

# Stepped wedge randomised trials

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What an interesting design !

useful

challenging

Mixture of cross-over trial

cluster

longitudinal

Randomized  
clusters  
(or individuals)

C	C	C	C	C	T
C	C	C	C	T	T
C	C	C	T	T	T
C	C	T	T	T	T
C	T	T	T	T	T

Time →

Vertical comparison

Horizontal comparison

Baseline – all C

Final – all T

C	C	T
C	T	T

SW CRT

**Varieties of cluster  
randomized trials**

C
T

Parallel group CRT

C	C
C	T

CRT with baseline

C	T
T	T

CRT with follow-up

## Cross-over cluster randomized trials

C	T
T	C

Cross-over CRT

C	C	T
C	T	C

Cross-over CRT with baseline

# Statistical advantages of SW design

1. Treatment effect is estimated both within and between clusters
2. Effect of between-cluster variability (ICC) is diminished
3. Can investigate the effect of duration of treatment

# Mdege, Taylor et al, J Clin Epidemiol 2011

Review of 25 SW CRTs (studies and protocols)

Statistical analysis (plans) were often unclear / vague / inadequate

7 mentioned hierarchical / multilevel modelling

1 mentioned repeated measures

2 mentioned GEEs

9 “not stated”

**Others:** e.g. t-tests / chi-squared tests / linear or logistic regression, comparing pre- and post-intervention periods

Simple comparison of pre- and post-intervention periods:

**Inadequate!** Need to address:

Clustering

Repeated measures

Confounding by time

Step-by-step assessment of intervention effect:

Helpful initial / exploratory analysis?



# General basic analysis model

$Y_{ijk}$  is continuous outcome for individual  $i$  in cluster  $j$  at step  $k$

## Model for SW cohort CRT (LMM)

$$Y_{ijk} = \alpha + u_j + \beta_k + v_{ij} + \theta T_{ijk} + e_{ijk}$$

where  $T_{ijk} = \begin{cases} 1 & \text{if cluster } j \text{ received treatment at step } k \\ 0 & \text{otherwise} \end{cases}$

$\alpha$ ,  $\beta_k$  and  $\theta$  are fixed effects

$u_j \sim N(0, \sigma_u^2)$  are random cluster effects

$v_{ij} \sim N(0, \sigma_v^2)$  are random individual effects

$e_{ijk} \sim N(0, \sigma_e^2)$  are residual errors

# Adaptations

(1) Binary outcomes:  $Y_{ijk} = 0 / 1$  (GLMM)

$$Y_{ijk} \sim \text{Bin}(1, \pi_{ijk})$$

$$\text{logit}(\pi_{ijk}) = \alpha + u_j + \beta_k + v_{ij} + \theta T_{ijk}$$

(2) No clusters  $j$  (SW individually randomized trial)

$$Y_{ik} = \alpha + \beta_k + v_i + \theta T_{ik} + e_{ik}$$

(3) SW repeated cross-sectional CRT

$$Y_{ijk} = \alpha + u_j + \beta_k + \theta T_{jk} + e_{ijk}$$

# Extensions

Duration m

0	0	0	0	0	1
0	0	0	0	1	2
0	0	0	1	2	3
0	0	1	2	3	4
0	1	2	3	4	5

- (1) Treatment duration:  
(e.g. delayed treatment effect)

Replace  $\theta$  by  $\theta_m$

- (2) Cluster variability  $\sigma_u^2$  depends on T=0/1  
Individual level variability  $\sigma_v^2$  or  $\sigma_e^2$  depends on T=0/1

- (3) Incorporating:

random cluster x time interaction

random cluster x treatment interaction

**Need a statistical analysis plan / explicit statistical model !**

# Analysis strategies

Hierarchical modelling is a natural approach

Cluster-level models are an option, especially for equally sized clusters

GEEs not good for multiple levels of clustering, or small numbers of clusters?

**Advantages of a Bayesian / MCMC approach:**

- propagates full uncertainty of variance components

- can use informative priors for ICC

- flexible framework for modelling extensions

# Other problems

Missing data / attrition

Survival outcomes: differential attrition

Non-compliance of individuals / clusters

Contamination

Lack of blinding

Use of cluster / individual level covariates

Adjusting for baseline

Model checking

# Conclusions

Write down the statistical analysis plan

Give principal statistical analysis model explicitly

Mention proposed extensions / sensitivity analyses

Base design / power calculation on principal statistical analysis model (analytically / by approximation / by simulation)