. of clusters
- $m$  = cluster size

# Results: Type I Error for Detecting Treatment Effect

fixed  $X_1$  effect, 30% missing,  $m = 30$ ,  $\theta = 0.3$



- Which methods perform the best in handling A-MAR data in partially clustered RCT?

### **Arm-specific MI methods**

If $X_1$ effect is...	Best Performing Method
Fixed	MI-JM-AS (joint modeling)
Random	MI-SM-AS (sequential modeling)

- Which methods perform the best in handling A-MAR data in partially clustered RCT?

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- Priors may have more influence on sequential modeling MI than joint modeling MI, given very few clusters (4 or 8).

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- MI of the entire sample assuming equal residual variance across arms (MI-JM-SIM) is not recommended.

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- MI of the entire sample assuming equal residual variance across arms (MI-JM-SIM) is not recommended.
- Sequential fully Bayesian approach is not recommended.



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# Thank you !

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