Package 'samplesizeestimator'

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Type Package

Title Calculate Sample Size for Various Scenarios

Version 1.0.0

Maintainer R Amala <amalar.statistics@gmail.com>

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%20sa

Imports stringi, stats

License GPL (>= 2)

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Author R Amala [aut, cre, cph],
G Kumarapandiyan [aut],
A Srividya [ctb],
M Rajeswari [ctb],
Ashwani Kumar [ctb]

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R topics documented:

`correl` *Sample Size for Testing Correlation Coefficient*

Description

Calculates minimum sample size needed to detect at least rho0-rho1 units difference in the hypothesized and reported correlation coefficient for desired level of significance and power

Usage

```
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)

R. Amala, Scientist-C, ICMR-VCRC, Puducherry & G. Kumarapandiyan, Asst. Prof., Madras Christian College, Chennai

References

Bujang, M. A., & Baharum, N. (2016). Sample size guideline for correlation analysis. World Journal of Social Science, 3(1), 37-46.

Examples

```
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

```
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

Hajian-Tilaki, K. (2014). Sample size estimation in diagnostic test studies of biomedical informatics. Journal of biomedical informatics, 48, 193-204.

Examples

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

`est.se` *Sample size for estimating sensitivity*

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)

R. Amala, Scientist-C, ICMR-VCRC, Puducherry & G. Kumarapandiyan, Asst. Prof., Madras Christian College, Chennai

References

Hajian-Tilaki, K. (2014). Sample size estimation in diagnostic test studies of biomedical informatics. Journal of biomedical informatics, 48, 193-204.

Examples

```
est.se(p = 0.10, se = 0.99, prec = 0.03, alp = 0.05)
```

estm *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)

R. Amala, Scientist-C, ICMR-VCRC, Puducherry & G. Kumarapandiyan, Asst. Prof., Madras Christian College, Chennai

References

Lwanga, S. K., Lemeshow, S., & World Health Organization. (1991). Sample size determination in health studies: a practical manual. World Health Organization.

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)
```

`estor` *Sample size for estimation of Odds Ratio with specified precision*

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

```
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)

R. Amala, Scientist-C, ICMR-VCRC, Puducherry & G. Kumarapandiyan, Asst. Prof., Madras Christian College, Chennai

References

Lwanga, S. K., Lemeshow, S., & World Health Organization. (1991). Sample size determination in health studies: a practical manual. World Health Organization.

Examples

```
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

```
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)

R. Amala, Scientist-C, ICMR-VCRC, Puducherry & G. Kumarapandiyan, Asst. Prof., Madras Christian College, Chennai

References

Lwanga, S. K., Lemeshow, S., & World Health Organization. (1991). Sample size determination in health studies: a practical manual. World Health Organization.

Examples

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

estRR *Sample size for estimation of Relative Risk*

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

p0	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)

R. Amala, Scientist-C, ICMR-VCRC, Puducherry & G. Kumarapandiyan, Asst. Prof., Madras Christian College, Chennai

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, lrneg, alp, pwr, k = 1)
```

Arguments

se	anticipated sensitivity of the diagnostic test
sp	anticipated specificity of the diagnostic test
lrneg	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)

R. Amala, Scientist-C, ICMR-VCRC, Puducherry & G. Kumarapandiyan, Asst. Prof., Madras Christian College, Chennai

References

Simel, D.L., Samsa, G.P. Matchar, D. B. (1991). Likelihood ratio with confidence: sample size estimation for diagnostic test studies. J Clin Epidemiol. 44: 763-70.

Examples

```
LRneg(se=0.9, sp=0.5,lrneg=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

```
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)

R. Amala, Scientist-C, ICMR-VCRC, Puducherry & G. Kumarapandiyan, Asst. Prof., Madras Christian College, Chennai

References

Simel, D.L., Samsa, G.P. Matchar, D. B. (1991). Likelihood ratio with confidence: sample size estimation for diagnostic test studies. J Clin Epidemiol. 44: 763-70.

Examples

```
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)

R. Amala, Scientist-C, ICMR-VCRC, Puducherry & G. Kumarapandiyan, Asst. Prof., Madras Christian College, Chennai

References

Lwanga, S. K., Lemeshow, S., & World Health Organization. (1991). Sample size determination in health studies: a practical manual. World Health Organization.

Examples

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

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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)

R. Amala, Scientist-C, ICMR-VCRC, Puducherry & G. Kumarapandiyan, Asst. Prof., Madras Christian College, Chennai

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)
```

`testor` *Sample size for testing Odds Ratio*

Description

When we try to associate multiple exposures to an outcome, we need to caluclate 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

```
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)

R. Amala, Scientist-C, ICMR-VCRC, Puducherry & G. Kumarapandiyan, Asst. Prof., Madras Christian College, Chennai

References

Lwanga, S. K., Lemeshow, S., & World Health Organization. (1991). Sample size determination in health studies: a practical manual. World Health Organization.

Examples

```
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)

R. Amala, Scientist-C, ICMR-VCRC, Puducherry & G. Kumarapandiyan, Asst. Prof., Madras Christian College, Chennai

Examples

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

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