
Sample size

Sample size and Power

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SAMPSIZE

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NAME

sampsiz - Computes sample size and power

SYNOPSIS

sampsiz

[-h] [-v] [-onesided] [-onesample] [-matched] [-cc continuity] [-pop pop] [-e precision] [-pr prevalence] [-level level] [-alpha alpha] [-power power] [-c ratio] [-or odds_ratio] [-exp exposed] [-cp comp] [-means means] [-rho rho] [-d delta] [-nob observed] [-bi binomial] [-n sample] [-obsclus obsclus] [-numclus numclus]

OPTIONS

- h** show usage information
- v** show program version
- onesided** one-sided test for comparisons
- onesample** one-sample test
- matched** 1:1 matched case-control study
- cc** continuity
- pop** target population size,
1 value between 0.0 and oo.
Default: '0'
- e** precision of estimate (%) -- prevalence study option,
1 value between 0.0 and 100.
- pr** prevalence (%) -- prevalence study option,
1 value between 0.0 and 100.
Default: '50'
- level** level of confidence interval (%),
1 value between 50.0 and 100.
Default: '95'
- alpha** Risk alpha (%),
1 value between 0.0 and 100.
Default: '5'
- power** Power of the test (%),
1 value between 50.0 and 100.
Default: '90'

- c** number of controls per case,
 1 integer value between 0 and oo with case control options, or
 1 value between 0.0 and oo with other relevant options,
 Default: '1'
- or** Odds Ratio -- case-control study option,
 1 value between 0.0 and oo.
- exp** Exposed controls (%) -- case-control study option,
 1 value between 0.0 and 100.
- cp** #p1 (%) #p2 (%) -- two sample comparison of percentages,
 2 consecutive values between 0.0 and 100.
- means** #m1 #m2 #sd1 #sd2 -- two sample comparison of means,
 3 values if onesample is selected or else, 4 consecutive values.
- rho** intraclass correlation coefficient -- cluster option
 1 value between 0.0 and 1, default 0
- nob** minimum number of events observed in the sample,
 1 integer value between 1 and 10000.
- bi** #obs #succ (binomial events, #obs >= #succ),
 2 integer values between 0 and oo.
- n** determine power from sample size,
 n = size of first group (two-group comparative studies)
 n = number of cases (unmatched case-control study)
 n = number of pairs (1:1 matched case-control study)
 1 integer value between 1 and oo.
- obsclus** number of observations per cluster
 1 integer value > 0
- numclus** minimum number of clusters
 1 integer value > 0
- d** delta critical value
 1 value between 0.0 and oo

DESCRIPTION

Sampsiz computes sample size and power for prevalence studies, sample size and power for one-sample and two-sample comparative studies of percentages and means, and for unmatched and 1:1 matched case-control studies.

USAGE

Prevalence Surveys

The following options are relevant to simple prevalence studies:

-e precision (%): we wish to obtain confidence limits equal to prevalence +/- precision

-pr prevalence (%), default 50%

-pop target population size, default 0 (infinite)

-level of confidence interval, default 95%

The population size is the total size of the population from which a sample will be drawn for a prevalence survey. If the population size is small, the correction for finite population will result in a reduced sample size. A prevalence study will need either the **-e** option for precision, or the **-nob** option to specify a finite number of events (see below).

Entering 50 (50%) for the estimated prevalence (**-pr 50**), which is the default value, will result in the highest estimated sample size. Entering 0 for the population size (**-pop 0**) will result in the programme using an infinite population size. If a null prevalence is entered (**-pr 0**), *sampsize* returns the estimated sample size needed for a 95% (default) confidence interval upper limit that is equal to the entered precision (option **-e**). Any other confidence interval may be selected instead of the 95% confidence interval, using the option **-level**. *Sampsize* will display the binomial exact confidence interval using the returned sample size unless a finite population size is specified. It may happen that this exact interval is larger than the expected interval (prevalence plus or minus precision), when the number of successful events is lower than 5, or when sample size minus that number is lower than 5, due to the lack of precision of the normal approximation formula with small numbers. In those instances, it is advisable to test different hypotheses of sample size and hypothetical numbers of successful binomial events using the **-bi** option (see below).

Minimum number of events to detect

This is a variation over the previous design: prevalence is low and the capacity to deal with a large sample often necessary to achieve a reasonable precision of the measured estimate is limited. We will rather want to detect with probability specified with **-level** at least *n* sampled units with the studied characteristic, given a probability of occurrence = prevalence (**-pr**). The option **-nob** instructs *sampsize* to return the sample size needed to observe at least **-nob** successful events, given a **-pr** probability of occurrence. Relevant options are:

-nob number to observe

-pr prevalence: probability (%) of occurrence of one event

-level probability of observing the given number of events

Binomial confidence intervals

The first design options may lead to small samples and the approximations used to estimate sample size are known to be non valid if less than 5 sampled units are expected to have the studied characteristic (equally problematic: all sampled units minus 5 or less have that characteristic). One alternative approach is to calculate the binomial exact confidence intervals that result from different sets of numbers. Relevant options are:

-bi two parameters: number of observations, number of successes

-level of confidence interval, default 95%

Comparison of percentages and means: sample size and power

Sampsize estimates the required sample size for studies comparing two groups. *Sampsize* can be used when comparing means or proportions for simple studies where only one measurement of the outcome is planned. *Sampsize* computes the sample size for two-sample comparison of means, where the postulated values of the means and standard deviations are **-means m1 m2 sd1 sd2**; one-sample comparison of mean to hypothesized value (option **-onesample** must be specified and only three parameters to the option **-means** are allowed in one-sample tests: m1, m2 and sd1); two-sample comparison of proportions (option **-cp** where the postulated values of the proportions are #1 and #2); and one-sample comparison of proportion to hypothesized value (option **-onesample** should be specified), where the hypothesized proportion (null hypothesis) is #1 and the postulated proportion (alternative hypothesis) is #2. Default power is 90%. If **-n** is specified, *sampsize* will compute power.

In the case of a cluster sampling design, a sample of natural groups of individuals is selected, rather than a random sample of the individuals themselves. Observations are no longer independent as we would expect had they been drawn randomly from the population. Nonindependence is measured by the intraclass correlation, which is specified with option **-rho** (between 0 and 1). One may then specify **-numclus**, the number of clusters (for instance, the number of physicians who will recruit the patients: typically, the intraclass correlation will be fairly small, often between 0 and 0.05), or alternatively, **-obsclus**, the minimum number of observations per cluster. The larger the number of clusters and the fewer observations per cluster, the less the effect on the standard error estimates. A sample of 250 consisting of 50 clusters with 5 observations per cluster will have better power than the same sample size consisting of 25 clusters with 10 observations per cluster. In fact, with only one observation per cluster, we are back to a simple random sample. If there is no intraclass correlation, there will be no increase in the sample size estimate.

By default, no continuity correction is applied when computing sample size or power for the comparison of two percentages. However, the correction may be applied with option **-cc**. The correction will result in a greater sample size and smaller power. Simulations showed that the correction is most often too conservative (Alzola C and Harrell F, An introduction to S and the Hmisc and Design Libraries: <http://hesweb1.med.virginia.edu/biostat/s/splus.html>).

Relevant options are (either **-cp** or **-means** must be specified, not both):

-cp percentages (%), two parameters for two proportions to compare

-means two means and two standard deviations (one if one-sample): m1 m2 sd1 [sd2]

-alpha alpha risk (%), default 5%

-n sample size of the first group (total sample size in one-sample comparison)

-power power of the comparison (%), default 90%

- onesided** one-sided test
- onesample** one-sample comparison against hypothesized value
- rho** intraclass correlation (between 0 and 1)
- obsclus** number of observations per cluster
- numclus** minimum number of cluster
- cc** continuity correction

Case-control studies

To specify a case-control design, we need to type the option **-exp**, which specifies the percentage of exposed controls. If we add the option **-or**, the odds-ratio that that we wish to detect, **sampsiz** will return the sample size for an unmatched design (option **-c** specifies the ratio of controls/cases, the default ratio is 1). The option **-matched** may be used to specify a 1:1 matched study design (**-c** may not be used with **-matched**). If we specify **-exp**, **-or**, and **-n**, **sampsiz** will return the power of the specified design. If one specifies **-exp** and **-n**, which is the number of cases, **sampsiz** will return the minimum detectable odds-ratio greater than one and the maximum detectable odds-ratio lower than one, an alternative to the power determination. Relevant options are:

- exp** percentage exposed among controls
- n** number of cases, or number of pairs if 1:1 matched case-control study
- or** odds-ratio to detect
- c** ratio of controls/cases (truncated to integer), default 1, not used if matched
- alpha** alpha risk (%), default 5%
- power** power of the comparison (%), default 90%
- onesided** one-sided test
- matched** 1:1 matched case-control study

Equivalence trials: sample size

The goal of an equivalence trial is to prove that two quantities are equal. The hypothesis framework for an equivalence trial requires the specification of no difference in the alternative and a difference in the null. It contains an additional parameter delta, **-d**, to indicate the maximum clinical difference allowed for an experimental therapy to be considered equivalent with a standard therapy. Binomial endpoints are defined as the positive difference of the probability of success for the standard group (**ps**) and the probability of success for the experimental group (**pt**) of patients. These probabilities are entered with **-cp #ps #pt** (percentages), and delta is entered as a percentage. In the case of a continuous endpoint, delta indicates the maximum clinical difference allowed for the comparison of two means, and is entered using the **-d** option. Means and standard deviations are to be entered the usual way with **-means ms me ss se**, with **ms** and **me** the means in the standard and experimental group, respectively, and **ss** and **se** the standard deviations.

There is a general misconception that it requires a larger sample to prove equivalence than difference. The veracity of this assumption is situation-specific and dependant upon the degree of difference, delta, one is willing to allow so that the standard and experimental treatments may still be considered equivalent. Relevant options are:

- cp** percentages (%), two parameters for two proportions to compare
- means** two means and two standard deviations (one if one-sample): m1 m2 sd1 [sd2]
- alpha** alpha risk (%), default 5%

EXAMPLES

Prevalence surveys

- * To calculate the sample size given a 50% prevalence (default) and infinite population size (also default), with 5% precision: the upper boundary of the confidence interval will equal the observed prevalence plus 5%, and the lower boundary will equal the observed prevalence minus 5%, i.e. [45% - 55%]:

```
cunegonde:~>sampsize -e 5
```

Assumptions:

```
Precision          = 5.00 %
Prevalence         = 50.00 %
Population size    = infinite
```

```
95% Confidence Interval specified limits [ 45%  --  55% ]
(these limits equal prevalence plus or minus precision)
```

Estimated sample size:

```
n =          385
```

```
95% Binomial Exact Confidence Interval with n =          385
and n * prevalence =          193 observed events:
[45.0212%  --  55.2365% ]
```

- * To get the needed sample size after correction for population size (n = 1500):

```
cunegonde:~>sampsize -e 5 -pop 1500
```

Assumptions:

```
Precision          = 5.00 %
Prevalence         = 50.00 %
Population size    = 1500
```

```
95% Confidence Interval specified limits [ 45%  --  55% ]
(these limits equal prevalence plus or minus precision)
```

Estimated sample size:
n = 306

- * Assuming a prevalence of 10%, a precision of 4% estimated using a 90% confidence interval, and a target population size of 2500:

```
cunegonde:~>sampsize -pr 10 -e 4 -pop 2500 -level 90
```

Assumptions:

Precision = 4.00 %
Prevalence = 10.00 %
Population size = 2500

90% Confidence Interval specified limits [6% -- 14%]
(these limits equal prevalence plus or minus precision)

Estimated sample size:
n = 144

- * Assuming that the observed prevalence in the sample will be null, for a 97.5% one-sided confidence interval upper limit that is equal to the entered precision (2% in this example), type:

```
cunegonde:~>sampsize -pr 0 -e 2
```

Assumptions:

Precision = 2.00 %
Prevalence = 0.00 %
Population size = infinite

A null prevalence was entered, we assume here that the observed prevalence in the sample will be null, and compute the sample size for an upper limit of the confidence interval equal to the entered precision. The population size is not taken into account even if a finite size was entered. Sample sizes are calculated using the binomial exact method.

97.5% one-sided Confidence Interval upper limit = 2.00

Estimated sample size:
n = 183

- * Assuming that the observed prevalence in the sample will be null, for 95% one-sided confidence interval upper limit equal to the entered precision (2% in this example), type:

```
cunegonde:~>sampsize -pr 0 -e 2 -level 90
```

Assumptions:

Precision = 2.00 %
Prevalence = 0.00 %
Population size = infinite

A null prevalence was entered, we assume here that the observed prevalence in the sample will be null, and compute the sample size for an upper limit of the confidence interval equal to the entered precision. The population size is not taken into account even if a finite size was entered. Sample sizes are calculated using the binomial exact method.

95% one-sided Confidence Interval upper limit = 2.00

Estimated sample size:
n = 149

- * A study on the hepatitis C virus aims at describing some characteristics of the virus strains. It is assumed that the prevalence of virus positive individuals is 10% in the population. The investigators wish to calculate the sample size needed to be 95% sure that at least 5 patients will harbour a virus.

cunegonde:~>sampsize -nob 5 -pr 10

Assumptions:

prevalence = 10%
minimum number of successes = 5 in the sample
with probability = 95%

Estimated sample size:
n = 90

- * You flip a coin 10 times and it comes up heads only once. You are shocked and decide to obtain a 99% confidence interval for this coin:

cunegonde:~>sampsize -bi 10 1

Assumptions:

number of observations = 10
number of successes = 1

Binomial Exact 95% Confidence Interval:
[0.252858% -- 44.5016%]

Comparative studies of proportions

- * Someone claims that US females are more likely than US males to study French. Our null hypothesis is that the proportion of female French students is 0.5. We wish to compute the sample size that will give us a 80% power to reject the null hypothesis if the true proportion of female French students is 75%.

```
cunegonde:~>sampsize -cp 50 75 -power 80 -onesample
```

Estimated sample size for one-sample comparison of percentage to hypothesized value

Test Ho: p = 50%, where p is the percentage in the population

Assumptions:

```
alpha = 5% (two-sided)
power = 80%
alternative p = 75%
```

Estimated sample size:

```
n = 29
```

- * We want to conduct a survey on people's opinions of the President's performance. Specifically, we want to determine whether members of the President's party have a different opinion from people with another party affiliation. We estimate that only 25% of members of the President's party will say that the President is doing a poor job, whereas 40% of other parties will rate the President's performance as poor. We compute the sample size for alpha = 5% (two-sided) and power = 90%:

```
cunegonde:~>sampsize -cp 25 40
```

Estimated sample size for two-sample comparison of percentages

Test H: p1 = p2, where p1 is the percentage in population 1 and p2 is the percentage in population 2

Assumptions:

```
alpha = 5% (two-sided)
power = 90%
p1 = 25%
p2 = 40%
```

Estimated sample size:

```
n1 = 203
n2 = 203
```

- * Following the calculation for the survey on the President's performance, we realize that we can sample only n1 = 300 members of the President's party and a sample of n2 = 150 members of other parties, due to time constraints. We wish to compute the power of our survey:

```
cunegonde:~>sampsize -n 300 -cp 25 40 -c 0.5
```

Estimated power for two-sample comparison of percentages

Test Ho: $p_1 = p_2$, where p_1 is the percentage in the population 1 and p_2 is the percentage in the population 2

Assumptions:

```
alpha =      5 (two-sided)
p1 =        25%
p2 =        40%
sample size n1 = 300
sample size n2 = 150
n2/n1 =      0.5
```

Estimated power:

```
power =      89.9001%
```

- * We wish to study the proportion of patients who have not recovered from a back pain by 4 weeks, and compare the outcome between patients in whom sciatica was diagnosed and patients without sciatica. We know that typically, about 20% of acute low back pain patients have not recovered by 4 weeks and think that the percentage may be 30% for patients who also have sciatica. The sample size we would need to detect this difference between the two groups, with a two-sided alpha of 5% and a power of 80% is 313:

```
cunegonde:~>sampsize -cp 20 30 -power 80
```

Estimated sample size for two-sample comparison of percentages

Test H: $p_1 = p_2$, where p_1 is the percentage in population 1 and p_2 is the percentage in population 2

Assumptions:

```
alpha =      5% (two-sided)
power =      80%
p1 =        20%
p2 =        30%
```

Estimated sample size:

```
n1 =        294
n2 =        294
```

- * Now we look at the same example using 10 observations per cluster and an intraclass correlation of 0.1:

```
cunegonde:~>sampsize -cp 20 30 -power 80 -obsclus 10 -rho 0.1
```

Estimated sample size for two-sample comparison of percentages

Test H: $p_1 = p_2$, where p_1 is the percentage in population 1 and p_2 is the percentage in population 2

Assumptions:

alpha = 5% (two-sided)
power = 80%
p1 = 20%
p2 = 30%

Estimated sample size:

n1 = 294
n2 = 294

Sample size adjusted for cluster design:

Intraclass correlation = 0.1
Average obs. per cluster = 10
Minimum number of clusters = 112

Estimated sample size per group:

n1 (corrected) = 559
n2 (corrected) = 559

- * Taking into account the cluster design of the study, our samples have increased to 595 per group and a total of 119 physicians (clusters). Finally, we try the calculation assuming only 40 physicians:

```
cunegonde:~>sampsize -cp 20 30 -power 80 -numclus 40 -rho 0.1
```

Sample size adjusted for cluster design:

Error: for rho = 0.1, the minimum number of clusters possible is:
numclus = 59

- * We got an error message telling us that, given these sets of sample size parameters, it is not possible to estimate a sample size with fewer than 63 clusters. We need to rerun `sampsize` with different parameters in order to get a manageable number of patients.

```
cunegonde:~>sampsize -cp 20 30 -power 80 -numclus 40 -rho 0.05
```

Sample size adjusted for cluster design:

Intraclass correlation = 0.05
Average obs. per cluster = 53
Minimum number of clusters = 40

Estimated sample size per group:

```
n1 (corrected) = 1059
n2 (corrected) = 1059
```

Comparative studies of means

- * We wish to test the effects of a low-fat diet on serum cholesterol levels. We will measure the difference in cholesterol level for each subject before and after being on the diet. Since there is only one group of subjects, all on diet, this is a one-sample test. Our null hypothesis is that the mean of individual differences in cholesterol level will be zero; i.e., $\text{mdiff} = 0\text{mg}/100\text{ml}$. If the effect of the diet is as large as a mean difference of $-10\text{mg}/100\text{ml}$, then we wish to have power of 95% for rejecting the null hypothesis. Since we expect a reduction in levels, we want to use a one-sided test with $\alpha = 2.5\%$. Based on past studies, we estimate that the standard deviation of the difference in cholesterol levels will be about $20\text{mg}/100\text{ml}$:

```
cunegonde:~>sampsize -means 0 -10 20 -onesample -alpha 2.5
-onesided -power 95
```

Estimated sample size for one-sample comparison of mean to hypothesized value

Test Ho: $m = 0$, where m is the mean in the population

Assumptions:

```
alpha = 2.5 (one-sided)
power = 95
alternative m = -10
sd = 20
```

Estimated sample size:

```
n = 52
```

- * We decide to conduct the cholesterol study with $n = 60$ subjects, and we wonder what the power will be at a one-sided significance level of $\alpha = 1\%$:

```
cunegonde:~>sampsize -n 60 -means 0 -10 20 -onesample -onesided
-alpha 1
```

Estimated power for one-sample comparison of mean to hypothesized value

Test Ho: $m = 0\%$, where m is the mean in the population

Assumptions:

```

alpha =          1% (one-sided)
alternative m =   -10
sd =             20
sample size =    60

```

Estimated power:

```
power = 93.9024%
```

- * We are doing a study of the relationship of oral contraceptives (OC) and blood pressure (BP) level for women ages 35-39. From a pilot study, it was determined that the mean and standard deviation BP of OC users were 132.86 and 15.34, respectively. The mean and standard deviation BP of OC users were 127.44 and 18.23. Since it is easier to find OC nonusers than users in the country were the study is conducted, we decide that n_2 , the size of the sample of OC users, should be twice n_1 , the size of the sample of OC users; that is, $c = n_2/n_1 = 2$. To compute the sample sizes for $\alpha = 5\%$ (two-sided) and the power of 80%:

```

cunegonde:~>sampsize -means 132.86 127.44 15.34 18.23 -power 80
-c 2

```

Estimated sample size for two-sample comparison of means

Test Ho: $m_1 = m_2$, where m_1 is the mean in population 1 and m_2 is the mean in population 2

Assumptions:

```

alpha =          5 (two-sided)
power =          80
m1 =          132.86
m2 =          127.44
sd1 =           15.34
sd2 =           18.23
n2/n1 =          2

```

Estimated sample size:

```

n1 =          108
n2 =          216

```

- * We now find that we only have enough money to study 100 subjects from each group for the above oral contraceptives study. We can compute the power for $n_1 = n_2 = 100$

```

cunegonde:~>sampsize -n 100 -means 132.86 127.44 15.34 18.23

```

Estimated power for two-sample comparison of means

Test Ho: $m_1 = m_2$, where m_1 is the mean in the population 1
and m_2 is the mean in the population 2

Assumptions:

```
alpha =          5% (two-sided)
m1 =          132.86
m2 =          127.44
sd1 =          15.34
sd2 =          18.23
sample size n1 =          100
sample size n2 =          100
n2/n1 =          1
```

Estimated power:

```
power =        62.3601%
```

- * Patients for the study on oral contraceptives and blood pressure will be recruited in 12 clinics, and we suspect some intraclass correlation (patients recruited in the same clinic are more alike than patients recruited from different clinics). Due to the cluster sampling design, patients are not independent observations, and we wish to correct the above sample size (sampsiz returned a sample size of 108 in the first group, and 216 in the second group). We think that the intraclass correlation is fairly small (0.02), and compute:

```
cunegonde:~>sampsiz -means 132.86 127.44 15.34 18.23 -power 80
-c 2 -numclus 12 -rho 0.02
```

Estimated sample size for two-sample comparison of means

Test Ho: $m_1 = m_2$, where m_1 is the mean in population 1
and m_2 is the mean in population 2

Assumptions:

```
alpha =          5 (two-sided)
power =          80
m1 =          132.86
m2 =          127.44
sd1 =          15.34
sd2 =          18.23
n2/n1 =          2
```

Estimated sample size:

```
n1 =          108
n2 =          216
```

Sample size adjusted for cluster design:

Intraclass correlation	=	0.02
Average obs. per cluster	=	58
Minimum number of clusters	=	12

Estimated sample size per group:

n1 (corrected)	=	232
n2 (corrected)	=	464

The design effect is rather important despite a small intraclass correlation, due to the small number of clusters. Sampsiz returned $n1 = 232$ and $n2 = 464$, more than twice the initial sample size.

Case-Control Studies

- * We wish to conduct a case control study to assess whether bladder cancer is associated with past exposure to cigarette smoking. Cases will be patients with bladder cancer and controls will be patients hospitalized for injury. It is assumed that 20% of controls will be smokers or past smokers, and we wish to detect an odds-ratio of 2 with power 90%. Three controls will be recruited for one case:

```
cunegonde:~>sampsiz -or 2 -exp 20 -c 3
```

Assumptions:

Odds ratio	=	2
Exposed controls	=	20%
Alpha risk	=	5%
Power	=	90%
Controls / Case ratio	=	3
Total exposed	=	23.3333%

Estimated sample size:

Number of cases	=	150
Number of controls	=	450
Total	=	600

- * The above study on bladder cancer needed a total sample size of 600. An alternative is to conduct a matched case-control study of bladder cancer and cigarette smoking rather than the above unmatched study design. One case will be matched to one control. Again, the percentage of exposed controls is 20%, and we wish to detect a two-fold increased risk ($OR = 2$). With these specifications, we need 226 pairs (total sample size 452).

```
cunegonde:~>sampsiz -or 2 -exp 20 -matched
```

Assumptions:

Odds ratio = 2
 Exposed controls = 20%
 Alpha risk = 5%
 Power = 90%
 Probability of an exposure-discordant pair = 40%

Estimated sample size (number of pairs):

Number of exposure discordant-pairs = 91
 Number of pairs = 226
 Total sample size = 452

* The following table (Kline et al., 1978) shows previous induced abortions among multi-gravid cases and controls. (Primiigravidae were excluded since these women did not have prior pregnancies.):

	Spontaneous abortions	Controls
PIA:		
yes	171	90
no	303	165
Total:	474	255

The power of the study for detecting a relative risk of $R = 1.5$ is calculated as follows: $c = 255/474 = 0.538$, percentage exposed in controls = $100 \times 90/255 = 35.29$:

```
cunegonde:~>sampsize -or 1.5 -exp 35.29 -c 0.538 -n 474
```

Assumptions:

Odds ratio = 1.5
 Exposed controls = 35.29%
 Alpha risk = 5%
 Controls / Case ratio = 0.538

 Total exposed = 41.6005%

 Number of cases = 474
 Number of controls = 255

 Total = 729

Estimated power:

power = 72.0774%

* Kessler and Clark (1978) studied 365 males with bladder cancer and an equal number of controls, 35 percent of whom reported past use of nonnutritive sweeteners. Using

a one-sided test at the $\alpha = 5\%$ level, the smallest relative risk greater than one that can be detected with 90% power is $RR = 1.55$:

```
cunegonde:~>sampsize -n 365 -exp 35 -onesided
```

Assumptions:

Exposed controls	=	35%
One-sided alpha risk	=	5%
Power	=	90
Number of cases	=	365
Number of controls	=	365
Total	=	730

Estimated smallest and highest detectable odds-ratio:

Highest odds-ratio < 1	=	0.623181
Smallest odds-ratio > 1	=	1.55439

Equivalence trials

- * Researchers want to show that a new treatment is "as good as" the standard one. The success rates of both treatments are expected to be approximately 90%. The researchers want to be sure that the new treatment is no worse than the standard treatment by an amount of 10%. Then, the sample size for each treatment group is 155 patients:

```
cunegonde:~>sampsize -cp 90 90 -d 10
```

Estimated sample size for two-sample non-inferiority comparison of percentages

Test H_0 : $p_2 < p_1 - \delta$, where p_1 is the percentage in population 1, p_2 is the percentage in population 2, and δ is the critical value

Assumptions:

alpha =	5% (two-sided)
power =	90%
p1 =	90%
p2 =	90%
delta =	10%

Estimated sample size per group:

n =	155
-----	-----

PRIMARY FTP SITE

The most recent distributions of **sampsize** can be found at:

<http://prdownloads.sourceforge.net/sampsize/>

sampsize project home page:

<http://sampsize.sourceforge.net/>

NOTES

Some parts of **sampsize** are translated and adapted from publicly available code written in the stata language (Statacorp Inc.).

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