Package ‘samplesizeestimator’

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**Type** Package  

**Title** Calculate Sample Size for Various Scenarios  

**Version** 1.0.0  

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**Description** Calculates sample size for various scenarios, such as sample size to estimate population proportion with stated absolute or relative precision, testing a single proportion with a reference value, to estimate the population mean with stated absolute or relative precision, testing single mean with a reference value and sample size for comparing two unpaired or independent means, comparing two paired means, the sample size for case control studies, estimating the odds ratio with stated precision, testing the odds ratio with a reference value, estimating relative risk with stated precision, testing relative risk with a reference value, testing a correlation coefficient with a specified value, etc.  

<https://www.academia.edu/39511442/Adequacy_of_Sample_Size_in_Health_Studies#:~:text=Determining%20the%20sample%20size%20for,may%20yield%20statistically%20inconclusive%20results.>.  

**Imports** stringi, stats  

**License** GPL (>= 2)  

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**Description**

Calculates minimum sample size needed to detect at least \( r_{0} - r_{1} \) units difference in the hypothesized and reported correlation coefficient for desired level of significance and power.

**Usage**

```r
 correl(rho0, rho1, alp, pwr)
```

**Arguments**

- `rho0`: magnitude of relationship between the two variables under study, set at null hypothesis
- `rho1`: anticipated magnitude of relationship between the two variables under study
- `alp`: level of significance or accepted level of probability of type I error
- `pwr`: desired level of power

**Value**

A list object with minimum required sample size along with description for reporting.

**Author(s)**

est.auc

References


Examples

```r
correl(rho0 = 0.5, rho1 = 0.7, alp = 0.05, pwr = 0.8)
```

---

**est.auc**  
*Sample size for estimating Area Under the ROC curve*

---

**Description**

Sample size for estimating Area Under the ROC curve

**Usage**

```r
est.auc(auc, alp, d)
```

**Arguments**

- `auc`  
  anticipated AUC of the diagnostic marker or test

- `alp`  
  level of significance or accepted level of probability of type I error

- `d`  
  Precision required on either side of the true AUC

**Value**

a list of total sample size based on AUC along with reporting

**References**


**Examples**

```r
est.auc(auc=0.7,alp=0.05,d=0.07)
```
Description

In diagnostic studies, the test yields a binary outcome and accuracy is evaluated by sensitivity and specificity. This function calculates sample size for estimating sensitivity when the diagnostic test yields a binary outcome.

Usage

est.se(p, se, prec, alp)

Arguments

p  Prevalence of disease
se  anticipated sensitivity of the test
prec  Precision required on either side of the true sensitivity
alp  level of significance or accepted level of probability of type I error

Value

a list of total sample size based on sensitivity along with reporting

Author(s)


References


Examples

est.se(p = 0.10, se = 0.99, prec = 0.03, alp = 0.05)
Sample size for estimating single mean

Description

This function computes adequate sample size based on the method of estimating mean with absolute or relative precision. It can be used for descriptive studies where the researcher wishes to describe the distribution of one or more quantitative outcome variables without looking at their causal relationship and hypothesis testing.

Usage

estm(mean, sig, prec, alp, relative = FALSE)

Arguments

- **mean**: anticipated population mean (required if relative precision is desired otherwise not required)
- **sig**: anticipated population standard deviation
- **prec**: desired level of precision on either side of the population mean
- **alp**: level of significance or accepted level of probability of type I error
- **relative**: a logical argument indicating relative or absolute precision (FALSE gives absolute precision)

Value

number needed to estimate mean within the desired precision level

Author(s)


References


Examples

```
estm(sig=6.3, prec=1.2, alp=0.05, relative=FALSE)
estm(mean=14, sig=8, prec=0.1, alp=0.05, relative = TRUE)
```
Description
Odds ratios are estimated in a case-control study design to assess the association of outcome with past exposure. This function estimates the sample size needed to estimate the true odds ratio with specified precision.

Usage
```r
estor(p0, or, alp, prec, k)
```

Arguments
- `p0`: Probability of exposure among the controls
- `or`: Anticipated Odds Ratio (OR)
- `alp`: level of significance or probability of claiming the association exists when in fact there is no association
- `prec`: Precision desired on either side of OR
- `k`: the number of controls for each case

Value
A list object, the required minimum sample size along with description for reporting

Author(s)

References

Examples
```r
estor(p0 = 0.35, or = 2, alp = 0.05, prec = 0.25, k = 1)
```
estp  

**Sample Size for Estimation of Single Proportion**

**Description**

This function may be used in case of a descriptive study design where the researcher wishes to describe the distribution of one or more categorical outcome variables without looking at their causal relationship and hypothesis testing.

**Usage**

```r
estp(prop, prec, alp = 0.05, relative = FALSE)
```

**Arguments**

- `prop`: Anticipated proportion of outcome or characteristic of interest in the population
- `prec`: Precision required on either side of the population proportion
- `alp`: Level of significance or accepted level of probability of type I error
- `relative`: a logical argument indicating relative or absolute precision (FALSE gives absolute precision)

**Value**

a list object with minimum required sample size along with description for reporting

**Author(s)**


**References**


**Examples**

```r
estp(prop = 0.8, prec = 0.1, alp = 0.01, relative = FALSE)
```
Description

Relative risks are estimated in a cohort study design to assess the association of exposure with the outcome. This function estimates the sample size needed to estimate the true relative risk with specified precision.

Usage

estRR(p0, RR, alp, prec, k)

Arguments

- \( p_0 \) Probability of outcome among unexposed
- \( RR \) anticipated Relative Risk (RR)
- \( alp \) level of significance or probability of claiming the association exists when in fact there is no association
- \( prec \) Precision desired on either side of RR
- \( k \) the number of unexposed for each exposed

Value

a list object, the required minimum sample size along with description for reporting

Author(s)


Examples

estRR(p0=0.2, RR=2, alp=0.05, prec=0.25, k=1)
**LRneg**  
*Sample Size for Estimating LR negative of a Single Diagnostic Test*

**Description**
Calculate sample size (cases) based on negative likelihood ratio an unified index for comparing the accuracy of two diagnostic tests.

**Usage**
```
LRneg(se, sp, lneg, alp, pwr, k = 1)
```

**Arguments**
- `se`: anticipated sensitivity of the diagnostic test
- `sp`: anticipated specificity of the diagnostic test
- `lneg`: anticipated LR negative value
- `alp`: level of significance
- `pwr`: desired level of power
- `k`: number of control(s) per case

**Value**
a list object with minimum required sample size with reporting

**Author(s)**

**References**

**Examples**
```
LRneg(se=0.9, sp=0.5, lneg=0.4, alp=0.05, pwr=0.8, k=1)
```
### LRpos

**Sample Size for Estimating LR Positive of a Single Diagnostic Test**

**Description**

Calculate sample size (cases) based on positive likelihood ratio an unified index for comparing the accuracy of two diagnostic tests.

**Usage**

```r
LRpos(se, sp, lrpos, alp, pwr, k = 1)
```

**Arguments**

- `se`: anticipated sensitivity of the diagnostic test
- `sp`: anticipated specificity of the diagnostic test
- `lrpos`: anticipated LR positive value
- `alp`: level of significance
- `pwr`: desired level of power
- `k`: number of control(s) per case

**Value**

A list object with minimum required sample size with reporting.

**Author(s)**


**References**


**Examples**

```r
LRpos(se=0.8, sp=0.70, lrpos=2, alp=0.05, pwr=0.8, k=1)
```
n.means

Sample Size for Comparing Independent and dependent means

Description

This function computes the sample size based on three different methods i) comparing mean with a specified value ii) comparing two independent means iii) comparing two dependent means

Usage

n.means(
  delta,
  sd,
  alp = 0.05,
  pwr = 0.8,
  type = "two",
  alternative = "two.sided",
  k = 1,
  paired = FALSE
)

Arguments

- **delta**: anticipated difference between the two groups
- **sd**: anticipated standard deviation
- **alp**: anticipated level of significance or accepted level of type I error alp=0.05 is default
- **pwr**: desired power pwr=0.80 is default
- **type**: string specifying the type of sample (one or two) type=two is default
- **alternative**: one or two sided alternative hypothesis "two.sided" is default
- **k**: the ratio of control to experimental patients k=1 is default
- **paired**: a logical argument indicating whether the sample is independent or dependent FALSE is default

Value

- a list object, the required minimum sample size along with description for reporting

Author(s)


References

Examples

n.means(delta = 1.5, sd = 1, alp = 0.05, pwr = 0.9, type ="two",
alternative= "two.sided", k = 1, paired = FALSE)

nprop

Estimate sample size for hypothesis testing on proportions

Description

This function computes the sample size based on two different methods i) comparing proportion
with a specified (reference) value ii) comparing two independent proportions

Usage

nprop(p1, p2, alp, pwr, type = "two", alternative = "two.sided", k = 1)

Arguments

p1       hypothesized or reported proportion
p2       anticipated proportion in the population of interest
alp      level of significance or accepted level of probability of type I error
pwr      desired level of power
type     character string stating number of groups i.e. one or two (default)
alternative a character string specifying the alternative hypothesis, must be one of two.sided (default) or one.sided
k        ratio of number of subjects in the two groups k=1 (default)

Value

a list object, the required minimum sample size along with description for reporting

Author(s)


Examples

nprop(p1=0.5, p2=0.4, alp=0.05, pwr=0.90, type="one",
alternative="one.sided", k=1)
nprop(p1=0.05, p2=0.15, alp=0.05, pwr=0.90, type="two",
alternative="one.sided", k=1)
**Description**

When we try to associate multiple exposures to an outcome, we need to calculate the odds ratio (OR) of a particular exposure in the presence of other exposures and test their relative importance in the model using a significance test based on OR. This function computes sample size based on testing OR for a case-control study design.

**Usage**

```r
testor(p0, or, alp, pwr, k)
```

**Arguments**

- `p0` Probability of exposure among the controls
- `or` Anticipated Odds Ratio
- `alp` Probability of type I error
- `pwr` Desired level of power
- `k` ratio of number of cases to controls to cases

**Value**

A list object, the required minimum sample size along with description for reporting.

**Author(s)**


**References**


**Examples**

```r
testor(p0=0.042, or=2.5, alp=0.05, pwr=0.8, k=1)
```
testRR

Sample size for testing relative risk

Description
When we try to associate multiple exposures to an outcome, we need to know the relative risk (RR) of a particular exposure in the presence of other exposures and test their importance in the model using a significance test based on RR. This function computes sample size based on testing RR for a cohort study design.

Usage
testRR(RR, p0, alp, pwr, k = 1)

Arguments
- RR: anticipated relative risk
- p0: probability of outcome among the unexposed
- alp: level of significance or accepted level of probability of type I error
- pwr: desired level of power
- k: number of unexposed for each exposed

Value
a list object with minimum required sample size along with description for reporting

Author(s)

Examples
testRR(p0 = 0.2, RR = 1.5, alp = 0.05, pwr = 0.84, k = 1)
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