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Supporting research to improve the lives of young people

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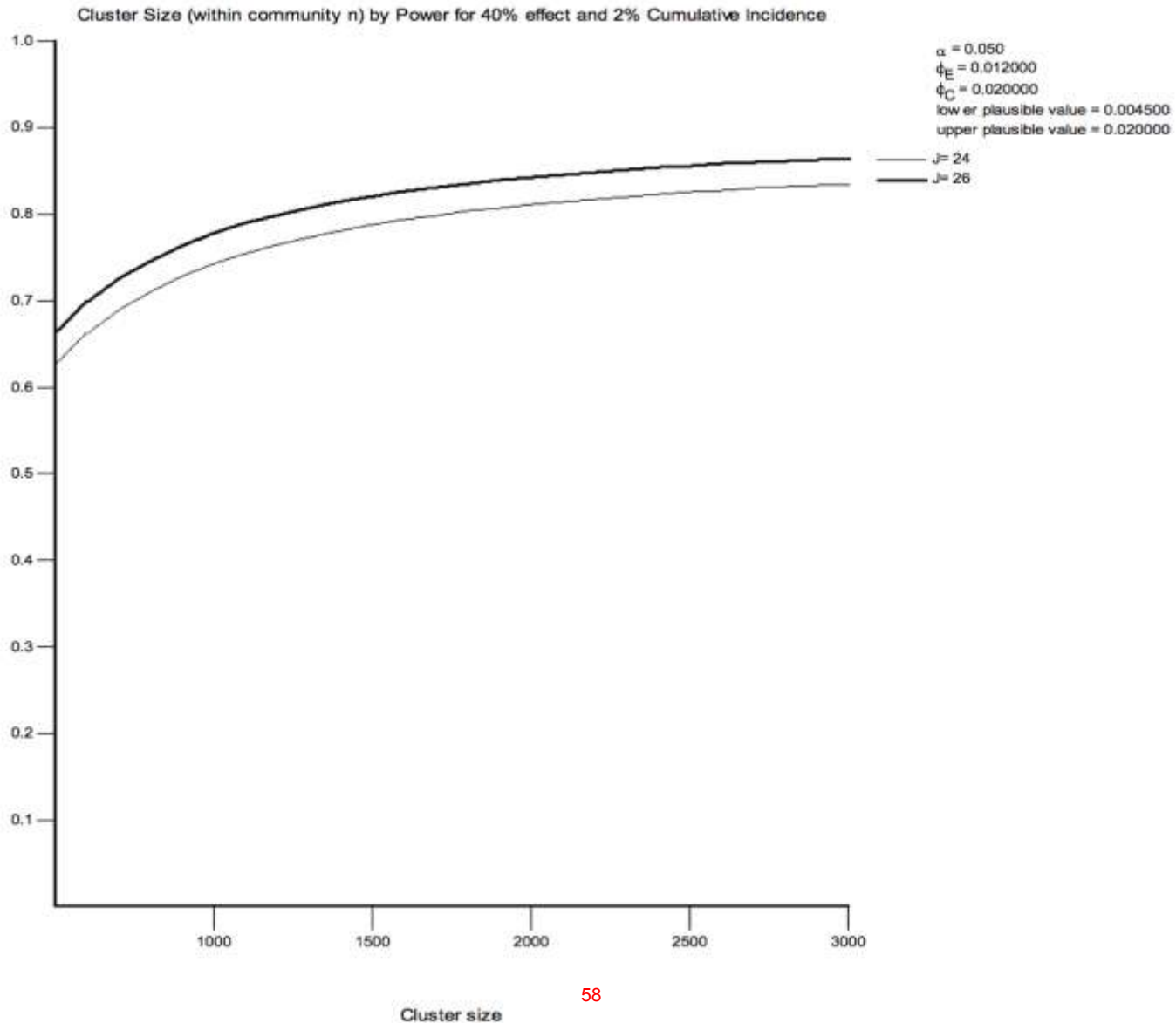
Consultation and Software Tools

We support a consultation service and software to aid in the design of group-randomized studies. The consultation service can also be used for help with assessing the reliability and validity of measures of social settings.

- • Consultation Service
- • Optimal Design Software

Consultation on Design of Group-Randomized Studies
The William T. Grant Foundation, in collaboration with Stephen Raudenbush and his colleagues, supports a free consultation service. The team encourages researchers, funders, and policymakers to send questions about the design of group-randomized studies of interventions designed to promote the development of youth between ages 8-25, and/or the assessment of reliability and validity of measures of social settings. Designs not involving randomization of groups or measures of social settings are beyond the scope of this service.

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Optimal Design Software

Cluster Size (within community n) by Power for 40% effect and 2% Cumulative Incidence

$\alpha = 0.050$
$\phi_E = 0.012000$
$\phi_C = 0.020000$
lower plausible value = 0.004500
upper plausible value = 0.020000

J= 24
J= 26

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Cluster size

SamClus Software

SAMCLUS v1.0

Sample size required in each group without clustering: 2021

Mean cluster size: 5000

ICC: .005

Smallest cluster size expected: 4500

Largest cluster size expected: 6000

SAMCLUS OUTPUT

Design effect: 26.135625

Number of individuals required per group: 52820.098125

Number of clusters required per group: 10.564019625

Analyse

Next calculation

Create Log File

Cancel

SampClus in Stata

```
. sampsi .02 .01, power(.8) onesided

Estimated sample size for two-sample comparison of proportions

Test Ho: p1 = p2, where p1 is the proportion in population 1
                  and p2 is the proportion in population 2
Assumptions:

        alpha =   0.0500  (one-sided)
        power =   0.8000
           p1 =   0.0200
           p2 =   0.0100
        n2/n1 =   1.00

Estimated required sample sizes:

           n1 =     2021
           n2 =     2021

. sampclus, obsclus(5000) rho(.005)

Sample Size Adjusted for Cluster Design

   n1 (uncorrected) = 2021
   n2 (uncorrected) = 2021

   Intraclass correlation    = .005

   Average obs. per cluster  = 5000
   Minimum number of clusters = 22


   Estimated sample size per group:

   n1 (corrected) = 52536
   n2 (corrected) = 52536
```

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Hayes Equations in R

```
[R.app GUI 1.31 (5537) i386-apple-darwin9.8.0]

[Workspace restored from /Users/echarlebois/.RData]

> get_clusters_matched_proportions <- function(p0, p1, k, m, za=1.96, zb=0.84) { 2 + (za + zb)^2 * (((p0*(1-p0)/m) + (p1*(1-p1)/m) + k^2 * (p0^2 + p1^2))/ (p0 - p1)^2) }
>
> get_clusters_matched_rates <- function(l0, l1, k, y, za=1.96, zb=0.84) { 2 + (za + zb)^2 * (((l0 + l1)/y) + k^2 * (l0^2 + l1^2) / (l0 -l1)^2) }
>
> get_clusters_unmatched_proportions <- function(p0, p1, k0, k1, m, za=1.96, zb=0.84) { 1 + (za + zb)^2 * (((p0*(1-p0)/m) + (p1*(1-p1)/m) + (k0^2 * p0^2 + k1^2 * p1^2))/ (p0 -
p1)^2) }
>
> get_clusters_unmatched_rates <- function(l0, l1, k0, k1, y, za=1.96, zb=0.84) { 1 + (za + zb)^2 * (((l0 + l1)/y) + (k0^2 * l0^2 + k1^2 * l1^2) / (l0 -l1)^2) }
>
>
> get_clusters_matched_proportions(.02,.01,.5,1000)
[1] 14.1128
>
> kseq<- seq(0,.55,by=.05)
> i<-0
> cluster<-1:11
> for (thisk in kseq) {
+    cluster[i]<-get_clusters_matched_proportions(.02,.01,thisk,1000)
+    i<-i+1
+    }
> kseq
 [1] 0.00 0.05 0.10 0.15 0.20 0.25 0.30 0.35 0.40 0.45 0.50 0.55
> cluster
 [1]  4.4108  4.7048  5.1948  5.8808  6.7628  7.8408  9.1148 10.5848 12.2508 14.1128 16.1708
>
```

Matched Pair Cluster Randomized Trial Cluster Sample Sizes

HIV Incidence in Control Arm	HIV Incidence in Intervention Arm	Coefficient of Variation Km	Cluster Size @ 80% Power	Total Sites
0.02	0.01	0	4.4108	10
0.02	0.01	0.05	4.7048	10
0.02	0.01	0.1	5.1948	12
0.02	0.01	0.15	5.8808	12
0.02	0.01	0.2	6.7628	14
0.02	0.01	0.25	7.8408	16
0.02	0.01	0.3	9.1148	20
0.02	0.01	0.35	10.5848	22
0.02	0.01	0.4	12.2508	26
0.02	0.01	0.45	14.1128	30
0.02	0.01	0.5	16.1708	34
0.03	0.015	0	3.6268	8
0.03	0.015	0.05	3.9208	8
0.03	0.015	0.1	4.4108	10
0.03	0.015	0.15	5.0968	12
0.03	0.015	0.2	5.9788	12
0.03	0.015	0.25	7.0568	16
0.03	0.015	0.3	8.3308	18
0.03	0.015	0.35	9.8008	20
0.03	0.015	0.4	11.4668	24
0.03	0.015	0.45	13.3288	28
0.03	0.015	0.5	15.3868	32
0.01	0.005	0	6.7628	14
0.01	0.005	0.05	7.0568	16
0.01	0.005	0.1	7.5468	16
0.01	0.005	0.15	8.2328	18
0.01	0.005	0.2	9.1148	20
0.01	0.005	0.25	10.1928	22
0.01	0.005	0.3	11.4668	24
0.01	0.005	0.35	12.9368	26
0.01	0.005	0.4	14.6028	30
0.01	0.005	0.45	16.4648	34
0.01	0.005	0.5	18.5228	38

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Simulation

- Using simulation to predict likely ranges of clustering effects

- Varying cluster effects, contamination, unmeasured external influences

Learning Objectives

Hopefully you now have knowledge of:

- a basic understanding of cluster randomized trials,

- what are the big issues in designing and analyzing CRTs, and

- where do you go to learn more and get the software tools you need to do sample size planning for CRTs.

Discussions

- Your experiences with Cluster Randomized Trials

- Other resources and experts

- Clarifications

- Getting copies of the resource items and locations

Thank You

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