power oneproportion, cluster — Power analysis for a one-sample proportion test, CRD

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Description

`power oneproportion, cluster` computes the number of clusters, cluster size, power, or target proportion for a one-sample proportion test in a cluster randomized design (CRD). It computes the number of clusters given cluster size, power, and the values of the null and alternative proportions. It also computes cluster size given the number of clusters, power, and the values of the null and alternative proportions. Alternatively, it computes power given the number of clusters, cluster size, and the values of the null and alternative proportions, or it computes the target proportion given the number of clusters, cluster size, power, and the null proportion. See [PSS] **power oneproportion** for a general discussion of power and sample-size analysis for a one-sample proportion test. Also see [PSS] **power** for a general introduction to the `power` command using hypothesis tests.

Quick start

Compute number of clusters for two-sided test of H_0: $\pi = 0.2$ versus H_a: $\pi \neq 0.2$ with null proportion $p_0 = 0.2$, alternative proportion $p_a = 0.1$, and cluster size of 5, using default intraclass correlation of 0.5, power of 0.8, and significance level $\alpha = 0.05$

```
power oneproportion 0.2 0.1, m(5)
```

As above, but with an intraclass correlation of 0.7

```
power oneproportion 0.2 0.1, m(5) rho(0.7)
```

As above, but the cluster size varies with a coefficient of variation of 0.6

```
power oneproportion 0.2 0.1, m(5) rho(0.7) cvcluster(0.6)
```

Compute cluster size when 52 clusters are sampled:

```
power oneproportion 0.2 0.1, k(52)
```

Power for 52 clusters with cluster size of 5

```
power oneproportion 0.2 0.1, k(52) m(5)
```

Power for 20, 30, 40, and 50 clusters

```
power oneproportion 0.2 0.1, k(20(10)50) m(5)
```

As above, but display results in a graph of power versus number of clusters

```
power oneproportion 0.2 0.1, k(20(10)50) m(5) graph
```

Effect size and target proportion for $p_0 = 0.2$ with 40 clusters of size 5, power of 0.9, and $\alpha = 0.01$, and default direction `upper`

```
power oneproportion 0.2, k(40) m(5) power(0.9) alpha(0.01)
```

Menu

Statistics > Power and sample size

Syntax

Compute number of clusters

```
power oneproportion p0 pa , {m(numlist) | n(numlist) cluster} [options]
```

Compute cluster size

```
power oneproportion p0 pa , k(numlist) [options]
```

Compute power

```
power oneproportion p0 pa , k(numlist) {m(numlist) | n(numlist)} [options]
```

Compute effect size and target proportion

```
power oneproportion p0 , k(numlist) {m(numlist) | n(numlist)} power(numlist)
    [options]
```

where p_0 is the null (hypothesized) proportion or the value of the proportion under the null hypothesis and p_a is the alternative (target) proportion or the value of the proportion under the alternative hypothesis. p_0 and p_a may each be specified either as one number or as a list of values in parentheses (see **[U] 11.1.8 numlist**).

options	Description
Main	
`cluster`	perform computations for a CRD; implied by `k()` or `m()`
* `alpha(`*numlist*`)`	significance level; default is `alpha(0.05)`
* `power(`*numlist*`)`	power; default is `power(0.8)`
* `beta(`*numlist*`)`	probability of type II error; default is `beta(0.2)`
* `k(`*numlist*`)`	number of clusters
* `m(`*numlist*`)`	cluster size
* `n(`*numlist*`)`	number of observations
`nfractional`	allow fractional number of clusters, cluster size, and sample size
* `diff(`*numlist*`)`	difference between the alternative proportion and the null proportion, $p_a - p_0$; specify instead of the alternative proportion p_a
* `rho(`*numlist*`)`	intraclass correlation; default is `rho(0.5)`
* `cvcluster(`*numlist*`)`	coefficient of variation for cluster sizes
`direction(upper`|`lower)`	direction of the effect for effect-size determination; default is `direction(upper)`, which means that the postulated value of the parameter is larger than the hypothesized value
`onesided`	one-sided test; default is two sided
`parallel`	treat number lists in starred options or in command arguments as parallel when multiple values per option or argument are specified (do not enumerate all possible combinations of values)
Table	
`[no]table[(`*tablespec*`)]`	suppress table or display results as a table; see [PSS] **power, table**
`saving(`*filename* `[, replace])`	save the table data to *filename*; use `replace` to overwrite existing *filename*
Graph	
`graph[(`*graphopts*`)]`	graph results; see [PSS] **power, graph**
Iteration	
`init(`#`)`	initial value for number of clusters, cluster size, or proportion
`iterate(`#`)`	maximum number of iterations; default is `iterate(500)`
`tolerance(`#`)`	parameter tolerance; default is `tolerance(1e-12)`
`ftolerance(`#`)`	function tolerance; default is `ftolerance(1e-12)`
`[no]log`	suppress or display iteration log
`[no]dots`	suppress or display iterations as dots
`notitle`	suppress the title

*Specifying a list of values in at least two starred options, or at least two command arguments, or at least one starred option and one argument results in computations for all possible combinations of the values; see [U] **11.1.8 numlist**. Also see the `parallel` option.

`notitle` does not appear in the dialog box.

where *tablespec* is

column [:*label*] [*column* [:*label*] [...]] [, *tableopts*]

column is one of the columns defined below, and *label* is a column label (may contain quotes and compound quotes).

column	Description	Symbol
`alpha`	significance level	α
`power`	power	$1-\beta$
`beta`	type II error probability	β
`K`	number of clusters	K
`M`	cluster size	M
`N`	number of observations	N
`delta`	effect size	δ
`p0`	null proportion	p_0
`pa`	alternative proportion	p_a
`diff`	difference between the alternative and null proportions	$p_a - p_0$
`rho`	intraclass correlation	ρ
`CV_cluster`	coefficient of variation for cluster sizes	$\mathrm{CV}_{\mathrm{cl}}$
`target`	target parameter; synonym for `pa`	
`_all`	display all supported columns	

Column `beta` is shown in the default table in place of column `power` if specified.

Columns `diff` and `CV_cluster` are shown in the default table if specified.

Options

Main

`cluster` specifies that computations should be performed for a CRD. This option is implied when either the `k()` or `m()` option is specified. It is required if the `n()` option is used to compute the number of clusters.

`alpha()`, `power()`, `beta()`; see [PSS] **power**.

`k(`*numlist*`)` specifies the number of clusters. This option is required to compute the cluster size, power, or effect size.

`m(`*numlist*`)` specifies the cluster size. This option or the `n()` option is required to compute the number of clusters, power, or effect size. `m()` may contain noninteger values. In this case or if the `cvcluster()` option is specified, `m()` represents the average cluster size.

`n(`*numlist*`)` specifies the number of observations. This option or the `m()` option is required to compute the number of clusters, power, or effect size.

`nfractional`; see [PSS] **power**. The `nfractional` option is allowed when computing the number of clusters and cluster size to display fractional (without rounding) values of the number of clusters, cluster size, and sample size.

diff(*numlist*) specifies the difference between the alternative proportion and the null proportion, $p_a - p_0$. You can specify either the alternative proportion p_a as a command argument or the difference between the two proportions in diff(). If you specify diff(#), the alternative proportion is computed as $p_a = p_0 + \#$. This option is not allowed with the effect-size determination.

rho(*numlist*) specifies the intraclass correlation. The default is rho(0.5).

cvcluster(*numlist*) specifies the coefficient of variation for cluster sizes. This option is used with varying cluster sizes.

direction(), onesided, parallel; see [PSS] **power**.

Table

table, table(), notable; see [PSS] **power, table**.

saving(); see [PSS] **power**.

Graph

graph, graph(); see [PSS] **power, graph**. Also see the *column* table for a list of symbols used by the graphs.

Iteration

init(#) specifies the initial value for the number of clusters or cluster size for sample-size determination or the initial value for the proportion for the effect-size determination. The default is to use a closed-form normal approximation to compute an initial value for the estimated parameter.

iterate(), tolerance(), ftolerance(), log, nolog, dots, nodots; see [PSS] **power**.

The following option is available with power oneproportion, cluster but is not shown in the dialog box:

notitle; see [PSS] **power**.

Remarks and examples

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Remarks are presented under the following headings:

Using power oneproportion, cluster
Computing number of clusters
Computing cluster size
Computing power
Computing effect size and target proportion
Performing hypothesis tests on proportion in a CRD

power oneproportion, cluster requests that computations for the power oneproportion command be done for a CRD. In a CRD, groups of subjects or clusters are randomized instead of individual subjects, so the sample size is determined by the number of clusters and the cluster size. The sample-size determination thus consists of the determination of the number of clusters given cluster size or the determination of cluster size given the number of clusters. For a general discussion of using power oneproportion, see [PSS] **power oneproportion**. The discussion below is specific to the CRD.

Using power oneproportion, cluster

If you specify the `cluster` option, include `k()` to specify the number of clusters or include `m()` to specify the cluster size, the `power oneproportion` command will perform computations for a one-sample proportion test in a CRD. The computations for a CRD are based on the large-sample Wald z test.

All computations are performed for a two-sided hypothesis test where, by default, the significance level is set to 0.05. You may change the significance level by specifying the `alpha()` option. You can specify the `onesided` option to request a one-sided test.

To compute the number of clusters, you must specify the proportions under the null and alternative hypotheses as command arguments p_0 and p_a, respectively, and specify the cluster size in the `m()` option. Instead of specifying the `m()` option, you may specify the sample size in the `n()` option and specify the `cluster` option, so that `power onemean` will perform its computation for a cluster randomized design instead of the default individual-level design. You may also specify the power of the test in the `power()` option.

To compute cluster size, you must specify the null proportion p_0, the alternative proportion p_a, and the number of clusters in the `k()` option. You may also specify the power of the test in the `power()` option.

To compute power, you must specify the number of clusters in the `k()` option, the cluster size in the `m()` option or the sample size in the `n()` option, the null proportion p_0, and the alternative proportion p_a.

Instead of the alternative proportion p_a, you may specify the difference $p_a - p_0$ between the alternative proportion and the null proportion in the `diff()` option when computing sample size or power.

The effect size δ is defined as the difference between the alternative and null proportions. In a CRD, the effect size δ is also adjusted for the cluster design; see *Methods and formulas*.

To compute effect size and the corresponding target proportion, you must specify the number of clusters in the `k()` option, the cluster size in the `m()` option or the sample size in the `n()` option, the power in the `power()` option, and the null proportion p_0. You may also specify the direction of the effect in the `direction()` option. The direction is upper by default, `direction(upper)`; see *Using power oneproportion* in [PSS] **power oneproportion** for other details.

All computations assume an intraclass correlation of 0.5. You can change this by specifying the `rho()` option. Also, all clusters are assumed to be of the same size unless the coefficient of variation for cluster sizes is specified in the `cvcluster()` option.

By default, the computed number of clusters, cluster size, and sample size is rounded up. However, you can specify the `nfractional` option to see the corresponding fractional values; see *Fractional sample sizes* in [PSS] **unbalanced designs** for an example. If the `cvcluster()` option is specified when computing cluster size, then cluster size represents the average cluster size and is thus not rounded. When sample size is specified in the `n()` option, fractional cluster size may be reported to accommodate the specified number of clusters and sample size.

Some of `power oneproportion, cluster`'s computations require iteration, such as to compute the number of clusters for a two-sided test; see *Methods and formulas* for details and [PSS] **power** for the descriptions of options that control the iteration procedure.

Computing number of clusters

To compute the number of clusters, you must specify the proportions under the null and alternative hypotheses as command arguments p_0 and p_a, respectively, and specify the cluster size in the `m()` option. Instead of specifying the `m()` option, you may specify the sample size in the `n()` option and specify the `cluster` option, so that `power onemean` will perform its computation for a cluster randomized design instead of the default individual-level design. You may also specify the power of the test in the `power()` option.

▷ Example 1: Number of clusters for a one-sample proportion test in a CRD, specifying cluster size

Ahn, Heo, and Zhang (2015, 33) demonstrate sample-size computations for a clustered binary outcome by using the data from Hujoel, Moulton, and Loesche (1990) as pilot data. The data recorded positive test results from an enzymatic diagnostic test (EDT) of a specific (target) infection. There were 29 subjects in the study, and each subject had multiple infected sites, as determined by a gold standard test, which were then retested for the presence of the target infection using the EDT. The number of infected sites varied among subjects with an average of 4.897 sites, and observations within a subject were correlated with an intraclass correlation of 0.2. Ahn, Heo, and Zhang (2015) used these estimates to compute the required number of clusters for a new study to test whether the proportion of infected sites detected by the EDT is 0.6, H_0: $p = 0.6$, against the alternative H_a: $p = 0.7$. We demonstrate how to use `power oneproportion, cluster` to compute the required number of clusters.

For simplicity, we assume a constant cluster size across subjects and use an integer cluster size of 5. To detect a proportion of 0.7 against the reference value of 0.6 with 80% power using a 5%-level two-sided test, we type

```
. power oneproportion 0.6 0.7, m(5) rho(0.2)
Performing iteration ...
Estimated number of clusters for a one-sample proportion test
Cluster randomized design, Wald z test
Ho: p = p0  versus  Ha: p != p0
Study parameters:
        alpha =    0.0500
        power =    0.8000
        delta =    0.1000
           p0 =    0.6000
           pa =    0.7000
Cluster design:
            M =         5
          rho =    0.2000
Estimated number of clusters and sample size:
            K =        60
            N =       300
```

We find that given 5 sites per subject, 60 subjects and thus a total of 300 infected sites are required to detect a proportion of 0.7 for the infection of interest against a reference proportion of 0.6 with 80% power using a 5%-level two-sided test. The effect size (`delta`) is calculated as the difference between the alternative and null proportions.

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▷ Example 2: Number of clusters for a one-sample proportion test in a CRD, with varying cluster sizes

Unlike the simplified case in example 1, in a practical study, the number of infected sites per subject may vary. We use the average number of infected sites of 4.897 and a coefficient of variation of 0.25. To account for varying cluster sizes, we specify `m(4.897)` and `cvcluster(0.25)`.

```
. power oneproportion 0.6 0.7, m(4.897) rho(0.2) cvcluster(0.25)
Performing iteration ...
Estimated number of clusters for a one-sample proportion test
Cluster randomized design, Wald z test
Ho: p = p0  versus  Ha: p != p0
Study parameters:
        alpha =    0.0500
        power =    0.8000
        delta =    0.1000
           p0 =    0.6000
           pa =    0.7000
Cluster design:
    Average M =    4.8970
          rho =    0.2000
        CV_cl =    0.2500
Estimated number of clusters and sample size:
            K =        61
            N =       299
```

We now need 61 subjects for a total of 299 sites to achieve the same power.

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Computing cluster size

To compute cluster size, you must specify the null proportion p_0, the alternative proportion p_a, and the number of clusters in the `k()` option. You may also specify the power of the test in the `power()` option.

▷ Example 3: Cluster size for a one-sample proportion test in a CRD

Continuing with example 1, suppose that we are designing a new study and would like to recruit 80 subjects in the study. We would like to get an idea of how many infected sites we need to achieve 80% power. Given the study parameters from example 1, we compute the number of infected sites by specifying 80 clusters in the `k()` option.

```
. power oneproportion 0.6 0.7, k(80) rho(0.2)
Performing iteration ...
Estimated cluster size for a one-sample proportion test
Cluster randomized design, Wald z test
Ho: p = p0  versus  Ha: p != p0
Study parameters:
        alpha =    0.0500
        power =    0.8000
        delta =    0.1000
           p0 =    0.6000
           pa =    0.7000
Cluster design:
            K =        80
          rho =    0.2000
Estimated cluster size and sample size:
            M =         3
            N =       240
```

To achieve the desired power with 80 subjects, we will need to observe 3 sites per subject.

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Computing power

To compute power, you must specify the number of clusters in the `k()` option, the cluster size in the `m()` option or the sample size in the `n()` option, the null proportion p_0, and the alternative proportion p_a.

▷ Example 4: Power for a one-sample proportion test in a CRD

Continuing with example 1, suppose that we have 80 subjects and each subject has 5 infected sites. Given the study parameters from example 1, we compute the power by specifying 80 clusters in the `k()` option and cluster size of 5 in the `m()` option:

```
. power oneproportion 0.6 0.7, k(80) m(5) rho(0.2)
Estimated power for a one-sample proportion test
Cluster randomized design, Wald z test
Ho: p = p0  versus  Ha: p != p0
Study parameters:
        alpha =    0.0500
        delta =    0.1000
           p0 =    0.6000
           pa =    0.7000
Cluster design:
            K =        80
            M =         5
            N =       400
          rho =    0.2000
Estimated power:
        power =    0.9020
```

The computed power is about 90%.

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▷ Example 5: Multiple values of study parameters

To investigate the effect of the number of clusters on power, we can specify a list of numbers in the `k()` option:

```
. power oneproportion 0.6 0.7, k(20(20)100) m(5) rho(0.2)

Estimated power for a one-sample proportion test
Cluster randomized design, Wald z test
Ho: p = p0  versus  Ha: p != p0

  +--------------------------------------------------------------------------+
  |   alpha    power        K       M        N   delta       p0       pa      rho |
  |--------------------------------------------------------------------------|
  |     .05    .3696       20       5      100      .1       .6       .7       .2 |
  |     .05    .6332       40       5      200      .1       .6       .7       .2 |
  |     .05    .8043       60       5      300      .1       .6       .7       .2 |
  |     .05     .902       80       5      400      .1       .6       .7       .2 |
  |     .05    .9532      100       5      500      .1       .6       .7       .2 |
  +--------------------------------------------------------------------------+
```

As expected, as the number of clusters increases, the power tends to get closer to 1.

For multiple values of parameters, the results are automatically displayed in a table, as we see above. For more examples of tables, see [PSS] **power, table**. If you wish to produce a power plot, see [PSS] **power, graph**.

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Computing effect size and target proportion

The effect size δ is defined as the difference between the alternative and null proportions. In a CRD, the effect size δ is also adjusted for the cluster design; see *Methods and formulas*.

To compute effect size and the corresponding target proportion, you must specify the number of clusters in the `k()` option, the cluster size in the `m()` option or the sample size in the `n()` option, the power in the `power()` option, and the null proportion p_0. You may also specify the direction of the effect in the `direction()` option. The direction is upper by default, `direction(upper)`; see *Using power oneproportion* in [PSS] **power oneproportion** for other details.

▷ Example 6: Effect size for a one-sample proportion test in a CRD

Continuing with example 4, we may also be interested in finding the minimum value of the proportion that can be detected with a sample of 80 subjects, 5 infected sites per subject, and 80% power. To compute this, we specify the null value of 0.6 as the command argument and the required options `k(80)`, `m(5)`, and `power(0.8)` and continue to use `rho(0.2)`.

```
. power oneproportion 0.6, k(80) m(5) power(0.8) rho(0.2)
Performing iteration ...
Estimated target proportion for a one-sample proportion test
Cluster randomized design, Wald z test
Ho: p = p0  versus  Ha: p != p0; pa > p0
Study parameters:
        alpha =    0.0500
        power =    0.8000
           p0 =    0.6000
Cluster design:
            K =        80
            M =         5
            N =       400
          rho =    0.2000
Estimated effect size and target proportion:
        delta =    0.0871
           pa =    0.6871
```

Given the null value of 0.6, the minimum detectable value of the proportion is about 0.69, which is slightly smaller than the alternative proportion of 0.7 used in previous examples, because here we use more subjects than, for instance, in example 1, more sites per subject than in example 3, and lower power than in example 4.

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Performing hypothesis tests on proportion in a CRD

power oneproportion, cluster performs PSS computations based on a large-sample test of proportion that accounts for a CRD or for clustered data. We can perform this test by using prtest, cluster(); see [R] **prtest**. In this section, we briefly demonstrate how to test the hypothesis that the proportion is different from a reference value on the collected clustered data by using prtest.

▷ Example 7: Testing for proportion with clustered data

Ahn, Heo, and Zhang (2015, 33) report the data from Hujoel, Moulton, and Loesche (1990) on positive test results from the EDT; see example 1 for details about the study. Let's use prtest to test the null hypothesis H_0: $p = 0.6$.

For clustered data, prtest requires that we specify the cluster identifier in the cluster() option and population intraclass correlation in the rho() option. We use the intraclass correlation of 0.2 as in Ahn, Heo, and Zhang (2015, 33).

```
. use http://www.stata-press.com/data/r15/infection
(Target infections detected by EDT (Hujoel, Moulton, and Loesche, 1990))

. prtest infection == 0.6, cluster(subject) rho(0.2)

One-sample test of proportion                   Number of obs      =       142
Cluster variable: subject                       Number of clusters =        29
                                                Avg. cluster size  =      4.90
                                                CV cluster size    =    0.2419
                                                Intraclass corr.   =    0.2000

------------------------------------------------------------------------------
    Variable |       Mean   Std. Err.                     [95% Conf. Interval]
-------------+----------------------------------------------------------------
   infection |   .6619718   .0537974                      .5565308    .7674129
------------------------------------------------------------------------------
    p = proportion(infection)                                     z =   1.1123
Ho: p = 0.6

     Ha: p < 0.6                 Ha: p != 0.6                   Ha: p > 0.6
 Pr(Z < z) = 0.8670         Pr(|Z| > |z|) = 0.2660          Pr(Z > z) = 0.1330
```

We do not find any statistical evidence to reject the null hypothesis of H_0: $p = 0.6$.

Suppose that we want to design a new similar study and use the estimates from this study to compute the required number of clusters. We are interested in detecting the alternative value of, say, 0.66 with 80% power for a 5%-level two-sided test. To compute the required number of clusters, we use the average cluster size of 4.9 as observed in this study.

```
. power oneproportion 0.6 0.66, m(4.9) rho(0.2)

Performing iteration ...

Estimated number of clusters for a one-sample proportion test
Cluster randomized design, Wald z test
Ho: p = p0  versus  Ha: p != p0

Study parameters:

        alpha =    0.0500
        power =    0.8000
        delta =    0.0600
           p0 =    0.6000
           pa =    0.6600

Cluster design:

    Average M =    4.9000
          rho =    0.2000

Estimated number of clusters and sample size:

            K =       178
            N =       873
```

We need 178 subjects to detect the 0.06 difference between the alternative and null proportions, given the null proportion of 0.6, with 80% power using a 5%-level two-sided test.

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Stored results

`power oneproportion, cluster` stores the following in `r()`:

Scalars

`r(alpha)`	significance level
`r(power)`	power
`r(beta)`	probability of a type II error
`r(delta)`	effect size
`r(K)`	number of clusters
`r(M)`	cluster size
`r(N)`	number of subjects
`r(nfractional)`	`1` if `nfractional` is specified; `0` otherwise
`r(onesided)`	`1` for a one-sided test; `0` otherwise
`r(p0)`	proportion under the null hypothesis
`r(pa)`	proportion under the alternative hypothesis
`r(diff)`	difference between the alternative and null proportions
`r(rho)`	intraclass correlation
`r(CV_cluster)`	coefficient of variation for cluster sizes
`r(init)`	initial value for estimated parameter
`r(maxiter)`	maximum number of iterations
`r(iter)`	number of iterations performed
`r(tolerance)`	requested parameter tolerance
`r(deltax)`	final parameter tolerance achieved
`r(ftolerance)`	requested distance of the objective function from zero
`r(function)`	final distance of the objective function from zero
`r(converged)`	`1` if iteration algorithm converged; `0` otherwise

Macros

`r(type)`	`test`
`r(method)`	`oneproportion`
`r(design)`	`CRD`
`r(test)`	`wald`
`r(direction)`	`upper` or `lower`
`r(columns)`	displayed table columns
`r(labels)`	table column labels
`r(widths)`	table column widths
`r(formats)`	table column formats

Matrices

`r(pss_table)`	table of results

Methods and formulas

The computation for a CRD is based on the Wald test under the large-sample normal approximation, adjusted for the cluster design; see *Large-sample normal approximation* under *Methods and formulas* in [PSS] **power oneproportion** for the common notation for a one-sample proportion test.

Methods and formulas are presented under the following headings:

Equal cluster sizes
Unequal cluster sizes

Equal cluster sizes

In a CRD, let K be the number of clusters, M be the number of observations in each cluster, and n be the total number of subjects, where $n = MK$. Let x_{ij} be the outcome of a Bernoulli trial of the jth ($j = 1, 2, \ldots, M$) observation from the ith cluster ($i = 1, 2, \ldots, K$). Let ρ be the intraclass correlation and DE be the design effect defined as

$$\mathrm{DE} = 1 + \rho(M - 1)$$

Let $P(x_{ij} = 1) = p$ denote the probability of a success in the population. Each individual observation is a Bernoulli trial with a success probability p. Let

$$\widehat{p} = \frac{1}{n}\sum_{i=1}^{K}\sum_{j=1}^{M} x_{ij} \qquad \text{and} \qquad \text{se}(\widehat{p}) = \sqrt{\frac{\widehat{p}(1-\widehat{p})\text{DE}}{n}}$$

denote the sample proportion and its standard error, respectively. Let p_0 and p_a denote the respective null and alternative values of the proportion parameters.

For a large sample, the distribution of the sample proportion $\widehat{p}$ may be approximated by the normal distribution with proportion p and variance $p(1-p)\text{DE}/n$. The Wald test statistic $z = (\widehat{p} - p_0)/\sqrt{\widehat{p}(1-\widehat{p})\text{DE}/n}$ under the null hypothesis follows a standard normal distribution; see, for example, Ahn, Heo, and Zhang (2015).

Let α be the significance level, β be the probability of a type II error, and $z_{1-\alpha}$ and z_β be the $(1-\alpha)$th and the βth quantiles of the standard normal distribution. Let

$$p_{\text{std}} = \frac{(p_a - p_0)}{\sqrt{p_a(1-p_a)\text{DE}}} \tag{1}$$

The power $\pi = 1 - \beta$ is computed using

$$\pi = \begin{cases} \Phi\left(\sqrt{n}p_{\text{std}} - z_{1-\alpha}\right) & \text{for an upper one-sided test} \\ \Phi\left(-\sqrt{n}p_{\text{std}} - z_{1-\alpha}\right) & \text{for a lower one-sided test} \\ \Phi\left(\sqrt{n}p_{\text{std}} - z_{1-\alpha/2}\right) + \Phi\left(-\sqrt{n}p_{\text{std}} - z_{1-\alpha/2}\right) & \text{for a two-sided test} \end{cases} \tag{2}$$

where $\Phi(\cdot)$ is the c.d.f. of the standard normal distribution.

Given the cluster size M, the number of clusters K for a one-sided test is computed by inverting a one-sided power equation from (2),

$$K = \left(\frac{z_{1-\alpha} - z_\beta}{p_{\text{std}}\sqrt{M}}\right)^2 \tag{3}$$

Given the sample size n, the number of clusters K for a one-sided test is computed as

$$K = \frac{n\left(p_a - p_0\right)^2}{\rho p_a(1-p_a)\left(z_{1-\alpha} - z_\beta\right)^2} - \frac{1}{\rho} + 1 \tag{4}$$

Given the number of clusters K, the cluster size M for a one-sided test is computed by solving (2), after substituting p_{std} from (1),

$$M = \frac{1-\rho}{\frac{K(p_a-p_0)^2}{p_a(1-p_a)(z_{1-\alpha}-z_\beta)^2} - \rho} \tag{5}$$

The number of clusters and cluster size for a two-sided test are computed iteratively using the two-sided power equation from (2). The initial values are obtained from (3), (4), and (5), with $\alpha/2$.

The minimum detectable value of the proportion is computed iteratively using the corresponding power equation from (2).

Unequal cluster sizes

For unequal cluster sizes, we assume that the cluster sizes are independent and identically distributed and are small relative to the number of clusters; see Ahn, Heo, and Zhang (2015) for details. Let the coefficient of variation of the cluster sizes be $\mathrm{CV}_{\mathrm{cl}}$. According to van Breukelen, Candel, and Berger (2007) and Campbell and Walters (2014), to adjust for varying cluster sizes, define the relative efficiency (RE) of unequal versus equal cluster sizes as

$$\mathrm{RE} = 1 - \lambda(1-\lambda)\mathrm{CV}_{\mathrm{cl}}^2$$

where $\lambda = \rho M/(\rho M + 1 - \rho)$. With unequal cluster sizes, p_{std} becomes

$$p_{\mathrm{std}} = \frac{(p_a - p_0)}{\sqrt{p_a(1-p_a)\mathrm{DE}/\mathrm{RE}}} \qquad (6)$$

With p_{std} as defined in (6), we can obtain the formula for computing the number of clusters given cluster size for a one-sided test using (3). In all other cases, parameters are computed iteratively using the power equations in (2) with p_{std} from (6).

References

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Also see

[PSS] **power oneproportion** — Power analysis for a one-sample proportion test

[PSS] **power** — Power and sample-size analysis for hypothesis tests

[PSS] **power, graph** — Graph results from the power command

[PSS] **power, table** — Produce table of results from the power command

[PSS] **Glossary**

[R] **prtest** — Tests of proportions