

Package ‘epiR’

May 10, 2011

Version 0.9-32

Date 2011-05-10

Title Functions for analysing epidemiological data

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Description A package for analysing epidemiological data. Contains
functions for directly and indirectly adjusting measures of
disease frequency, quantifying measures of association on the
basis of single or multiple strata of count data presented in a
contingency table, and computing confidence intervals around
incidence risk and incidence rate estimates. Miscellaneous
functions for use in meta-analysis, diagnostic test interpretation, and sample size calculations.

Depends R (>= 2.0.0)

License GPL (>= 2)

URL <http://epicentre.massey.ac.nz>

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epi.2by2

Summary measures for count data presented in a 2 by 2 table

Description

Computes summary measures of risk and a chi-squared test for difference in the observed proportions from count data presented in a 2 by 2 table. Multiple strata may be represented by additional rows of count data and in this case crude and Mantel-Haenszel adjusted measures of risk are calculated and chi-squared tests of homogeneity are performed.

Usage

```
epi.2by2(dat, method = "cohort.count", conf.level = 0.95,
          units = 100, verbose = FALSE)
```

Arguments

<code>dat</code>	an object of class <code>table</code> with the individual cell frequencies.
<code>method</code>	a character string indicating the experimental design on which the tabular data has been based. Options are <code>cohort.count</code> , <code>cohort.time</code> , <code>case.control</code> , or <code>cross.sectional</code> .
<code>conf.level</code>	magnitude of the returned confidence interval. Must be a single number between 0 and 1.
<code>units</code>	multiplier for prevalence and incidence estimates.
<code>verbose</code>	logical indicating whether detailed or summary results are to be returned.

Details

Where `method` is `cohort.count`, `case.control`, or `cross.sectional` the 2 by 2 table format required is:

	Disease +	Disease -
Expose +	a	b
Expose -	c	d

Where `method` is `cohort.time` the 2 by 2 table format required is:

	Disease +	Time at risk
Expose +	a	b
Expose -	c	d

Value

When `method` equals `cohort.count` the following measures of association are returned: the incidence risk ratio (RR), the odds ratio (OR), the attributable risk (AR), the attributable risk in the population (ARp), the attributable fraction in the exposed (AF_e), and the attributable fraction in the population (AF_p).

When `method` equals `cohort.time` the following measures of association are returned: the incidence rate ratio (IRR), the attributable rate (AR), the attributable rate in the population (ARp), the attributable fraction in the exposed (AF_e), and the attributable fraction in the population (AF_p).

When `method` equals `case.control` the following measures of association are returned: the odds ratio (OR), the attributable prevalence (AR), the attributable prevalence in population (ARp), the estimated attributable fraction in the exposed (AF_{est}), and the estimated attributable fraction in the population (AF_p).

When `method` equals `cross.sectional` the following measures of association are returned: the prevalence ratio (PR), the odds ratio (OR), the attributable prevalence (AR), the attributable prevalence in the population (ARp), the attributable fraction in the exposed (AF_e), and the attributable fraction in the population (AF_p).

When there are multiple strata, the function returns the appropriate measure of association for each strata (e.g. OR), the crude measure of association across all strata (e.g. OR.crude) and the Mantel-Haenszel adjusted measure of association (e.g. OR.summary). Strata-level weights (i.e. inverse variance of the strata-level measures of association) are provided — these are useful to understand the relationship between the crude strata-level measures of association and the Mantel-Haenszel

adjusted measure of association. `chisq` returns the results of a chi-squared test for difference in exposed and non-exposed proportions for each strata. `chisq.summary` returns the results of a chi-squared test for difference in exposed and non-exposed proportions across all strata. The chi-squared test of homogeneity (e.g. `OR.homogeneity`) provides a test of homogeneity of the strata-level measures of association.

Note

Measures of strength of association include the prevalence ratio, the incidence risk ratio, the incidence rate ratio and the odds ratio. The incidence risk ratio is the ratio of the incidence risk of disease in the exposed group to the incidence risk of disease in the unexposed group. The odds ratio (also known as the cross-product ratio) is an estimate of the incidence risk ratio. When the incidence of an outcome in the study population is low (say, less than 5%) the odds ratio will provide a reliable estimate of the incidence risk ratio. The more frequent the outcome becomes, the more the odds ratio will overestimate the incidence risk ratio when it is greater than 1 or underestimate the incidence risk ratio when it is less than 1.

Measures of effect include the attributable risk (or prevalence) and the attributable fraction. The attributable risk is the risk of disease in the exposed group minus the risk of disease in the unexposed group. The attributable risk provides a measure of the absolute increase or decrease in risk associated with exposure. The attributable fraction is the proportion of disease in the exposed group attributable to exposure.

Measures of total effect include the population attributable risk (or prevalence) and the population attributable fraction (also known as the aetiologic fraction). The population attributable risk is the risk of disease in the population that may be attributed to exposure. The population attributable fraction is the proportion of the disease in the population that is attributable to exposure.

Point estimates and confidence intervals for the summary prevalence ratio, incidence risk ratio, incidence rate ratio, and odds ratio are based on formulae provided by Rothman (2002, p 152). The point estimate and confidence intervals for the population attributable fraction are based on formulae provided by Jewell (2004, p 84 - 85). The point estimate and confidence intervals for the summary risk differences are based on formulae provided by Rothman and Greenland (1998, p 271).

The function checks each strata for cells with zero frequencies. If a zero frequency is found in any cell, 0.5 is added to all cells within the strata.

The chi-squared test of homogeneity is equivalent to the Breslow Day test for interaction. Mantel-Haenszel adjusted measures of association are valid when the measures of association across the different strata are similar (homogenous), that is when the chi-squared test of homogeneity is not significant.

Author(s)

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References

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- Elwood JM (2007). *Critical Appraisal of Epidemiological Studies and Clinical Trials*. Oxford University Press, London.
- Feychting M, Osterlund B, Ahlbom A (1998). Reduced cancer incidence among the blind. *Epidemiology* 9: 490 - 494.

Hanley JA (2001). A heuristic approach to the formulas for population attributable fraction. *Journal of Epidemiology and Community Health* 55: 508 - 514.

Jewell NP (2004). *Statistics for Epidemiology*. Chapman & Hall/CRC, London, pp. 84 - 85.

Martin SW, Meek AH, Willeberg P (1987). *Veterinary Epidemiology Principles and Methods*. Iowa State University Press, Ames, Iowa, pp. 130.

McNutt L, Wu C, Xue X, Hafner JP (2003). Estimating the relative risk in cohort studies and clinical trials of common outcomes. *American Journal of Epidemiology* 157: 940 - 943.

Robbins AS, Chao SY, Fonesca VP (2002). What's the relative risk? A method to directly estimate risk ratios in cohort studies of common outcomes. *Annals of Epidemiology* 12: 452 - 454.

Rothman KJ (2002). *Epidemiology An Introduction*. Oxford University Press, London, pp. 130 - 143.

Rothman KJ, Greenland S (1998). *Modern Epidemiology*. Lippincott Williams, & Wilkins, Philadelphia, pp. 271.

Willeberg P (1977). Animal disease information processing: Epidemiologic analyses of the feline urologic syndrome. *Acta Veterinaria Scandinavica*. Suppl. 64: 1 - 48.

Woodward MS (2005). *Epidemiology Study Design and Data Analysis*. Chapman & Hall/CRC, New York, pp. 163 - 214.

Zhang J, Yu KF (1998). What's the relative risk? A method for correcting the odds ratio in cohort studies of common outcomes. *Journal of the American Medical Association* 280: 1690 - 1691.

Examples

```
## EXAMPLE 1
## A cross sectional study investigating the relationship between dry cat
## food (DCF) and feline urologic syndrome (FUS) was conducted (Willeberg
## 1977). Counts of individuals in each group were as follows:

## DCF-exposed cats (cases, non-cases) 13, 2163
## Non DCF-exposed cats (cases, non-cases) 5, 3349

dat <- as.table(matrix(c(13,2163,5,3349), nrow = 2, byrow = TRUE))
epi.2by2(dat = dat, method = "cross.sectional",
  conf.level = 0.95, units = 100, verbose = FALSE)

## Prevalence ratio:
## The prevalence of FUS in DCF exposed cats is 4.01 times (95% CI 1.43 to
## 11.23) greater than the prevalence of FUS in non-DCF exposed cats.

## Attributable fraction:
## In DCF exposed cats, 75% of FUS is attributable to DCF (95% CI 30% to 91%).

## Population attributable fraction:
## Fifty-four percent of FUS cases in the cat population are attributable
## to DCF (95% CI 4% to 78%).

## EXAMPLE 2
## This example shows how the table function can be used to pass data to
## epi.2by2. Generate a case-control data set comprise of 1000 subjects.
## The probability of exposure is 0.50. The probability of disease in the
## exposed is 0.75, the probability of disease in the unexposed is 0.45.
```

```

n <- 1000; p.exp <- 0.50; pd.exp <- 0.75; pd.exn <- 0.45
dat <- data.frame(exp = rep(0, times = n), stat = rep(0, times = n))
dat$exp <- rbinom(n = n, size = 1, prob = p.exp)
dat$stat[dat$exp == 1] <- rbinom(n = length(dat$stat[dat$exp == 1]),
  size = 1, prob = pd.exp)
dat$stat[dat$exp == 0] <- rbinom(n = length(dat$stat[dat$exp == 0]),
  size = 1, prob = pd.exn)
dat$exp <- factor(dat$exp, levels = c("1", "0"))
dat$stat <- factor(dat$stat, levels = c("1", "0"))
head(dat)

## Create a 2 by 2 table from this simulated data set:
dat <- table(dat$exp, dat$stat, dnn = c("Exposure", "Disease"))
dat

## 2 by 2 table analysis:
epi.2by2(dat = dat, method = "case.control",
  conf.level = 0.95, units = 100, verbose = FALSE)

## EXAMPLE 3
## A study was conducted by Feychting et al (1998) comparing cancer occurrence
## among the blind with occurrence among those who were not blind but had
## severe visual impairment. From these data we calculate a cancer rate of
## 136/22050 person-years among the blind compared with 1709/127650 person-
## years among those who were visually impaired but not blind.

dat <- as.table(matrix(c(136,22050,1709,127650), nrow = 2, byrow = TRUE))
rval <- epi.2by2(dat = dat, method = "cohort.time", conf.level = 0.90,
  units = 1000, verbose = TRUE)
round(rval$AR, digits = 3)

## The incidence rate of cancer was 7.22 cases per 1000 person-years less in the
## blind, compared with those who were not blind but had severe visual impairment
## (90% CI 6.20 to 8.24 cases per 1000 person-years).

round(rval$IRR, digits = 3)

## The incidence rate of cancer in the blind group was less than half that of the
## comparison group (incidence rate ratio 0.46, 90% CI 0.40 to 0.53).

## EXAMPLE 4
## The results of an unmatched case control study of the association between
## smoking and cervical cancer were stratified by age. Counts of individuals
## in each group were as follows:

## Age group 20 - 29 years (cases, controls)
## Smokers: 41, 6
## Non-smokers: 13, 53

## Age group 30 - 39 years (cases, controls)
## Smokers: 66, 25
## Non-smokers: 37, 83

## Age +40 years (cases, controls)
## Smokers: 23, 14

```

```
## Non-smokers: 37, 62

## Coerce the count data that has been provided into tabular format:
dat <- data.frame(strata = rep(c("20-29 yrs", "30-39 yrs", "+40 yrs"), each = 2),
  exp = rep(c("+", "-"), times = 3), dis = rep(c("+", "-"), times = 3))
dat$exp <- factor(dat$exp, levels = c("+", "-"))
dat$dis <- factor(dat$dis, levels = c("+", "-"))
dat <- table(dat$exp, dat$dis, dat$strata,
  dnn = c("Exposure", "Disease", "Strata"))

dat[1,1,] <- c(41,66,23)
dat[1,2,] <- c(6,25,14)
dat[2,1,] <- c(13,37,37)
dat[2,2,] <- c(53,83,62)

tmp.2by2 <- epi.2by2(dat = dat, method = "case.control", conf.level = 0.95,
  units = 100, verbose = TRUE)
tmp.2by2

## Crude odds ratio:
## 6.57 (95% CI 4.31 to 10.03)

## Mantel-Haenszel adjusted odds ratio:
## 6.27 (95% CI 3.52 to 11.17)

## Summary chi-squared test for difference in proportions:
## Test statistic 83.31; df = 1; P < 0.01

## Test of homeogeneity of odds ratios:
## Test statistic 2.09; df = 2; P = 0.35

## We accept the null hypothesis that the strata level odds ratios
## are homogenous. The crude odds ratio is 6.57 (95% CI 4.31 -- 10.03).
## The Mantel-Haenszel adjusted odds ratio is 6.27 (95% CI 3.52 to 11.17).
## The crude odds ratio is 1.05 times the magnitude of the Mantel-Haenszel
## adjusted odds ratio so we conclude that age does not confound the association
## between smoking and risk of cervical cancer (using a ratio of greater
## than 1.10 or less than 0.90 as indicative of the presence of confounding).

## Now plot the individual strata-level odds ratio and compare them with the
## Mantel-Haenszel adjusted odds ratio.

## Not run:
## Not run: library(latticeExtra)
nstrata <- 1:dim(dat)[3]
strata.lab <- paste("Strata ", nstrata, sep = "")
y.at <- c(nstrata, max(nstrata) + 1)
y.labels <- c("Mantel-Haenszel", strata.lab)
x.labels <- c(0.5, 1, 2, 4, 8, 16, 32, 64, 128)

or.l <- c(tmp.2by2$OR.summary$lower, tmp.2by2$OR$lower)
or.u <- c(tmp.2by2$OR.summary$upper, tmp.2by2$OR$upper)
or.p <- c(tmp.2by2$OR.summary$est, tmp.2by2$OR$est)
vert <- 1:length(or.p)

segplot(vert ~ or.l + or.u, centers = or.p, horizontal = TRUE,
  aspect = 1/2, col = "grey",
```

```

ylim = c(0,vert + 1),
xlab = "Odds ratio", ylab = "",
scales = list(y = list(at = y.at, labels = y.labels, ticks = FALSE)),
main = "Strata level and summary measures of association")
## End(Not run)
## End(Not run)

## In this example the precision of both strata 2 and 3 odds ratio estimates is
## high (i.e. the confidence intervals are narrow) so strata 2 and 3 carry most
## of the weight in determining the value of the Mantel-Haenszel adjusted
## odds ratio.

```

epi.about

The library epiR: summary information

Description

Functions for quantitative epidemiology.

Usage

```
epi.about()
```

Details

The most recent version of the epiR package can be obtained from: <http://epicentre.massey.ac.nz/>

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epi.asc

Write matrix to an ASCII raster file

Description

Writes a data frame to an ASCII raster file, suitable for display in ArcView or ArcGIS.

Usage

```
epi.asc(dat, file, xllcorner, yllcorner, cellsize, na = -9999)
```


Arguments

<code>dat</code>	a matrix with data suitable for plotting using the <code>image</code> function.
<code>file</code>	character string specifying the name and path of the ASCII raster output file.
<code>xllcorner</code>	the easting coordinate corresponding to the lower left hand corner of the matrix.
<code>yllcorner</code>	the northing coordinate corresponding to the lower left hand corner of the matrix.
<code>cellsize</code>	number, defining the size of each matrix cell.
<code>na</code>	scalar, defines null values in the matrix. NAs are converted to this value.

Value

Writes an ASCII raster file (typically with `*.asc` extension), suitable for display in a GIS package.

Note

The `image` function in R rotates tabular data counter clockwise by 90 degrees for display. A matrix of the form:

```
1  3
2  4
```

is displayed (using `image`) as:

```
3  4
1  2
```

It is recommended that the source data for this function is a matrix. Replacement of NAs in a data frame extends processing time for this function.

epi.bohning

Bohning's test for overdispersion of Poisson data

Description

A test for overdispersion of Poisson data.

Usage

```
epi.bohning(obs, exp, alpha = 0.05)
```

Arguments

<code>obs</code>	the observed number of cases in each area.
<code>exp</code>	the expected number of cases in each area.
<code>alpha</code>	alpha level to be used for the test of significance. Must be a single number between 0 and 1.

Value

A data frame with two elements: `test.statistic` Bohning's test statistic, `p.value` the associated P-value.

References

Bohning D (2000). Computer-assisted Analysis of Mixtures and Applications. Chapman and Hall, Boca Raton.

Ugarte MD, Ibanez B, Militino AF (2006). Modelling risks in disease mapping. Statistical Methods in Medical Research 15: 21 - 35.

Examples

```
data(epi.SClip)
obs <- epi.SClip$cases
pop <- epi.SClip$population
exp <- (sum(obs) / sum(pop)) * pop

epi.bohning(obs, exp, alpha = 0.05)
```

epi.ccc

Concordance correlation coefficient

Description

Calculates Lin's (1989, 2000) concordance correlation coefficient for agreement on a continuous measure.

Usage

```
epi.ccc(x, y, ci = "z-transform", conf.level = 0.95)
```

Arguments

<code>x</code>	a vector, representing the first set of measurements.
<code>y</code>	a vector, representing the second set of measurements.
<code>ci</code>	a character string, indicating the method to be used. Options are <code>z-transform</code> or <code>asymptotic</code> .
<code>conf.level</code>	magnitude of the returned confidence interval. Must be a single number between 0 and 1.

Details

Computes Lin's (1989, 2000) concordance correlation coefficient for agreement on a continuous measure obtained by two methods. The concordance correlation coefficient combines measures of both precision and accuracy to determine how far the observed data deviate from the line of perfect concordance (that is, the line at 45 degrees on a square scatter plot). Lin's coefficient increases in value as a function of the nearness of the data's reduced major axis to the line of perfect concordance (the accuracy of the data) and of the tightness of the data about its reduced major axis (the precision of the data).

Both x and y values need to be present for a measurement pair to be included in the analysis. If either or both values are missing (i.e. coded NA) then the measurement pair is deleted before analysis.

Value

A list containing the following:

<code>rho.c</code>	the concordance correlation coefficient.
<code>s.shift</code>	the scale shift.
<code>l.shift</code>	the location shift.
<code>C.b</code>	a bias correction factor that measures how far the best-fit line deviates from a line at 45 degrees. No deviation from the 45 degree line occurs when $C.b = 1$. See Lin (1989, page 258).
<code>blalt</code>	a data frame with two columns: <code>mean</code> the mean of each pair of measurements, <code>delta</code> vector y minus vector x .
<code>nmissing</code>	a count of the number of measurement pairs ignored due to missingness.

References

- Bland J, Altman D (1986). Statistical methods for assessing agreement between two methods of clinical measurement. *The Lancet* 327: 307 - 310.
- Bradley E, Blackwood L (1989). Comparing paired data: a simultaneous test for means and variances. *American Statistician* 43: 234 - 235.
- Dunn G (2004). *Statistical Evaluation of Measurement Errors: Design and Analysis of Reliability Studies*. London: Arnold.
- Hsu C (1940). On samples from a normal bivariate population. *Annals of Mathematical Statistics* 11: 410 - 426.
- Krippendorff K (1970). Bivariate agreement coefficients for reliability of data. In: Borgatta E, Bohrnstedt G (eds) *Sociological Methodology*. San Francisco: Jossey-Bass, pp. 139 - 150.
- Lin L (1989). A concordance correlation coefficient to evaluate reproducibility. *Biometrics* 45: 255 - 268.
- Lin L (2000). A note on the concordance correlation coefficient. *Biometrics* 56: 324 - 325.
- Pitman E (1939). A note on normal correlation. *Biometrika* 31: 9 - 12.
- Reynolds M, Gregoire T (1991). Comment on Bradley and Blackwood. *American Statistician* 45: 163 - 164.
- Snedecor G, Cochran W (1989). *Statistical Methods*. Ames: Iowa State University Press.

Examples

```
## Concordance correlation plot:
set.seed(seed = 1234)
method1 <- rnorm(n = 100, mean = 0, sd = 1)
method2 <- method1 + runif(n = 100, min = 0, max = 1)

## Introduce some missing values:
method1[50] <- NA
method2[75] <- NA

tmp.ccc <- epi.ccc(method1, method2, ci = "z-transform",
```

```

conf.level = 0.95)

lab <- paste("CCC: ", round(tmp.ccc$rho.c[,1], digits = 2), " (95% CI ",
  round(tmp.ccc$rho.c[,2], digits = 2), " - ",
  round(tmp.ccc$rho.c[,3], digits = 2), ")", sep = "")
z <- lm(method2 ~ method1)

par(pty = "s")
plot(method1, method2, xlim = c(0, 5), ylim = c(0,5), xlab = "Method 1",
  ylab = "Method 2", pch = 16)
abline(a = 0, b = 1, lty = 2)
abline(z, lty = 1)
legend(x = "topleft", legend = c("Line of perfect concordance",
  "Reduced major axis"), lty = c(2,1), lwd = c(1,1), bty = "n")
text(x = 1.55, y = 3.8, labels = lab)

## Bland and Altman plot (Figure 2 from Bland and Altman 1986):
x <- c(494,395,516,434,476,557,413,442,650,433,417,656,267,
  478,178,423,427)

y <- c(512,430,520,428,500,600,364,380,658,445,432,626,260,
  477,259,350,451)

tmp.ccc <- epi.ccc(x, y, ci = "z-transform", conf.level = 0.95)
tmp.mean <- mean(tmp.ccc$blalt$delta)
tmp.sd <- sqrt(var(tmp.ccc$blalt$delta))

plot(tmp.ccc$blalt$mean, tmp.ccc$blalt$delta, pch = 16,
  xlab = "Average PEFR by two meters (L/min)",
  ylab = "Difference in PEFR (L/min)", xlim = c(0,800),
  ylim = c(-140,140))
abline(h = tmp.mean, lty = 1, col = "gray")
abline(h = tmp.mean - (2 * tmp.sd), lty = 2, col = "gray")
abline(h = tmp.mean + (2 * tmp.sd), lty = 2, col = "gray")
legend(x = "topleft", legend = c("Mean difference",
  "Mean difference +/- 2SD"), lty = c(1,2), bty = "n")
legend(x = 0, y = 125, legend = c("Difference"), pch = 16,
  bty = "n")

```

epi.cluster1size *Sample size under one-stage cluster sampling*

Description

Returns the required number of clusters to be sampled using a one-stage cluster sampling strategy.

Usage

```
epi.cluster1size(n, mean, var, epsilon.r, method = "mean",
  conf.level = 0.95)
```

Arguments

n integer, representing the total number of clusters in the population.

mean	number, representing the population mean of the variable of interest.
var	number, representing the population variance of the variable of interest.
epsilon.r	the maximum relative difference between our estimate and the unknown population value.
method	a character string indicating the method to be used. Options are <code>total</code> , <code>mean</code> or <code>mean.per.unit</code> .
conf.level	scalar, defining the level of confidence in the computed result.

Value

Returns an integer defining the required number of clusters to be sampled.

References

Levy PS, Lemeshow S (1999). Sampling of Populations Methods and Applications. Wiley Series in Probability and Statistics, London, pp. 258.

Examples

```
## We intend to conduct a survey of residents to estimate the total number
## over 65 years of age that require the services of a nurse. There are
## five housing complexes in the study area and we expect that there might
## be a total of around 34 residents meeting this criteria (variance 6.8).
## We would like the estimated sample size to provide us with an estimate
## that is within 10% of the true value. How many housing complexes (clusters)
## should be sampled?

epi.cluster1size(n = 5, mean = 34, var = 6.8, epsilon.r = 0.10, method =
  "total", conf.level = 0.999)

## We would need to sample 3 housing complexes to meet the specifications
## for this study.
```

epi.cluster2size *Sample size under under two-stage cluster sampling*

Description

Returns the required number of clusters to be sampled using a two-stage cluster sampling strategy.

Usage

```
epi.cluster2size(nbar, n, mean, var, epsilon.r, method = "mean",
  conf.level = 0.95)
```

Arguments

<code>nbar</code>	integer, representing the total number of primary sampling units to be selected from each cluster.
<code>n</code>	vector of length two, specifying the total number of clusters in the population and the total number of primary sampling units in each cluster, respectively.
<code>mean</code>	vector of length two, specifying the mean of the variable of interest at the cluster level and the mean of the variable of interest at the primary sampling unit level, respectively.
<code>var</code>	vector of length two, specifying the variance of the variable of interest at the cluster level and the variance of the variable of interest at the primary sampling unit level, respectively.
<code>epsilon.r</code>	the maximum relative difference between our estimate and the unknown population value.
<code>method</code>	a character string indicating the method to be used. Options are <code>total</code> , or <code>mean</code> .
<code>conf.level</code>	scalar, defining the level of confidence in the computed result.

Details

In simple two-stage cluster sampling the desired number of primary sampling units to be selected from each cluster is determined on the basis of cost and on the basis of the relative sizes of the first- and second-stage variance components. Once the number of primary sampling units is fixed we might then wish to determine the total number of clusters to be selected at the first stage of sampling in order to be confident of obtaining estimates that reflect the true population value.

Value

Returns an integer defining the required number of clusters to be sampled.

References

Levy PS, Lemeshow S (1999). Sampling of Populations Methods and Applications. Wiley Series in Probability and Statistics, London, pp. 292.

Examples

```
## We intend to conduct a survey of nurse practitioners to estimate the
## average number of patients seen by each nurse. There are five health
## centres in the study area, each with three nurses. We intend to sample
## two nurses from each health centre. We would like to be 95% confident
## of obtaining an estimate that is within 30% of the true population value.
## We expect that the mean number of patients seen at the health centre level
## is 84 (var 567) and the mean number of patients seen at the nurse
## level is 28 (var 160). How many health centres should we sample?

nbar <- 2; n <- c(5, 3); mean <- c(84, 28); var <- c(567, 160)
epi.cluster2size(nbar, n, mean, var, epsilon.r = 0.3, method = "mean",
  conf.level = 0.95)

## We would need a simple two-stage cluster sample of 3 health centres to
## meet these specifications.
```

epi.clustersize	<i>Sample size for cluster-sample surveys</i>
-----------------	---

Description

Estimates the number of clusters to be sampled using a cluster-sample design.

Usage

```
epi.clustersize(p, b, rho, epsilon, conf.level = 0.95)
```

Arguments

<code>p</code>	the estimated prevalence of disease in the population.
<code>b</code>	the number of units to be sampled per cluster.
<code>rho</code>	the intra-cluster correlation, a measure of the variation between clusters compared with the variation within clusters.
<code>epsilon</code>	scalar, the acceptable absolute error.
<code>conf.level</code>	scalar, defining the level of confidence in the computed result.

Value

A list containing the following:

<code>clusters</code>	the estimated number of clusters to be sampled.
<code>units</code>	the total number of units to be sampled.
<code>design</code>	the design effect.

Note

The intra-cluster correlation (`rho`) will be higher for those situations where the between-cluster variation is greater than within-cluster variation. The design effect is dependent on `rho` and `b` (the number of units sampled per cluster): $\text{rho} = (D - 1) / (b - 1)$. Design effects of 2, 4, and 7 can be used to estimate `rho` when intra-cluster correlation is low, medium, and high (respectively). A design effect of 7.5 should be used when the intra-cluster correlation is unknown.

References

Otte J, Gumm I (1997). Intra-cluster correlation coefficients of 20 infections calculated from the results of cluster-sample surveys. Preventive Veterinary Medicine 31: 147 - 150.

Bennett S, Woods T, Liyanage WM, Smith DL (1991). A simplified general method for cluster-sample surveys of health in developing countries. Rapport trimestriel de statistiques sanitaires modiales 44: 98 - 106.

Examples

```
## The expected prevalence of disease in a population of cattle is 0.10.
## We wish to conduct a survey, sampling 50 animals per farm. No data
## are available to provide an estimate of rho, though we suspect
## the intra-cluster correlation for this disease to be relatively high.
## We wish to be 95% certain of being within 10% of the true population
## prevalence of disease. How many herds should be sampled?

p <- 0.10
b <- 50
D <- 7
rho <- (D - 1) / (b - 1)
epi.clustersize(p = 0.10, b = 50, rho = rho, epsilon = 0.10, conf.level = 0.95)

## We need to sample 485 herds (24250 samples in total).
```

epi.conf

Confidence intervals for means, proportions, incidence, and standardised mortality ratios

Description

Computes confidence intervals for means, proportions, incidence, and standardised mortality ratios.

Usage

```
epi.conf(dat, ctype = "mean.single", method, N, design = 1,
         conf.level = 0.95)
```

Arguments

dat	the data, either a vector or a matrix depending on the method chosen.
ctype	a character string indicating the type of confidence interval to calculate. Options are mean.single, mean.unpaired, mean.paired, prop.single, prop.unpaired, prop.paired, prevalence, inc.risk, inc.rate, and smr.
method	a character string indicating the method to use. Where ctype = "inc.risk" or ctype = "prevalence" options are exact, wilson and fleiss. Where ctype = "inc.rate" options are exact and byar.
N	scalar, representing the population size.
design	scalar, representing the design effect.
conf.level	magnitude of the returned confidence interval. Must be a single number between 0 and 1.

Details

Method mean.single requires a vector as input. Method mean.unpaired requires a two-column data frame; the first column defining the groups must be a factor. Method mean.paired requires a two-column data frame; one column for each group. Method prop.single requires a two-column matrix; the first column specifies the number of positives, the second column specifies the number of negatives. Methods prop.unpaired and prop.paired require a four-column

matrix; columns 1 and 2 specify the number of positives and negatives for the first group, columns 3 and 4 specify the number of positives and negatives for the second group. Method `prevalence` and `inc.risk` require a two-column matrix; the first column specifies the number of positives, the second column specifies the total number tested. Method `inc.rate` requires a two-column matrix; the first column specifies the number of positives, the second column specifies individual time at risk. Method `smr` requires a two-column matrix; the first column specifies the total number of positives, the second column specifies the total number tested.

The methodology implemented here follows Altman, Machin, Bryant, and Gardner (2000). Where method is `inc.risk`, `prevalence` or `inc.rate` if the numerator equals zero the lower bound of the confidence interval estimate is set to zero. Where method is `smr` the method of Dobson et al. (1991) is used. A summary of the methods used for each of the confidence interval calculations is as follows:

cotype-method	Reference
<code>mean.single</code>	Altman et al. (2000)
<code>mean.unpaired</code>	Altman et al. (2000)
<code>mean.paired</code>	Altman et al. (2000)
<code>prop.single</code>	Altman et al. (2000)
<code>prop.unpaired</code>	Altman et al. (2000)
<code>prop.paired</code>	Altman et al. (2000)
<code>inc.risk, exact</code>	Collett (1999)
<code>inc.risk, wilson</code>	Rothman (2002)
<code>inc.risk, fleiss</code>	Fleiss (1981)
<code>prevalence, exact</code>	Collett (1999)
<code>prevalence, wilson</code>	Rothman (2002)
<code>prevalence, fleiss</code>	Fleiss (1981)
<code>inc.rate, exact</code>	Collett (1999)
<code>inc.rate, byar</code>	Rothman (2002)
<code>smr</code>	Dobson et al. (1991)

The design effect is used to adjust the confidence interval around a prevalence or incidence risk estimate in the presence of clustering. The design effect is a measure of the variability between clusters and is calculated as the ratio of the variance calculated assuming a complex sample design divided by the variance calculated assuming simple random sampling. Adjustment for the effect of clustering can only be done on those prevalence and incidence risk methods that return a standard error (i.e. `method = "wilson"` or `method = "fleiss"`).

References

- Altman DG, Machin D, Bryant TN, and Gardner MJ (2000). Statistics with Confidence, second edition. British Medical Journal, London, pp. 28 - 29 and pp. 45 - 56.
- Collett D (1999). Modelling Binary Data. Chapman & Hall/CRC, Boca Raton Florida, p. 24.
- Dobson AJ, Kuulasmaa K, Eberle E, and Scherer J (1991). Confidence intervals for weighted sums of Poisson parameters. Statistics in Medicine 10: 457 - 462.
- Fleiss JL (1981). Statistical Methods for Rates and Proportions. 2nd edition. John Wiley & Sons, New York.
- Killip S, Mahfoud Z, Pearce K (2004). What is an intraclass correlation coefficient? Crucial concepts for primary care researchers. Annals of Family Medicine 2: 204 - 208.
- Otte J, Gumm I (1997). Intra-cluster correlation coefficients of 20 infections calculated from the results of cluster-sample surveys. Preventive Veterinary Medicine 31: 147 - 150.

Rothman KJ (2002). *Epidemiology An Introduction*. Oxford University Press, London, pp. 130 - 143.

Examples

```
## EXAMPLE 1
dat <- rnorm(n = 100, mean = 0, sd = 1)
epi.conf(dat, ctype = "mean.single")

## EXAMPLE 2
group <- c(rep("A", times = 5), rep("B", times = 5))
val = round(c(rnorm(n = 5, mean = 10, sd = 5),
              rnorm(n = 5, mean = 7, sd = 5)), digits = 0)
dat <- data.frame(group = group, val = val)
epi.conf(dat, ctype = "mean.unpaired")

## EXAMPLE 3
grp1 <- as.vector(round(rnorm(n = 100, mean = 10, sd = 5), digits = 0))
grp2 <- as.vector(round(rnorm(n = 100, mean = 7, sd = 5), digits = 0))
dat <- data.frame(cbind(grp1 = grp1, grp2 = grp2))
epi.conf(dat, ctype = "mean.paired")

## EXAMPLE 4
## Single sample (Altman et al. 2000, page 47):
## Out of 263 giving their views on the use of personal computers in
## general practice, 81 thought that the privacy of their medical file
## had been reduced.

pos <- 81
neg <- (263 - 81)
dat <- as.matrix(cbind(pos, neg))
round(epi.conf(dat, ctype = "prop.single"), digits = 3)

## The 95% confidence interval for the population value of the proportion
## of patients thinking their privacy was reduced was from 0.255 to 0.366.

## EXAMPLE 5
## Two samples, unpaired (Altman et al. 2000, page 49):
## Goodfield et al. report adverse effects in 85 patients receiving either
## terbinafine or placebo treatment for dermatophyte onychomycosis.
## Out of 56 patients receiving terbinafine, 5 patients experienced
## adverse effects. Out of 29 patients receiving a placebo, none experienced
## adverse effects.

grp1 <- matrix(cbind(5, 51), ncol = 2)
grp2 <- matrix(cbind(0, 29), ncol = 2)
dat <- as.matrix(cbind(grp1, grp2))
round(epi.conf(dat, ctype = "prop.unpaired"), digits = 3)

## The 95% confidence interval for the difference between the two groups is
## from -0.038 to +0.193.

## EXAMPLE 6
## Two samples, paired (Altman et al. 2000, page 53):
## In a reliability exercise, 41 patients were randomly selected from those
## who had undergone a thallium-201 stress test. The 41 sets of images were
## classified as normal or not by the core thallium laboratory and,
```

```
## independently, by clinical investigators from different centres.
## Of the 19 samples identified as ischaemic by clinical investigators
## 5 were identified as ischaemic by the laboratory. Of the 22 samples
## identified as normal by clinical investigators 0 were identified as
## ischaemic by the laboratory.
```

```
## Clinic      | Laboratory   |           |
##             | Ischaemic    | Normal    | Total
## -----
## Ischaemic   | 14           | 5         | 19
## Normal      | 0            | 22        | 22
## -----
## Total       | 14           | 27        | 41
## -----
```

```
dat <- as.matrix(cbind(14, 5, 0, 22))
round(epi.conf(dat, ctype = "prop.paired", conf.level = 0.95), digits = 3)
```

```
## The 95% confidence interval for the population difference in
## proportions is 0.011 to 0.226 or approximately +1% to +23%.
```

```
## EXAMPLE 7
## A herd of 1000 cattle were tested for brucellosis. Two samples out of 200
## test returned a positive result. Assuming 100% test sensitivity and
## specificity, what is the estimated prevalence of brucellosis in this
## group of animals?
```

```
pos <- 4; pop <- 200
dat <- as.matrix(cbind(pos, pop))
epi.conf(dat, ctype = "prevalence", method = "exact", N = 1000,
  design = 1, conf.level = 0.95) * 100
```

```
## The estimated prevalence of brucellosis in this herd is 2 cases
## per 100 cattle (95% CI 0.54 -- 5.0 cases per 100 cattle).
```

```
## EXAMPLE 8
## The observed disease counts and population size in four areas are provided
## below. What are the the standardised morbidity ratios of disease for each
## area and their 95% confidence intervals?
```

```
obs <- c(5, 10, 12, 18); pop <- c(234, 189, 432, 812)
dat <- as.matrix(cbind(obs, pop))
round(epi.conf(dat, ctype = "smr"), digits = 2)
```

```
## EXAMPLE 9
## A survey has been conducted to determine the proportion of broilers
## protected from a given disease following vaccination. We assume that
## the intra-cluster correlation coefficient for protection (also known as the
## rate of homogeneity, rho) is 0.4 and the average number of birds per
## flock is 30. A total of 5898 birds from a total of 10363 were identified
## as protected. What proportion of birds are protected and what is the 95%
## confidence interval for this estimate?
```

```
## Calculate the design effect, given rho = (design - 1) / (nbar - 1), where
## nbar equals the average number of individuals per cluster:
```

```
design <- 0.4 * (30 - 1) + 1
```

```
## The design effect is 12.6. Now calculate the proportion protected:

dat <- as.matrix(cbind(5898, 10363))
epi.conf(dat, ctype = "prevalence", method = "fleiss", N = 1000000,
         design = design, conf.level = 0.95)

## The estimated proportion of the population protected is 0.57 (95% CI
## 0.53 -- 0.60). If we had mistakenly assumed that data were a simple random
## sample the confidence interval would have been 0.56 -- 0.58.
```

epi.convgrid	<i>Convert British National Grid georeferences to easting and northing coordinates</i>
--------------	--

Description

Convert British National Grid georeferences to easting and northing coordinates.

Usage

```
epi.convgrid(os.refs)
```

Arguments

<code>os.refs</code>	a vector of character strings listing the British National Grid georeferences to be converted.
----------------------	--

Note

If an invalid georeference is encountered in the vector `os.ref` the method returns a NA.

Examples

```
os.refs <- c("SJ505585", "SJ488573", "SJ652636")
epi.convgrid(os.refs)
```

epi.cp	<i>Extract unique covariate patterns from a data set</i>
--------	--

Description

Extract the set of unique patterns from a set of covariates.

Usage

```
epi.cp(dat)
```

Arguments

`dat` an i row by j column data frame where the i rows represent individual observations and the m columns represent covariates.

Details

A covariate pattern is a unique combination of values of predictor variables. For example, if a model contains two dichotomous predictors, there will be four covariate patterns possible: $(1, 1)$, $(1, 0)$, $(0, 1)$, and $(0, 0)$. This function extracts the n unique covariate patterns from a data set comprised of i observations, labelling them from 1 to n . A vector of length m is also returned, listing the covariate pattern identifier for each observation.

Value

A list containing the following:

`cov.pattern` a data frame with columns: `id` the unique covariate patterns, `n` the number of occasions each of the listed covariate pattern appears in the data, and the unique covariate combinations.

`id` a vector listing the covariate pattern identifier for each observation.

References

Dohoo I, Martin W, Stryhn H (2003). Veterinary Epidemiologic Research. AVC Inc, Charlottetown, Prince Edward Island, Canada.

Examples

```
## Generate a set of covariates:
set.seed(seed = 1234)
obs <- round(runif(n = 100, min = 0, max = 1), digits = 0)
v1 <- round(runif(n = 100, min = 0, max = 4), digits = 0)
v2 <- round(runif(n = 100, min = 0, max = 4), digits = 0)
dat <- as.data.frame(cbind(obs, v1, v2))

dat.glm <- glm(obs ~ v1 + v2, family = binomial, data = dat)
dat.mf <- model.frame(dat.glm)

## Covariate pattern:
epi.cp(dat.mf[-1])

## There are 25 covariate patterns in this data set. Subject 100 has
## covariate pattern 21.
```

Description

Returns covariate pattern residuals and delta betas from a logistic regression model.

Usage

```
epi.cpresids(obs, fit, covpattern)
```

Arguments

obs	a vector of observed values (i.e. counts of ‘successes’) for each covariate pattern).
fit	a vector defining the predicted (i.e. fitted) probability of success for each covariate pattern.
covpattern	a epi.cp object.

Value

A data frame with 13 elements: `cpid` the covariate pattern identifier, `n` the number of subjects in this covariate pattern, `obs` the observed number of successes, `pred` the predicted number of successes, `raw` the raw residuals, `sraw` the standardised raw residuals, `pearson` the Pearson residuals, `spearson` the standardised Pearson residuals, `deviance` the deviance residuals, `leverage` leverage, `deltabeta` the delta-betas, `sdeltabeta` the standardised delta-betas, and `deltachi` delta chi statistics.

References

Hosmer DW, Lemeshow S (1989). Applied Logistic Regression. John Wiley & Sons, New York, USA, pp. 137 - 138.

See Also

[epi.cp](#)

Examples

```
infert.glm <- glm(case ~ spontaneous + induced, data = infert,
  family = binomial())

infert.mf <- model.frame(infert.glm)
infert.cp <- epi.cp(infert.mf[-1])

infert.obs <- as.vector(by(infert$case, as.factor(infert.cp$id),
  FUN = sum))
infert.fit <- as.vector(by(fitted(infert.glm), as.factor(infert.cp$id),
  FUN = min))
infert.res <- epi.cpresids(obs = infert.obs, fit = infert.fit,
  covpattern = infert.cp)
```

epi.descriptives *Descriptive statistics*

Description

Computes descriptive statistics from a vector of numbers.

Usage

```
epi.descriptives(dat, quantile = c(0.025, 0.975))
```

Arguments

`dat` vector for which descriptive statistics will be calculated.

`quantile` vector of length two specifying quantiles to be calculated.

Examples

```
tmp <- rnorm(1000, mean = 0, sd = 1)
epi.descriptives(tmp, quantile = c(0.025, 0.975))
```

<code>epi.detectsize</code>	<i>Sample size to detect disease</i>
-----------------------------	--------------------------------------

Description

Estimates the required sample size to detect disease. The method adjusts sample size estimates on the basis of test sensitivity and specificity and can account for series and parallel test interpretation.

Usage

```
epi.detectsize(N, prev, se, sp, interpretation = "series",
  covar = c(0,0), conf.level = 0.95, finite.correction = TRUE)
```

Arguments

`N` a vector of length one or two defining the size of the population. The first element of the vector defines the number of clusters, the second element defining the mean number of sampling units per cluster.

`prev` a vector of length one or two defining the prevalence of disease in the population. The first element of the vector defines the between-cluster prevalence, the second element defines the within-cluster prevalence.

`se` a vector of length one or two defining the sensitivity of the test(s) used.

`sp` a vector of length one or two defining the specificity of the test(s) used.

`interpretation` a character string indicating how test results should be interpreted. Options are `series` or `parallel`.

`covar` a vector of length two defining the covariance between test results for disease positive and disease negative groups. The first element of the vector is the covariance between test results for disease positive subjects. The second element of the vector is the covariance between test results for disease negative subjects. Use `covar = c(0, 0)` (the default) if these values are not known.

`conf.level` scalar, defining the level of confidence in the computed result.

`finite.correction` logical, should a finite correction factor be applied?

Value

A list containing the following:

performance The sensitivity and specificity of the testing strategy.
 sample.size The number of clusters, units, and total number of units to be sampled.

Note

The finite correction factor reduces the variance of the sample as the sample size approaches the population size. As a rule of thumb, set `finite.correction = TRUE` when the sample size is greater than 5% of the population size.

Define `se1` and `se2` as the sensitivity for the first and second test, `sp1` and `sp2` as the specificity for the first and second test, `p111` as the proportion of disease-positive subjects with a positive test result to both tests and `p000` as the proportion of disease-negative subjects with a negative test result to both tests. The covariance between test results for the disease-positive group is $p111 - se1 * se2$. The covariance between test results for the disease-negative group is $p000 - sp1 * sp2$.

References

Dohoo I, Martin W, Stryhn H (2003). Veterinary Epidemiologic Research. AVC Inc, Charlottetown, Prince Edward Island, Canada, pp. 47 and pp 102 - 103.

Examples

```
## EXAMPLE 1
## We would like to confirm the absence of disease in a single 1000-cow
## dairy herd. We expect the prevalence of disease in the herd to be 5%.
## We intend to use a single test with a sensitivity of 0.90 and a
## specificity of 0.80. How many samples should we take to be 95% certain
## that, if all tests are negative, the disease is not present?

epi.detectsize(N = 1000, prev = 0.05, se = 0.90, sp = 0.80, interpretation =
  "series", covar = c(0,0), conf.level = 0.95, finite.correction = TRUE)

## We need to sample 59 cows.

## EXAMPLE 2
## We would like to confirm the absence of disease in a study area. If the
## disease is present we expect the between-herd prevalence to be 8% and the
## within-herd prevalence to be 5%. We intend to use two tests: the first has
## a sensitivity and specificity of 0.90 and 0.80, respectively. The second
## has a sensitivity and specificity of 0.95 and 0.85, respectively. The two
## tests will be interpreted in parallel. How many herds and cows within herds
## should we sample to be 95% certain that the disease is not present in the
## study area if all tests are negative? There area is comprised of
## approximately 5000 herds and the average number of cows per herd is 100.

epi.detectsize(N = c(5000, 100), prev = c(0.08, 0.05), se = c(0.90, 0.95),
  sp = c(0.80, 0.85), interpretation = "parallel", covar = c(0,0),
  conf.level = 0.95, finite.correction = TRUE)

## We need to sample 31 cows from 38 herds (a total of 1178 samples).
## The sensitivity of this testing regime is 99%. The specificity of this
## testing regime is 68%.
```



```
## EXAMPLE 3
## You want to document the absence of Mycoplasma from a 200-sow pig herd.
## Based on your experience and the literature, a minimum of 20% of sows
## would have seroconverted if Mycoplasma were present in the herd. How many
## sows do you need to sample?

epi.detectsize(N = 200, prev = 0.20, se = 1.00, sp = 1.00, conf.level = 0.95,
  finite.correction = TRUE)

## If you test 12 sows and all test negative you can state that you are 95%
## confident that the prevalence rate of Mycoplasma in the herd is less than
## 20%.
```

epi.dgamma

*Estimate the precision of a [structured] heterogeneity term***Description**

Returns the precision of a [structured] heterogeneity term after one has specified the amount of variation *a priori*.

Usage

```
epi.dgamma(rr, quantiles = c(0.05, 0.95))
```

Arguments

<code>rr</code>	the lower and upper limits of relative risk, estimated <i>a priori</i> .
<code>quantiles</code>	a vector of length two defining the quantiles of the lower and upper relative risk estimates.

Value

Returns the precision (the inverse variance) of the heterogeneity term.

References

Best, NG. WinBUGS 1.3.1 Short Course, Brisbane, November 2000.

Examples

```
## Suppose we are expecting the lower 5% and upper 95% confidence interval
## of relative risk in a data set to be 0.5 and 3.0, respectively.
## A prior guess at the precision of the heterogeneity term would be:

tau <- epi.dgamma(rr = c(0.5, 3.0), quantiles = c(0.05, 0.95))
tau

## This can be translated into a gamma distribution. We set the mean of the
## distribution as tau and specify a large variance (that is, we are not
## certain about tau).
```

```

mean <- tau
var <- 1000
shape <- mean^2 / var
inv.scale <- mean / var

## In WinBUGS the precision of the heterogeneity term may be parameterised
## as tau ~ dgamma(shape, inv.scale). Plot the probability density function
## of tau:

z <- seq(0.01, 10, by = 0.01)
fz <- dgamma(z, shape = shape, scale = 1/inv.scale)
plot(z, fz, type = "l", ylab = "Probability density of tau")

```

epi.directadj

Directly adjusted measures of disease frequency

Description

Compute directly adjusted rates, on the basis of a specified standard population.

Usage

```
epi.directadj(obs, pop, std, conf.level = 0.95)
```

Arguments

<code>obs</code>	a matrix representing the observed number of events. Rows represent strata (e.g. areas) and the columns represent the covariates to be adjusted for (e.g. age, herd type). The sum of each row will equal the total number of events for each stratum. If there are no stratification variables <code>obs</code> will be a one column matrix.
<code>pop</code>	a matrix representing the population size. Rows represent the strata (e.g. areas) and the columns represent the covariates to be adjusted for (e.g. age, herd type). The sum of each row will equal the total population size within each stratum. If there are no stratification variables <code>pop</code> will be a one column matrix.
<code>std</code>	a matrix representing the standard population size in each areal unit. In this matrix the rows represent each strata and the columns represent each covariate. Each cell of the matrix gives the strata and covariate specific standardised population size. The sum of each row will equal the total standardised population size within each strata. If there are no stratification variables <code>std</code> will be a one column matrix.
<code>conf.level</code>	magnitude of the returned confidence interval. Must be a single number between 0 and 1.

Value

A list containing the following:

`crude.strata` the crude rates for each strata.

```

crude.summary
                the crude rates across all strata.
adj.strata      the directly adjusted rates for each strata.
adj.summary     the directly adjusted rates across all strata.

```

References

Fay M, Feuer E (1997). Confidence intervals for directly standardized rates: A method based on the gamma distribution. *Statistics in Medicine* 16: 791 - 801.

Examples

```

## A study was conducted to estimate the seroprevalence of leptospirosis
## in dogs in Glasgow and Edinburgh, Scotland. The following data were
## obtained:

obs <- matrix(data = c(61,69), nrow = 2, byrow = TRUE,
              dimnames = list(c("ED", "GL"), NULL))
pop <- matrix(data = c(260,251), nrow = 2, byrow = TRUE,
              dimnames = list(c("ED", "GL"), NULL))

## Compute directly adjusted seroprevalence estimates, using a standard
## population size of 500:

std <- matrix(data = c(250,250), nrow = 2, byrow = TRUE,
              dimnames = list(c("ED", "GL"), NULL))

epi.directadj(obs, pop, std, conf.level = 0.95)

## > $crude.area
## >      est      se  est.025  est.975
## > ED 0.2346154 0.01455023 0.1769231 0.2961538
## > GL 0.2749004 0.01735156 0.2111554 0.3426295

## > $crude.summary
## >      est      se  est.025  est.975
## > 1 0.2544031 0.01125413 0.2113503 0.2994129

## > $adj.summary
## >      est      var  est.025  est.975
## > 1 0.2547579 0.0004993969 0.2128434 0.3025123

## The crude prevalence data suggests that Glasgow has a slightly higher
## seroprevalence of leptospirosis in its dog population. We now stratify
## the data by sex:

obs <- matrix(data = c(15,46,53,16), nrow = 2, byrow = TRUE,
              dimnames = list(c("ED", "GL"), c("M", "F")))
pop <- matrix(data = c(48,212,180,71), nrow = 2, byrow = TRUE,
              dimnames = list(c("ED", "GL"), c("M", "F")))

## Compute directly adjusted seroprevalence estimates, using a standard
## population size of 500:

std <- matrix(data = c(250,250,250,250), nrow = 2, byrow = TRUE,
              dimnames = list(c("ED", "GL"), c("M", "F")))

```

```

epi.directadj(obs, pop, std, conf.level = 0.95)

## > $crude.area
## >      est      se  est.025  est.975
## > ED 0.2346154 0.01455023 0.1769231 0.2961538
## > GL 0.2749004 0.01735156 0.2111554 0.3426295

## > $crude.summary
## >      est      se  est.025  est.975
## > 1 0.2544031 0.01125413 0.2113503 0.2994129

## > $adj.strata
## >      est      var  est.025  est.975
## > ED 0.2647406 0.0001323703 0.2426680 0.2882815
## > GL 0.2598983 0.0001299491 0.2380329 0.2832322

## > $adj.summary
## >      est      se  est.025  est.975
## > 1 0.2623194 0.008295268 0.231 0.295

## The confounding effect of sex has been removed by producing gender-
## adjusted prevalence estimates.

```

epi.dms

Decimal degrees and degrees, minutes and seconds conversion

Description

Converts decimal degrees to degrees, minutes and seconds. Converts degrees, minutes and seconds to decimal degrees.

Usage

```
epi.dms(dat)
```

Arguments

dat	the data. A one-column matrix is assumed when converting decimal degrees to degrees, minutes, and seconds. A two-column matrix is assumed when converting degrees and decimal minutes to decimal degrees. A three-column matrix is assumed when converting degrees, minutes and seconds to decimal degrees.
-----	---

Examples

```

## EXAMPLE 1 Degrees, minutes, seconds to decimal degrees:
dat <- matrix(c(41, 38, 7.836, -40, 40, 27.921),
  byrow = TRUE, nrow = 2)
epi.dms(dat)

## EXAMPLE 2 Decimal degrees to degrees, minutes, seconds
dat <- matrix(c(41.63551, -40.67442), nrow = 2)
epi.dms(dat)

```

epi.dsl

*Mixed-effects meta-analysis of binary outcomes using the DerSimonian and Laird method***Description**

Computes individual study odds or risk ratios for binary outcome data. Computes the summary odds or risk ratio using the DerSimonian and Laird method. Performs a test of heterogeneity among trials. Performs a test for the overall difference between groups (that is, after pooling the studies, do treated groups differ significantly from controls?).

Usage

```
epi.dsl(ev.trt, n.trt, ev.ctrl, n.ctrl, names, method = "odds.ratio",
        alternative = c("two.sided", "less", "greater"), conf.level = 0.95)
```

Arguments

ev.trt	observed number of events in the treatment group.
n.trt	number in the treatment group.
ev.ctrl	observed number of events in the control group.
n.ctrl	number in the control group.
names	character string identifying each trial.
method	a character string indicating the method to be used. Options are <code>odds.ratio</code> or <code>risk.ratio</code> .
alternative	a character string specifying the alternative hypothesis, must be one of <code>two.sided</code> , <code>greater</code> or <code>less</code> .
conf.level	magnitude of the returned confidence interval. Must be a single number between 0 and 1.

Details

`alternative = "greater"` tests the hypothesis that the DerSimonian and Laird summary measure of association is greater than 1.

Value

A list containing the following:

OR	the odds ratio for each trial, the standard error of the odds ratio for each trial, and the lower and upper bounds of the confidence interval of the odds ratio for each trial.
RR	the risk ratio for each trial, the standard error of the risk ratio for each trial, and the lower and upper bounds of the confidence interval of the risk ratio for each trial.
OR.summary	the DerSimonian and Laird summary odds ratio, the standard error of the DerSimonian and Laird summary odds ratio, the lower and upper bounds of the confidence interval of the DerSimonian and Laird summary odds ratio.

<code>RR.summary</code>	the DerSimonian and Laird summary risk ratio, the standard error of the DerSimonian and Laird summary risk ratio, the lower and upper bounds of the confidence interval of the DerSimonian and Laird summary risk ratio.
<code>weights</code>	the inverse variance and DerSimonian and Laird weights for each trial.
<code>heterogeneity</code>	a vector containing <code>Q</code> the heterogeneity test statistic, <code>df</code> the degrees of freedom and its associated P-value.
<code>Hsq</code>	the relative excess of the heterogeneity test statistic <code>Q</code> over the degrees of freedom <code>df</code> .
<code>Isq</code>	the percentage of total variation in study estimates that is due to heterogeneity rather than chance.
<code>tau.sq</code>	the variance of the treatment effect among trials.
<code>effect</code>	a vector containing <code>z</code> the test statistic for overall treatment effect and its associated P-value.

Note

Under the random-effects model, the assumption of a common treatment effect is relaxed, and the effect sizes are assumed to have a normal distribution with variance `tau.sq`.

Using this method, the DerSimonian and Laird weights are used to compute the pooled odds ratio.

The function checks each strata for cells with zero frequencies. If a zero frequency is found in any cell, 0.5 is added to all cells within the strata.

References

Deeks JJ, Altman DG, Bradburn MJ (2001). Statistical methods for examining heterogeneity and combining results from several studies in meta-analysis. In: Egger M, Davey Smith G, Altman D (eds). Systematic Review in Health Care Meta-Analysis in Context. British Medical Journal, London, 2001, pp. 291 - 299.

DerSimonian R, Laird N (1986). Meta-analysis in clinical trials. Controlled Clinical Trials 7: 177 - 188.

Higgins J, Thompson S (2002). Quantifying heterogeneity in a meta-analysis. Statistics in Medicine 21: 1539 - 1558.

See Also

[epi.iv](#), [epi.mh](#), [epi.smd](#)

Examples

```
data(epi.epidural)
epi.dsl(ev.trt = epi.epidural$ev.trt, n.trt = epi.epidural$n.trt,
        ev.ctrl = epi.epidural$ev.ctrl, n.ctrl = epi.epidural$n.ctrl,
        names = as.character(epi.epidural$trial), method = "odds.ratio",
        alternative = "two.sided", conf.level = 0.95)
```

epi.edr	<i>Estimated dissemination ratio</i>
---------	--------------------------------------

Description

Computes estimated dissemination ratio on the basis of a vector of numbers (usually counts of incident cases identified on each day of an epidemic).

Usage

```
epi.edr(dat, n = 4, conf.level = 0.95, nsim = 99, na.zero = TRUE)
```

Arguments

<code>dat</code>	a numeric vector listing the number of incident cases for each day of an epidemic.
<code>n</code>	scalar, defining the number of days to be used when computing the estimated dissemination ratio.
<code>conf.level</code>	magnitude of the returned confidence interval. Must be a single number between 0 and 1.
<code>nsim</code>	scalar, defining the number of simulations to be used for the confidence interval calculations.
<code>na.zero</code>	logical, replace NaN or Inf values with zeros?

Details

In infectious disease epidemics the n -day estimated dissemination ratio (EDR) at day i equals the total number of incident cases between day i and day $[i - (n - 1)]$ (inclusive) divided by the total number of incident cases between day $(i - n)$ and day $(i - 2n) + 1$ (inclusive). EDR values are often calculated for each day of an epidemic and presented as a time series analysis. If the EDR is consistently less than unity, the epidemic is said to be ‘under control.’

A simulation approach is used to calculate confidence intervals around each daily EDR estimate. The numerator and denominator of the EDR estimate for each day is taken in turn and a random number drawn from a Poisson distribution, using the calculated numerator and denominator value as the mean. EDR is then calculated for these simulated values and the process repeated `nsim` times. Confidence intervals are then derived from the vector of simulated values for each day.

Value

Returns the point estimate of the EDR and the lower and upper bounds of the confidence interval of the EDR.

Examples

```
set.seed(123)
dat <- rpois(n = 50, lambda = 2)
edr.04 <- epi.edr(dat, n = 4, conf.level = 0.95, nsim = 99, na.zero = TRUE)

## Plot:
plot(1:50, 1:50, xlim = c(0,25), ylim = c(0, 10), xlab = "Days",
     ylab = "Estimated dissemination ratio", type = "n", main = "")
```

```
lines(1:50, edr.04[,1], type = "l", lwd = 2, lty = 1, col = "blue")
lines(1:50, edr.04[,2], type = "l", lwd = 1, lty = 2, col = "blue")
lines(1:50, edr.04[,3], type = "l", lwd = 1, lty = 2, col = "blue")
```

epi.empbayes	<i>Empirical Bayes estimates</i>
--------------	----------------------------------

Description

Computes empirical Bayes estimates of observed event counts using the method of moments.

Usage

```
epi.empbayes(obs, pop)
```

Arguments

<code>obs</code>	a vector representing the observed disease counts in each region of interest.
<code>pop</code>	a vector representing the population count in each region of interest.

Details

The gamma distribution is sometimes parameterised in terms of shape and rate parameters. The rate parameter equals the inverse of the scale parameter. The mean of the distribution equals δ/α . The variance of the distribution equals δ/α^2 . The empirical Bayes estimate of the proportion affected in each area equals $(obs + \delta)/(pop + \alpha)$.

Value

A data frame with four elements: `gamma` mean observed event count, `phi` variance of observed event count, `alpha` shape parameter of gamma distribution, and `delta` scale parameter of gamma distribution.

References

Bailey TC, Gatrell AC (1995). Interactive Spatial Data Analysis. Longman Scientific & Technical. London.

Langford IH (1994). Using empirical Bayes estimates in the geographical analysis of disease risk. Area 26: 142 - 149.

Examples

```
data(epi.SClip)
obs <- epi.SClip$cases
pop <- epi.SClip$population

est <- epi.empbayes(obs, pop)
empbayes.prop <- (obs + est[4]) / (pop + est[3])
raw.prop <- (obs) / (pop)
rank <- rank(raw.prop)
dat <- as.data.frame(cbind(rank, raw.prop, empbayes.prop))
```



```
plot(dat$rank, dat$raw.prop, type = "n", xlab = "Rank", ylab = "Proportion")
points(dat$rank, dat$raw.prop, pch = 16, col = "red")
points(dat$rank, dat$empbayes.prop, pch = 16, col = "blue")
legend(5, 0.00025, legend = c("Raw estimate", "Bayes adjusted estimate"),
      col = c("red", "blue"), pch = c(16, 16), bty = "n")
```

epi.epidural

Rates of use of epidural anaesthesia in trials of caregiver support

Description

This data set provides results of six trials investigating rates of use of epidural anaesthesia during childbirth. Each trial is made up of a group where a caregiver (midwife, nurse) provided support intervention and a group where standard care was provided. The objective was to determine if there were higher rates of epidural use when a caregiver was present at birth.

Usage

```
data(epi.epidural)
```

Format

A data frame with 6 observations on the following 5 variables.

trial the name and year of the trial.

ev.trt number of births in the caregiver group where an epidural was used.

n.trt number of births in the caregiver group.

ev.ctrl number of births in the standard care group where an epidural was used.

n.ctrl number of births in the standard care group.

Source

Deeks JJ, Altman DG, Bradburn MJ (2001). Statistical methods for examining heterogeneity and combining results from several studies in meta-analysis. In: Egger M, Davey Smith G, Altman D (eds). Systematic Review in Health Care Meta-Analysis in Context. British Medical Journal, London, pp. 291 - 299.

epi.herdtest

Estimate herd test characteristics

Description

When tests are applied to individuals within a group we may wish to designate the group as being either diseased or non-diseased on the basis of these individual test results. This function estimates sensitivity and specificity of this testing regime at the group (or herd) level.

Usage

```
epi.herdtest(se, sp, P, N, n, k)
```

Arguments

se	a vector of length one defining the sensitivity of the individual test used.
sp	a vector of length one defining the specificity of the individual test used.
P	scalar, defining the estimated true prevalence.
N	scalar, defining the herd size.
n	scalar, defining the number of individuals to be tested per group (or herd).
k	scalar, defining the critical number of individuals testing positive that will denote the group as test positive.

Value

A data frame with four elements: APpos the probability of obtaining a positive test, APneg the probability of obtaining a negative test, HSe the estimated group (herd) sensitivity, and HSp the estimated group (herd) specificity.

Note

The method implemented in this function is based on the hypergeometric distribution.

Author(s)

Ron Thornton, MAF New Zealand, PO Box 2526 Wellington, New Zealand.

References

Dohoo I, Martin W, Stryhn H (2003). Veterinary Epidemiologic Research. AVC Inc, Charlottetown, Prince Edward Island, Canada, pp. 113 - 115.

Examples

```
## EXAMPLE 1
## We wish to estimate the herd-level sensitivity and specificity of
## a testing regime using an individual animal test of sensitivity 0.391
## and specificity 0.964. The estimated true prevalence of disease is 0.12.
## Assume that 60 individuals will be tested per herd and we have
## specified that two or more positive test results identify the herd
## as positive.

epi.herdtest(se = 0.391, sp = 0.964, P = 0.12, N = 1E06, n = 60, k = 2)

## This testing regime gives a herd sensitivity of 0.95 and a herd
## specificity of 0.36. With a herd sensitivity of 0.95 we can be
## confident that we will declare a herd infected if it is infected.
## With a herd specificity of only 0.36, we will declare 0.64 of disease
## negative herds as infected, so false positives are a problem.
```

epi.incin*Laryngeal and lung cancer cases in Lancashire 1974 - 1983*

Description

Between 1972 and 1980 an industrial waste incinerator operated at a site about 2 kilometres south-west of the town of Coppull in Lancashire, England. Addressing community concerns that there were greater than expected numbers of laryngeal cancer cases in close proximity to the incinerator Diggle et al. (1990) conducted a study investigating risks for laryngeal cancer, using recorded cases of lung cancer as controls. The study area is 20 km x 20 km in size and includes location of residence of patients diagnosed with each cancer type from 1974 to 1983. The site of the incinerator was at easting 354500 and northing 413600.

Usage

```
data(epi.incin)
```

Format

A data frame with 974 observations on the following 3 variables.

xcoord easting coordinate (in metres) of each residence.

ycoord northin coordinate (in metres) of each residence.

status disease status: 0 = lung cancer, 1 = laryngeal cancer.

Source

Bailey TC and Gatrell AC (1995). Interactive Spatial Data Analysis. Longman Scientific & Technical. London.

References

Diggle P, Gatrell A, and Lovett A (1990). Modelling the prevalence of cancer of the larynx in Lancashire: A new method for spatial epidemiology. In: Thomas R (Editor), Spatial Epidemiology. Pion Limited, London, pp. 35 - 47.

Diggle P (1990). A point process modelling approach to raised incidence of a rare phenomenon in the vicinity of a prespecified point. Journal of the Royal Statistical Society, A, 153: 349 - 362.

Diggle P, Rowlingson B (1994). A conditional approach to point process modelling of elevated risk. Journal of the Royal Statistical Society, A, 157: 433 - 440.

epi.indirectadj *Indirectly adjusted rates*

Description

Compute standardised mortality ratios and indirectly adjusted rates.

Usage

```
epi.indirectadj(obs, pop, std = "NA", type = "risk",
  conf.level = 0.95)
```

Arguments

<code>obs</code>	a matrix representing the observed number of events. Rows represent strata (e.g. areas) and the columns represent the covariates to be adjusted for (e.g. age, herd type). The sum of each row will equal the total number of events for each stratum. If there are no stratification variables <code>obs</code> will be a one column matrix.
<code>pop</code>	a matrix representing the population size. Rows represent the strata (e.g. areas) and the columns represent the covariates to be adjusted for (e.g. age, herd type). The sum of each row will equal the total population size within each stratum. If there are no stratification variables <code>pop</code> will be a one column matrix.
<code>std</code>	a vector specifying the standard risks/rates to be applied. The length of <code>std</code> should be one plus the number of covariates to be adjusted for.
<code>type</code>	a character string indicating the type of data. Options are <code>risk</code> (number of cases per population at risk), or <code>rate</code> (number of cases per population-time at risk).
<code>conf.level</code>	magnitude of the returned confidence interval. Must be a single number between 0 and 1.

Details

Confidence intervals for the standardised mortality ratio for risks are based on the Poisson distribution. Confidence intervals for the standardised mortality ratio for rates are based on formulae provided by Dohoo, Martin, and Stryhn (2003, p 78).

Value

A list containing the following:

<code>crude.risk</code>	the crude risks for each stratum.
<code>adj.risk</code>	the indirectly adjusted risk for each stratum.
<code>crude.smr</code>	the crude standardised mortality ratio for each stratum.
<code>adj.smr</code>	the indirectly adjusted standardised mortality ratio for each stratum.

Author(s)

Thanks to Dr. Telmo Nunes (UISEE/DETSa, Faculdade de Medicina Veterinária - UTL, Rua Prof. Cid dos Santos, 1300-477 Lisboa Portugal) for details and code for the confidence interval calculations.

References

- Breslow NE, Day NE (1987). Statistical Methods in Cancer Research: Volume II - The Design and Analysis of Cohort Studies. Lyon: International Agency for Cancer Research.
- Dohoo I, Martin W, Stryhn H (2003). Veterinary Epidemiologic Research. AVC Inc, Charlottetown, Prince Edward Island, Canada, pp. 76 - 81.
- Rothman KJ, Greenland S (1998). Modern Epidemiology, second edition. Lippincott Williams & Wilkins, Philadelphia.
- Sahai H, Khurshid A (1993). Confidence intervals for the mean of a Poisson distribution: A review. Biometrical Journal 35: 857 - 867.
- Sahai H, Khurshid A (1996). Statistics in Epidemiology. Methods, Techniques and Applications. CRC Press, Baton Roca.

Examples

```
## EXAMPLE 1
## Data have been collected on the incidence of tuberculosis in two
## areas, for two herd types: dairy and beef.

obs <- matrix(data = c(17, 41, 10, 120), nrow = 2, byrow = TRUE,
  dimnames = list(c("A", "B"), c("beef", "dairy")))
pop <- matrix(data = c(550, 450, 500, 1500), nrow = 2, byrow = TRUE,
  dimnames = list(c("A", "B"), c("beef", "dairy")))
epi.indirectadj(obs, pop, std = "NA", type = "rate", conf.level = 0.05)

## The crude incidence risk of tuberculosis in area A was 0.058 cases per year.
## The crude incidence risk of tuberculosis in area B was 0.065 cases per year.
## The indirectly adjusted incidence risk of tuberculosis in area A was 0.071
## cases per year. The indirectly adjusted incidence risk of tuberculosis in
## area B was 0.059 cases per year.

## Repeat the analysis, explicitly defining the standard incidence risks
## for beef, dairy, and the total population as 0.025, 0.085, and 0.060
## cases per herd per year, respectively:

std <- c(0.025, 0.085, 0.060)
epi.indirectadj(obs, pop, std = std, type = "rate", conf.level = 0.05)

## The indirectly adjusted incidence risk of tuberculosis in area A was 0.067
## cases per year. The indirectly adjusted incidence risk of tuberculosis in
## area B was 0.056 cases per year.
```

epi.insthaz

Instantaneous hazard computed on the basis of a Kaplan-Meier survival function

Description

Compute the instantaneous hazard on the basis of a Kaplan-Meier survival function.

Usage

```
epi.insthaz(survfit.obj, conf.level = 0.95)
```

Arguments

`survfit.obj` a `survfit` object, computed using the `survival` package.

`conf.level` magnitude of the returned confidence interval. Must be a single number between 0 and 1.

Details

Computes the instantaneous hazard of failure, equivalent to the proportion of the population failing per unit time.

Value

A data frame with three elements: `time` the observed failure times, `est` the proportion of the population failing per unit time, `lower` the lower bounds of the confidence interval, and `upper` the upper bounds of the confidence interval.

References

Venables W, Ripley B (2002). *Modern Applied Statistics with S*, fourth edition. Springer, New York, pp. 353 - 385.

Singer J, Willett J (2003). *Applied Longitudinal Data Analysis Modeling Change and Event Occurrence*. Oxford University Press, London, pp. 348.

Examples

```
library(survival)
ovarian.km <- survfit(Surv(futime,fustat) ~ 1, data = ovarian)

ovarian.haz <- epi.insthaz(ovarian.km, conf.level = 0.95)
plot(ovarian.haz$time, ovarian.haz$est, xlab = "Days",
     ylab = "Instantaneous hazard", type = "b", pch = 16)
```

<code>epi.interaction</code>	<i>Relative excess risk due to interaction in a case-control study</i>
------------------------------	--

Description

Computes the relative excess risk due to interaction, the proportion of disease among those with both exposures attributable to interaction, and the synergy index for case-control data. Confidence interval calculations are based on those described by Hosmer and Lemeshow (1992).

Usage

```
epi.interaction(model, coeff, conf.level = 0.95)
```

Arguments

<code>model</code>	an object of class <code>glm</code> .
<code>coeff</code>	a vector specifying the position of the two coefficients of their interaction term in the model.
<code>conf.level</code>	magnitude of the returned confidence interval. Must be a single number between 0 and 1.

Details

Interaction is defined as a departure from additivity of effects in epidemiologic studies. This function calculates three indices defined by Rothman (1998): (1) the relative excess risk due to interaction (RERI), (2) the proportion of disease among those with both exposures that is attributable to their interaction (AP[AB]), and (3) the synergy index (S). The synergy index measures the interaction between two risk factors expressed as the ratio of the relative excess risk for the combined effect of the risk factors and the sum of the relative excess risks for each separate effect of the two risk factors. In the absence of interaction both RERI and AP[AB] = 0 and S = 1.

These measures can be used to assess additive interaction when the odds ratio estimates the risk ratio. However, it is recognised that odds ratios from case-control studies that are not designed to directly estimate the risk or rate ratio (and only do so well when the outcome is rare).

Value

A list containing the following:

<code>reri</code>	the relative excess risk due to interaction.
<code>apab</code>	the proportion of disease among those with both exposures that is attributable to interaction.
<code>S</code>	the synergy index.

References

- Chen S-C, Wong R-H, Shiu L-J, Chiou M-C, Lee H (2008). Exposure to mosquito coil smoke may be a risk factor for lung cancer in Taiwan. *Journal of Epidemiology* 18: 19 - 25.
- Hosmer DW, Lemeshow S (1992). Confidence interval estimation of interaction. *Epidemiology* 3: 452 - 456.
- Kalilani L, Atashili J (2006). Measuring additive interaction using odds ratios. *Epidemiologic Perspectives & Innovations* doi:10.1186/1742-5573-3-5.
- Rothman K, Greenland S (1998). *Modern Epidemiology*. Lippincott - Raven Philadelphia, USA.
- Rothman K, Keller AZ (1972). The effect of joint exposure to alcohol and tobacco on risk of cancer of the mouth and pharynx. *Journal of Chronic Diseases* 23: 711 - 716.

Examples

```
## Data from Rothman and Keller (1972) evaluating the effect of joint exposure
## to alcohol and tobacco on risk of cancer of the mouth and pharynx (cited in
## Hosmer and Lemeshow, 1992):

can <- c(rep(1, times = 231), rep(0, times = 178), rep(1, times = 11),
         rep(0, times = 38))
smk <- c(rep(1, times = 225), rep(0, times = 6), rep(1, times = 166),
         rep(0, times = 12), rep(1, times = 8), rep(0, times = 3), rep(1, times = 18),
```

```

    rep(0, times = 20))
alc <- c(rep(1, times = 409), rep(0, times = 49))
dat <- as.data.frame(cbind(alc, smk, can))

## Table 2 of Hosmer and Lemeshow (1992):

dat.glm01 <- glm(can ~ alc + smk + alc:smk, family = binomial, data = dat)
summary(dat.glm01)

## Rothman suggested an alternative coding scheme to be employed for
## parameterising an interaction term. Using this approach, instead of using
## two risk factors and one product term to represent the interaction (as
## above) the risk factors are combined into one variable with four levels:

## a.neg b.neg: 0 0 0
## a.pos b.neg: 1 0 0
## a.neg b.pos: 0 1 0
## a.pos b.pos: 0 0 1

dat$d <- rep(NA, times = nrow(dat))
dat$d[dat$alc == 0 & dat$smk == 0] <- 0
dat$d[dat$alc == 1 & dat$smk == 0] <- 1
dat$d[dat$alc == 0 & dat$smk == 1] <- 2
dat$d[dat$alc == 1 & dat$smk == 1] <- 3
dat$d <- factor(dat$d)

## Table 3 of Hosmer and Lemeshow (1992):

dat.glm02 <- glm(can ~ d, family = binomial, data = dat)
summary(dat.glm02)

epi.interaction(model = dat.glm02, coeff = c(2,3,4), conf.level = 0.95)

## Page 455 of Hosmer and Lemeshow (1992):
## RERI: 3.73 (95% CI -1.83 -- 9.31).
## AP[AB]: 0.41 (95% CI -0.07 -- 0.90).
## S: 1.87 (95% CI 0.54 -- 5.41).

```

epi.iv

Fixed-effect meta-analysis of binary outcomes using the inverse variance method

Description

Computes individual study odds or risk ratios for binary outcome data. Computes the summary odds or risk ratio using the inverse variance method. Performs a test of heterogeneity among trials. Performs a test for the overall difference between groups (that is, after pooling the studies, do treated groups differ significantly from controls?).

Usage

```

epi.iv(ev.trt, n.trt, ev.ctrl, n.ctrl, names, method = "odds.ratio",
       alternative = c("two.sided", "less", "greater"), conf.level = 0.95)

```


Arguments

<code>ev.trt</code>	observed number of events in the treatment group.
<code>n.trt</code>	number in the treatment group.
<code>ev.ctrl</code>	observed number of events in the control group.
<code>n.ctrl</code>	number in the control group.
<code>names</code>	character string identifying each trial.
<code>method</code>	a character string indicating the method to be used. Options are <code>odds.ratio</code> or <code>risk.ratio</code> .
<code>alternative</code>	a character string specifying the alternative hypothesis, must be one of <code>two.sided</code> , <code>greater</code> or <code>less</code> .
<code>conf.level</code>	magnitude of the returned confidence interval. Must be a single number between 0 and 1.

Details

Using this method, the inverse variance weights are used to compute the pooled odds ratios and risk ratios. The inverse variance weights should be used to indicate the weight each trial contributes to the meta-analysis.

`alternative = "greater"` tests the hypothesis that the inverse variance summary measure of association is greater than 1.

Value

A list containing:

<code>OR</code>	the odds ratio for each trial, the standard error of the odds ratio for each trial, and the lower and upper bounds of the confidence interval of the odds ratio for each trial.
<code>RR</code>	the risk ratio for each trial, the standard error of the risk ratio for each trial, and the lower and upper bounds of the confidence interval of the risk ratio for each trial.
<code>OR.summary</code>	the inverse variance summary odds ratio, the standard error of the inverse variance summary odds ratio, the lower and upper bounds of the confidence interval of the inverse variance summary odds ratio.
<code>RR.summary</code>	the inverse variance summary risk ratio, the standard error of the inverse variance summary risk ratio, the lower and upper bounds of the confidence interval of the inverse variance summary risk ratio.
<code>weights</code>	the raw and inverse variance weights assigned to each trial.
<code>heterogeneity</code>	a vector containing <code>Q</code> the heterogeneity test statistic, <code>df</code> the degrees of freedom and its associated P-value.
<code>Hsq</code>	the relative excess of the heterogeneity test statistic <code>Q</code> over the degrees of freedom <code>df</code> .
<code>Isq</code>	the percentage of total variation in study estimates that is due to heterogeneity rather than chance.
<code>effect</code>	a vector containing <code>z</code> the test statistic for overall treatment effect and its associated P-value.

Note

The inverse variance method performs poorly when data are sparse, both in terms of event rates being low and trials being small. The Mantel-Haenszel method ([epi.mh](#)) is more robust when data are sparse.

Using this method, the inverse variance weights are used to compute the pooled odds ratios and risk ratios.

The function checks each strata for cells with zero frequencies. If a zero frequency is found in any cell, 0.5 is added to all cells within the strata.

References

Deeks JJ, Altman DG, Bradburn MJ (2001). Statistical methods for examining heterogeneity and combining results from several studies in meta-analysis. In: Egger M, Davey Smith G, Altman D (eds). Systematic Review in Health Care Meta-Analysis in Context. British Medical Journal, London, 2001, pp. 291 - 299.

Higgins JP, Thompson SG (2002). Quantifying heterogeneity in a meta-analysis. Statistics in Medicine 21: 1539 - 1558.

See Also

[epi.dsl](#), [epi.mh](#), [epi.smd](#)

Examples

```
data(epi.epidural)
epi.iv(ev.trt = epi.epidural$ev.trt, n.trt = epi.epidural$n.trt,
       ev.ctrl = epi.epidural$ev.ctrl, n.ctrl = epi.epidural$n.ctrl,
       names = as.character(epi.epidural$trial), method = "odds.ratio",
       alternative = "two.sided", conf.level = 0.95)
```

epi.kappa

Kappa statistic

Description

Computes the kappa statistic and its confidence interval.

Usage

```
epi.kappa(a, b, c, d, conf.level = 0.95)
```

Arguments

a	number of observations where observer 1 positive and observer 2 positive.
b	number of observations where observer 1 negative and observer 2 positive.
c	number of observations where observer 1 positive and observer 2 negative.
d	number of observations where observer 1 negative and observer 2 negative.
conf.level	magnitude of the returned confidence interval. Must be a single number between 0 and 1.

Details

Kappa is a measure of agreement beyond the level of agreement expected by chance alone. The observed agreement is the proportion of samples for which both methods (or observers) agree.

Common interpretations for the kappa statistic are as follows: < 0.2 slight agreement, 0.2 - 0.4 fair agreement, 0.4 - 0.6 moderate agreement, 0.6 - 0.8 substantial agreement, > 0.8 almost perfect agreement.

Value

A list containing the following:

kappa	a data frame with the kappa statistic and the lower and upper bounds of the confidence interval for the kappa statistic.
mcnemar	a data frame containing McNemar's test statistic and its associated P-value.

Note

	Obs1 +	Obs1 -	Total
Obs 2 +	a	b	a + b
Obs 2 -	c	d	c + d
Total	a + c	b + d	a + b + c + d

McNemar's test is used to test for the presence of bias. Bias would be present if the proportion positive to each test differed. A non-significant McNemar's test would indicate that the two proportions do not differ, and that the kappa statistic is a valid measure of agreement

References

Altman DG, Machin D, Bryant TN, Gardner MJ (2000). Statistics with Confidence, second edition. British Medical Journal, London, pp. 116 - 118.

Dohoo I, Martin W, Stryhn H (2003). Veterinary Epidemiologic Research. AVC Inc, Charlottetown, Prince Edward Island, Canada, pp. 92.

Examples

```
## Kidney samples from 291 salmon were split with one half of the
## samples sent to each of two laboratories where an IFAT test
## was run on each sample. The following results were obtained:

## Lab 1 positive, lab 2 positive: 19
## Lab 1 positive, lab 2 negative: 10
## Lab 1 negative, lab 2 positive: 6
## Lab 1 negative, lab 2 negative: 256

epi.kappa(a = 19, b = 10, c = 6, d = 256, conf.level = 0.95)

## The McNemar's chi-squared test statistic is 1.00 (P = 0.32). We
## conclude that there is little evidence that the two laboratories
## found different proportions positive.

## The proportion of agreements after chance has been excluded is
## 0.67 (95% CI 0.52 to 0.83). We conclude that, on the basis of
```

```
## this sample, that there is substantial agreement between the two
## laboratories.
```

epi.ltd

Lactation to date and standard lactation milk yields

Description

Calculate lactation to date and standard lactation (that is, 305 or 270 day) milk yields.

Usage

```
epi.ltd(dat, std = "305")
```

Arguments

dat	an eight column data frame listing (in order) cow identifier, herd test identifier, lactation number, herd test days in milk, lactation length (NA if lactation incomplete), herd test milk yield (litres), herd test fat (percent), and herd test protein (percent).
std	std = "305" returns 305-day milk volume, fat, and protein yield. std = "270" returns 270-day milk volume, fat, and protein yield.

Details

Lactation to date yields will only be calculated if there are four or more herd test events.

Value

A data frame with nine elements: ckey cow identifier, lact lactation number, llen lactation length, vltld milk volume (litres) to last herd test or dry off date (computed on the basis of lactation length, fltd fat yield (kilograms) to last herd test or dry off date (computed on the basis of lactation length, pltld protein yield (kilograms) to last herd test or dry off date (computed on the basis of lactation length, vstd 305-day or 270-day milk volume yield (litres), fstd 305-day or 270-day milk fat yield (kilograms), and pstd 305-day or 270-day milk protein yield (kilograms).

Author(s)

Nicolas Lopez-Villalobos and Mark Stevenson (IVABS, Massey University, Palmerston North New Zealand).

References

Kirkpatrick M, Lofsvold D, Bulmer M (1990). Analysis of the inheritance, selection and evolution of growth trajectories. *Genetics* 124: 979 - 993.

Examples

```
## Generate herd test data:
ckey <- rep(1, times = 12)
pkey <- 1:12
lact <- rep(1:2, each = 6)
dim <- c(25, 68, 105, 145, 200, 240, 30, 65, 90, 130, 190, 220)
llen <- c(280, 280, 280, 280, 280, 280, NA, NA, NA, NA, NA, NA)
vol <- c(18, 30, 25, 22, 18, 12, 20, 32, 27, 24, 20, 14)
fat <- c(4.8, 4.3, 4.5, 4.7, 4.8, 4.9, 4.8, 4.3, 4.5, 4.7, 4.8, 4.9)/100
pro <- c(3.7, 3.5, 3.6, 3.7, 3.8, 3.9, 3.7, 3.5, 3.6, 3.7, 3.8, 3.9)/100
dat <- as.data.frame(cbind(ckey, pkey, lact, dim, llen, vol, fat, pro))

## Lactation to date and 305-day milk, fat, and protein yield:
epi.ltd(dat, std = "305")

## Lactation to date and 270-day milk, fat, and protein yield:
epi.ltd(dat, std = "270")
```

epi.mh	<i>Fixed-effects meta-analysis of binary outcomes using the Mantel-Haenszel method</i>
--------	--

Description

Computes individual study odds or risk ratios for binary outcome data. Computes the summary odds or risk ratio using the Mantel-Haenszel method. Performs a test of heterogeneity among trials. Performs a test for the overall difference between groups (that is, after pooling the studies, do treated groups differ significantly from controls?).

Usage

```
epi.mh(ev.trt, n.trt, ev.ctrl, n.ctrl, names, method = "odds.ratio",
       alternative = c("two.sided", "less", "greater"), conf.level = 0.95)
```

Arguments

ev.trt	observed number of events in the treatment group.
n.trt	number in the treatment group.
ev.ctrl	observed number of events in the control group.
n.ctrl	number in the control group.
names	character string identifying each trial.
method	a character string indicating the method to be used. Options are <code>odds.ratio</code> or <code>risk.ratio</code> .
alternative	a character string specifying the alternative hypothesis, must be one of <code>two.sided</code> , <code>greater</code> or <code>less</code> .
conf.level	magnitude of the returned confidence interval. Must be a single number between 0 and 1.

Details

`alternative = "greater"` tests the hypothesis that the Mantel-Haenszel summary measure of association is greater than 1.

Value

A list containing the following:

<code>OR</code>	the odds ratio for each trial, the standard error of the odds ratio for each trial, and the lower and upper bounds of the confidence interval of the odds ratio for each trial.
<code>RR</code>	the risk ratio for each trial, the standard error of the risk ratio for each trial, and the lower and upper bounds of the confidence interval of the risk ratio for each trial.
<code>OR.summary</code>	the Mantel-Haenszel summary odds ratio, the standard error of the Mantel-Haenszel summary odds ratio, the lower and upper bounds of the confidence interval of the Mantel-Haenszel summary odds ratio.
<code>RR.summary</code>	the Mantel-Haenszel summary risk ratio, the standard error of the Mantel-Haenszel summary risk ratio, the lower and upper bounds of the confidence interval of the Mantel-Haenszel summary risk ratio.
<code>weights</code>	the raw and inverse variance weights assigned to each trial.
<code>heterogeneity</code>	a vector containing Q the heterogeneity test statistic, <code>df</code> the degrees of freedom and its associated P-value.
<code>Hsq</code>	the relative excess of the heterogeneity test statistic Q over the degrees of freedom <code>df</code> .
<code>Isq</code>	the percentage of total variation in study estimates that is due to heterogeneity rather than chance.
<code>effect</code>	a vector containing z the test statistic for overall treatment effect and its associated P-value.

Note

Using this method, the pooled odds and risk ratios are computed using the raw individual study weights. The methodology for computing the Mantel-Haenszel summary odds ratio follows the approach described in Deeks, Altman and Bradburn MJ (2001, pp 291 - 299).

The function checks each strata for cells with zero frequencies. If a zero frequency is found in any cell, 0.5 is added to all cells within the strata.

References

Deeks JJ, Altman DG, Bradburn MJ (2001). Statistical methods for examining heterogeneity and combining results from several studies in meta-analysis. In: Egger M, Davey Smith G, Altman D (eds). Systematic Review in Health Care Meta-Analysis in Context. British Medical Journal, London, 2001, pp. 291 - 299.

Higgins JP, Thompson SG (2002). Quantifying heterogeneity in a meta-analysis. Statistics in Medicine 21: 1539 - 1558.

See Also

[epi.dsl](#), [epi.iv](#), [epi.smd](#)

Examples

```
data(epi.epidural)
epi.mh(ev.trt = epi.epidural$ev.trt, n.trt = epi.epidural$n.trt,
       ev.ctrl = epi.epidural$ev.ctrl, n.ctrl = epi.epidural$n.ctrl,
       names = as.character(epi.epidural$trial), method = "odds.ratio",
       alternative = "two.sided", conf.level = 0.95)
```

epi.nomogram

*Post-test probability of disease given sensitivity and specificity of a test***Description**

Computes the post-test probability of disease given sensitivity and specificity of a test.

Usage

```
epi.nomogram(se, sp, pre.pos, verbose = FALSE)
```

Arguments

se	test sensitivity (0 - 1).
sp	test specificity (0 - 1).
pre.pos	the pre-test probability of disease in the patient.
verbose	logical, indicating whether detailed or summary results are to be returned.

Value

A list containing the following:

likelihood.ratio	the likelihood ratio of a positive and negative test.
prob	the post-test probability of disease given a positive and negative test.

References

Hunink M, Glasziou P (2001). Decision Making in Health and Medicine - Integrating Evidence and Values. Cambridge University Press, pp. 128 - 156.

Examples

```
## You are presented with a dog with lethargy, exercise intolerance,
## weight gain and bilaterally symmetric truncal alopecia. You are
## suspicious of hypothyroidism and take a blood sample to measure
## basal serum thyroxine (T4).

## You believe that around 5% of dogs presented to your clinic with
## a signalment of general debility have hypothyroidism. The serum T4
## has a sensitivity of 0.89 and specificity of 0.85 for diagnosing
## hypothyroidism in the dog. The laboratory reports a serum T4
## concentration of 22.0 nmol/L (reference range 19.0 to 58.0 nmol/L).
## What is the post-test probability that this dog is hypothyroid?
```

```
epi.nomogram(se = 0.89, sp = 0.85, pre.pos = 0.05, verbose = FALSE)

## The post-test probability that this dog is hypothyroid is 24%.
```

epi.offset	Create offset vector
------------	----------------------

Description

Creates an offset vector based on a list.

Usage

```
epi.offset(id.names)
```

Arguments

`id.names` a list identifying the [location] of each case. This must be a factor.

Details

This function is useful for supplying spatial data to WinBUGS.

Value

A vector of length (1 + length of `id`). The first element of the offset vector is 1, corresponding to the position at which data for the first factor appears in `id`. The second element of the offset vector corresponds to the position at which the second factor appears in `id` and so on. The last element of the offset vector corresponds to the length of the `id` list.

References

Bailey TC, Gatrell AC (1995). Interactive Spatial Data Analysis. Longman Scientific & Technical. London.

Langford IH (1994). Using empirical Bayes estimates in the geographical analysis of disease risk. Area 26: 142 - 149.

Examples

```
dat <- c(1,1,1,2,2,2,2,3,3,3)
dat <- as.factor(dat)

offset <- epi.offset(dat)
offset
## [1] 1 4 8 10
```


epi.pooled

*Estimate herd test characteristics when pooled sampling is used***Description**

We may wish to designate a group of individuals (e.g. a herd) as being either diseased or non-diseased on the basis of pooled samples. This function estimates sensitivity and specificity of this testing regime at the group (or herd) level.

Usage

```
epi.pooled(se, sp, P, m, r)
```

Arguments

se	a vector of length one defining the sensitivity of the individual test used.
sp	a vector of length one defining the specificity of the individual test used.
P	scalar, defining the estimated true prevalence.
m	scalar, defining the number of individual samples to make up a pooled sample.
r	scalar, defining the number of pooled samples per group (or herd).

Value

A list containing the following:

HAPneg	the apparent prevalence in a disease negative herd.
HSe	the estimated group (herd) level sensitivity.
HSp	the estimated group (herd) level specificity.

References

Dohoo I, Martin W, Stryhn H (2003). Veterinary Epidemiologic Research. AVC Inc, Charlottetown, Prince Edward Island, Canada, pp. 115 - 117 .

Christensen J, Gardner IA (2000). Herd-level interpretation of test results for epidemiologic studies of animal diseases. Preventive Veterinary Medicine 45: 83 - 106.

Examples

```
## We want to test dairy herds for Johne's disease using faecal culture
## which has a sensitivity and specificity of 0.647 and 0.981, respectively.
## Suppose we pool faecal samples from five cows together and use six pooled
## samples per herd. What is the herd level sensitivity and specificity
## based on this approach (assuming homogenous mixing)?

epi.pooled(se = 0.647, sp = 0.981, P = 0.12, m = 5 , r = 6)

## Herd level sensitivity is 0.927, herd level specificity is 0.562.
## Sensitivity at the herd level is increased using the pooled sampling
## approach; herd level specificity is decreased.
```

epi.popsiz	<i>Estimate population size</i>
------------	---------------------------------

Description

Estimates population size on the basis of capture-recapture sampling.

Usage

```
epi.popsiz(T1, T2, T12, conf.level = 0.95, verbose = FALSE)
```

Arguments

T1	an integer representing the number of individuals tested in the first round.
T2	an integer representing the number of individuals tested in the second round.
T12	an integer representing the number of individuals tested in both the first and second round.
conf.level	magnitude of the returned confidence interval. Must be a single number between 0 and 1.
verbose	logical indicating whether detailed or summary results are to be returned.

Value

Returns the estimated population size and an estimate of the numbers of individuals that remain untested.

References

Cannon RM, Roe RT (1982). Livestock Disease Surveys A Field Manual for Veterinarians. Australian Government Publishing Service, Canberra, pp. 34.

Examples

```
## In a field survey 400 feral pigs are captured, marked and then released.
## On a second occasion 40 of the original capture are found when another 400
## pigs are captured. Estimate the size of this feral pig population. Estimate
## the number of feral pigs that have not been tested.

epi.popsiz(T1 = 400, T2 = 400, T12 = 40, conf.level = 0.95, verbose = FALSE)

## Estimated population size: 4000 (95% CI 3125 - 5557)
## Estimated number of untested pigs: 3240 (95% CI 2365 - 4797)
```

epi.prcc

*Partial rank correlation coefficients***Description**

Compute partial rank correlation coefficients.

Usage

```
epi.prcc(dat, sided.test = 2)
```

Arguments

<code>dat</code>	a data frame comprised of $K + 1$ columns and N rows, where K represents the number of model parameters being evaluated and N represents the number of replications of the model. The last column of the data frame (i.e. column $K + 1$) provides the model output.
<code>sided.test</code>	use a one- or two-sided test? Use a two-sided test if you wish to evaluate whether or not the partial rank correlation coefficient is greater than or less than zero. Use a one-sided test to evaluate whether or not the partial rank correlation coefficient is greater than zero.

Details

If the number of parameters K is greater than the number of model replications N an error will be returned.

Value

A data frame with three elements: `gamma` the partial rank correlation coefficient between each input parameter and the outcome, `test.statistic` the test statistic used to determine the significance of non-zero values of `gamma`, and `p.value` the associated P-value.

References

Blower S, Dowlatabadi H (1994). Sensitivity and uncertainty analysis of complex models of disease transmission: an HIV model, as an example. *International Statistical Review* 62: 229 - 243.

Sanchez M, Blower S (1997) Uncertainty and sensitivity analysis of the basic reproductive rate. *American Journal of Epidemiology*, 145: 1127 - 1137.

Examples

```
## Create a matrix of simulation results:
x1 <- as.data.frame(rnorm(n = 10, mean = 120, sd = 10))
x2 <- as.data.frame(rnorm(n = 10, mean = 80, sd = 5))
x3 <- as.data.frame(rnorm(n = 10, mean = 40, sd = 20))
y <- 2 + (0.5 * x1) + (0.7 * x2) + (0.2 * x3)

dat <- as.data.frame(cbind(x1, x2, x3, y))
names(dat) <- c("X1", "X2", "X3", "Y")

epi.prcc(dat, sided.test = 2)
```

epi.prev

Estimate true prevalence

Description

Computes the true prevalence of a disease in a population on the basis of an imperfect test.

Usage

```
epi.prev(pos, tested, se, sp, conf.level = 0.95)
```

Arguments

pos	the number of positives.
tested	the number tested.
se	test sensitivity (0 - 1).
sp	test specificity (0 - 1).
conf.level	magnitude of the returned confidence interval. Must be a single number between 0 and 1.

Details

Exact binomial confidence limits are calculated for apparent prevalence (see Collett 1999 for details).

Value

A list containing the following:

ap	the point estimate of apparent prevalence, the standard error of the apparent prevalence, and the lower and upper bounds of the confidence interval around the apparent prevalence estimate.
tp	the point estimate of the true prevalence, the standard error of the true prevalence, and the lower and upper bounds of the confidence interval around the true prevalence estimate.

Note

This function uses apparent prevalence, test sensitivity and test specificity to estimate true prevalence (after Rogan and Gladen, 1978). The standard error of the Rogan Gladen true prevalence estimate is based on Abel (1993) and discussed in Messam et al. (2008). It is assumed that test sensitivity and specificity are known with certainty.

The Rogan Gladen true prevalence estimate is unreliable for small sample sizes and when true prevalence is believed to be close to zero. The algorithm implemented here makes no correction to the Rogan Gladen estimate of true prevalence if it is less than zero or greater than one (simply to remind the user that it provides unreliable estimates of true prevalence under these conditions). In this situation one is advised to adopt a Bayesian approach to true prevalence estimation. See Messam et al. (2008) for a very readable introduction.

References

- Abel U (1993). Die Bewertung Diagnostischer Tests. Hippokrates, Stuttgart.
- Collett D (1999). Modelling Binary Data. Chapman & Hall/CRC, Boca Raton Florida, p. 24.
- Gardener IA, Greiner M (1999). Advanced Methods for Test Validation and Interpretation in Veterinary Medicine. Freie Universität Berlin, ISBN 3-929619-22-9; 80 pp.
- Messam L, Branscum A, Collins M, Gardner I (2008) Frequentist and Bayesian approaches to prevalence estimation using examples from Johne's disease. Animal Health Research Reviews 9: 1 - 23.
- Rogan W, Gladen B (1978). Estimating prevalence from results of a screening test. American Journal of Epidemiology 107: 71 - 76.

Examples

```
## A simple random sample of 150 cows from a herd of 2560 is taken.
## Each cow is given a screening test for brucellosis which has a
## sensitivity of 96% and a specificity of 89%. Of the 150 cows tested
## 23 were positive to the screening test. What is the estimated prevalence
## of brucellosis in this herd (and its 95% confidence interval)?

epi.prev(pos = 23, tested = 150, se = 0.96, sp = 0.89, conf.level = 0.95)

## The estimated true prevalence of brucellosis in this herd is 5.1 cases per
## 100 cows (95% CI 0 -- 12 cases per 100 cows).
```

epi.RtoBUGS

R to WinBUGS data conversion

Description

Writes data from an R list to a text file in WinBUGS-compatible format.

Usage

```
epi.RtoBUGS(datalist, towhere)
```

Arguments

datalist	a list (normally, with named elements) which may include scalars, vectors, matrices, arrays of any number of dimensions, and data frames.
towhere	a character string identifying where the file is to be written.

Details

Does not check to ensure that only numbers are being produced. In particular, factor labels in a data frame will be output to the file, which normally won't be desired.

Author(s)

Terry Elrod (Terry.Elrod@UAlberta.ca), Kenneth Rice.

References

Best, NG. WinBUGS 1.3.1 Short Course, Brisbane, November 2000.

epi.SClip

Lip cancer in Scotland 1975 - 1980

Description

This data set provides counts of lip cancer diagnoses made in Scottish districts from 1975 to 1980. In addition to district-level counts of disease events and estimates of the size of the population at risk, the data set contains (for each district) an estimate of the percentage of the population involved in outdoor industry (agriculture, fishing, and forestry). It is known that exposure to sunlight is a risk factor for cancer of the lip and high counts are to be expected in districts where there is a high proportion of the workforce involved in outdoor industry.

Usage

```
data(epi.SClip)
```

Format

A data frame with 56 observations on the following 6 variables.

gridcode alternative district identifier.

id numeric district identifier (1 to 56).

district district name.

cases number of lip cancer cases diagnosed 1975 - 1980.

population total person years at risk 1975 - 1980.

prop.ag percent of the population engaged in outdoor industry.

Source

This data set has been analysed by a number of authors including Clayton and Kaldor (1987), Conlon and Louis (1999), Stern and Cressie (1999), and Carlin and Louis (2000, p 270).

References

Clayton D, Kaldor J (1987). Empirical Bayes estimates of age-standardized relative risks for use in disease mapping. *Biometrics*, 43: 671 - 681.

Conlon EM, Louis TA (1999). Addressing multiple goals in evaluating region-specific risk using Bayesian methods. In: Lawson AB (Editor), *Disease Mapping and Risk Assessment for Public Health*. John Wiley & Sons, Ltd, Chichester, pp. 31 - 47.

Stern H, Cressie N (1999). Inference in extremes in disease mapping. In: Lawson AB (Editor), *Disease Mapping and Risk Assessment for Public Health*. John Wiley & Sons, Ltd, Chichester, pp. 63 - 84.

Carlin BP, Louis TA (2000). *Bayes and Empirical Bayes Methods for Data Analysis - Monographs on Statistics and Applied Probability* 69. Chapman and Hall, London, pp. 270.

epi.simplesize	<i>Sample size under under simple random sampling</i>
----------------	---

Description

Estimates the required sample size under under simple random sampling.

Usage

```
epi.simplesize(N = 1E+06, Vsqr, Py, epsilon.r, method = "mean",
  conf.level = 0.95)
```

Arguments

N	scalar, representing the population size.
Vsq	scalar, if method is <code>total</code> or <code>mean</code> this is the relative variance of the variable to be estimated (i.e. var/mean^2).
Py	scalar, if method is <code>proportion</code> this is an estimate of the unknown population proportion.
epsilon.r	the maximum relative difference between our estimate and the unknown population value.
method	a character string indicating the method to be used. Options are <code>total</code> , <code>mean</code> , or <code>proportion</code> .
conf.level	scalar, defining the level of confidence in the computed result.

Value

Returns an integer defining the size of the sample is required.

Note

If the calculated sample size is greater than 10% of the population, an adjusted sample size is returned.

`epsilon.r` defines the maximum relative difference between our estimate and the unknown population value. The sample estimate should not differ in absolute value from the true unknown population parameter d by more than $\text{epsilon.r} * d$.

References

- Levy PS, Lemeshow S (1999). Sampling of Populations Methods and Applications. Wiley Series in Probability and Statistics, London, pp. 70 - 75.
- Scheaffer RL, Mendenhall W, Lyman Ott R (1996). Elementary Survey Sampling. Duxbury Press, New York, pp. 95.
- Otte J, Gumm I (1997). Intra-cluster correlation coefficients of 20 infections calculated from the results of cluster-sample surveys. Preventive Veterinary Medicine 31: 147 - 150.

Examples

```
## EXAMPLE 1
## A city contains 20 neighbourhood health clinics and it is desired to take a
## sample of clinics to estimate the total number of persons from all these
## clinics who have been given, during the past 12 month period, prescriptions
## for a recently approved antidepressant. If we assume that the average number
## of people seen at these clinics is 1500 per year with the standard deviation
## equal to 300, and that approximately 5% of patients (regardless of clinic)
## are given this drug, how many clinics need to be sampled to yield an estimate
## that is within 20% of the true population value?

pmean <- 1500 * 0.05; pvar <- (300 * 0.05)^2
epi.simplesize(N = 20, Vsqr = (pvar / pmean^2), Py = NA, epsilon.r = 0.20,
  method = "total", conf.level = 0.95)

## Three clinics need to be sampled to meet the survey requirements.

## EXAMPLE 2
## We want to estimate the mean bodyweight of deer on a farm. There are 278
## animals present. We anticipate the mean body weight to be around 200 kg
## and the standard deviation of body weight to be 30 kg. We would like to
## be 95% certain that our estimate is within 10 kg of the true mean. How
## many deer should be sampled?

epi.simplesize(N = 278, Vsqr = 30^2 / 200^2, Py = NA, epsilon.r = 10/200,
  method = "mean", conf.level = 0.95)

## A total of 28 deer need to be sampled to meet the survey requirements.

## EXAMPLE 3
## We want to estimate the seroprevalence of Brucella abortus in a population
## of cattle. An estimate of the unknown prevalence of B. abortus in this
## population is 0.15. We would like to be 95% certain that our estimate is
## within 20% of the true proportion of the population that is seropositive
## to B. abortus. Calculate the required sample size.

n.crude <- epi.simplesize(N = 1E+06, Vsqr = NA, Py = 0.15, epsilon.r = 0.20,
  method = "proportion", conf.level = 0.95)
n.crude

## A total of 544 cattle need to be sampled to meet the survey requirements.

## EXAMPLE 3 (continued)
## Being seropositive to brucellosis is likely to cluster within herds.
## Otte and Gumm (1997) cite the intraclass correlation coefficient of
## Brucella abortus to be in the order of 0.09. Adjust the sample size
## estimate to account for clustering at the herd level. Assume that, on
## average, herds in your area of interest are comprised of 100 animals.

## rho = (design - 1) / (nbar - 1)
## D <- rho * (nbar - 1) + 1

## Above, rho equals the intraclass correlation coefficient and nbar equals
## the average number of individuals per cluster.

rho <- 0.09; nbar <- 100
```



```

D <- rho * (nbar - 1) + 1

n.adj <- ceiling(n.crude * D)
n.adj

## After accounting for the presence of clustering at the herd level we
## estimate that a total of 5392 cattle need to be sampled to meet
## the survey requirements.

```

epi.smd	<i>Fixed-effect meta-analysis of continuous outcomes using the standardised mean difference method</i>
---------	--

Description

Computes the standardised mean difference and confidence intervals of the standardised mean difference for continuous outcome data.

Usage

```

epi.smd(mean.trt, sd.trt, n.trt, mean.ctrl, sd.ctrl, n.ctrl,
        names, method = "cohens", conf.level = 0.95)

```

Arguments

mean.trt	a vector, defining the mean outcome in the treatment group.
sd.trt	a vector, defining the standard deviation of the outcome in the treatment group.
n.trt	a vector, defining the number of subjects in the treatment group.
mean.ctrl	a vector, defining the mean outcome in the control group.
sd.ctrl	a vector, defining the standard deviation of the outcome in the control group.
n.ctrl	a vector, defining the number of subjects in the control group.
names	character string identifying each trial.
method	a character string indicating the method to be used. Options are <code>cohens</code> or <code>hedges</code> and <code>glass</code> .
conf.level	magnitude of the returned confidence interval. Must be a single number between 0 and 1.

Value

A list containing the following:

md	standardised mean difference and its confidence interval computed for each trial.
md.invar	the inverse variance (fixed effects) summary standardised mean difference.
md.dsl	the DerSimonian and Laird (random effects) summary standardised mean difference.
heterogeneity	a vector containing Q the heterogeneity test statistic, df the degrees of freedom and its associated P-value.

Note

The standardised mean difference method is used when trials assess the same outcome, but measure it in a variety of ways. For example: a set of trials might measure depression scores in psychiatric patients but use different methods to quantify depression. In this circumstance it is necessary to standardise the results of the trials to a uniform scale before they can be combined. The standardised mean difference method expresses the size of the treatment effect in each trial relative to the variability observed in that trial.

References

Deeks JJ, Altman DG, Bradburn MJ (2001). Statistical methods for examining heterogeneity and combining results from several studies in meta-analysis. In: Egger M, Davey Smith G, Altman D (eds). Systematic Review in Health Care Meta-Analysis in Context. British Medical Journal, London, pp. 290 - 291.

See Also

[epi.dsl](#), [epi.iv](#), [epi.mh](#)

Examples

```
## EXAMPLE 1
## A systematic review comparing assertive community treatment (ACT) for the
## severely mentally ill was compared to standard care. A systematic review
## comparing ACT to standard care found three trials that assessed mental
## status after 12 months. All three trials used a different scoring system,
## so standardisation is required before they can be compared.

names <- c("Audini", "Morse", "Lehman")
mean.trt <- c(41.4, 0.95, -4.10)
mean.ctrl <- c(42.3, 0.89, -3.80)
sd.trt <- c(14, 0.76, 0.83)
sd.ctrl <- c(12.4, 0.65, 0.87)
n.trt <- c(30, 37, 67)
n.ctrl <- c(28, 35, 58)

epi.smd(mean.trt, sd.trt, n.trt, mean.ctrl, sd.ctrl, n.ctrl,
        names, method = "cohens", conf.level = 0.95)
```

epi.stratasize

Sample size under under stratified random sampling

Description

Estimates the required sample size under under stratified random sampling.

Usage

```
epi.stratasize(strata.n, strata.mean, strata.var, strata.py, epsilon.r,
               method = "mean", conf.level = 0.95)
```

Arguments

<code>strata.n</code>	vector, defining the size of each strata.
<code>strata.mean</code>	vector, representing the expected means in each strata. Only used when <code>method = "mean", "total" or "pps"</code> .
<code>strata.var</code>	vector, representing the expected variance in each strata. Only used when <code>method = "mean", "total" or "pps"</code> .
<code>strata.Py</code>	vector, representing the expected proportions in each strata. Only used when <code>method = "proportion"</code> .
<code>epsilon.r</code>	the maximum relative difference between our estimate and the unknown population value.
<code>method</code>	a character string indicating the method to be used. Options are <code>mean</code> , <code>total</code> , <code>proportion</code> , or <code>pps</code> .
<code>conf.level</code>	scalar, defining the level of confidence in the computed result.

Value

A list containing the following:

<code>strata.sample</code>	the estimated sample size for each strata.
<code>strata.total</code>	the estimated total size.
<code>strata.stats</code>	<code>mean</code> the mean across all strata, <code>sigma.bx</code> the among-strata variance, <code>sigma.wx</code> the within-strata variance, and <code>sigma.x</code> the among-strata variance plus the within-strata variance, <code>rel.var</code> the within-strata variance divided by the square of the mean, and <code>gamma</code> the ratio of among-strata variance to within-strata variance.

Note

Use method `proportion` to estimate sample size using stratified random sampling with equal weights (see Levy and Lemeshow, page 176). Use method `pps` to estimate sample size using proportional stratified random sampling with proportional allocation (see Levy and Lemeshow, page 179).

Where `method = "proportion"` the vectors `strata.mean` and `strata.var` are ignored.

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References

Levy PS, Lemeshow S (1999). Sampling of Populations Methods and Applications. Wiley Series in Probability and Statistics, London, pp. 175 - 179.

Examples

```
## EXAMPLE 1
## Hospital episodes (Levy and Lemeshow 1999, page 176 -- 178)
## We plan to take a sample of the members of a health maintenance
## organisation (HMO) for purposes of estimating the average number
## of hospital episodes per person per year. The sample will be selected
## from membership lists according to age (under 45 years, 45 -- 64 years,
## 65 years and over). The number of members in each strata are 600, 500,
## and 400 (respectively). Previous data estimates the mean number of
## hospital episodes per year for each strata as 0.164, 0.166, and 0.236
## (respectively). The variance of these estimates are 0.245, 0.296, and
## 0.436 (respectively). How many from each strata should be sampled to be
## 95% that the sample estimate of hospital episodes is within 20% of the
## true value?

strata.n <- c(600, 500, 400)
strata.mean <- c(0.164, 0.166, 0.236)
strata.var <- c(0.245, 0.296, 0.436)
epi.stratasize(strata.n, strata.mean, strata.var, strata.py,
  epsilon.r = 0.20, method = "mean", conf.level = 0.95)

## The number allocated to the under 45 years, 45 -- 64 years, and 65 years
## and over strata should be 223, 186, and 149 (a total of 558). These
## results differ from the worked example provided in Levy and Lemeshow where
## certainty is set to approximately 99%.

## EXAMPLE 2
## Dairies are to be sampled to determine the proportion of herd managers
## using foot bathes. Herds are stratified according to size (small, medium,
## and large). The number of herds in each strata are 1500, 2500, and 4000
## (respectively). A review of the literature indicates that use of foot bathes
## on farms is in the order of 0.50, with the probability of usage increasing
## as herds get larger. How many dairies should be sampled?

strata.n <- c(1500, 2500, 4000)
strata.py <- c(0.50, 0.60, 0.70)
epi.stratasize(strata.n, strata.mean, strata.var, strata.py,
  epsilon.r = 0.20, method = "proportion", conf.level = 0.95)

## A total of 54 herds should be sampled: 10 small, 17 medium, and 27 large.
```

epi.studysize

Estimate the sample size to compare means, proportions, and survival

Description

Computes the sample size, power, and minimum detectable difference for cohort studies (using count data), case control studies, when comparing means and survival.

Usage

```
epi.studysize(treat, control, n, sigma, power, r = 1,
  conf.level = 0.95, sided.test = 2, method = "means")
```

Arguments

<code>treat</code>	the expected value for the treatment group (see below).
<code>control</code>	the expected value for the control group (see below).
<code>n</code>	scalar, defining the total number of subjects in the study (i.e. the number in the treatment and control group).
<code>sigma</code>	when <code>method = "means"</code> this is the expected standard deviation of the variable of interest for both treatment and control groups. When <code>method = "case.control"</code> this is the expected proportion of study subjects exposed to the risk factor of interest. This argument is ignored when <code>method = "proportions"</code> , <code>method = "survival"</code> , or <code>method = "cohort.count"</code> .
<code>power</code>	scalar, the required study power.
<code>r</code>	scalar, the number in the treatment group divided by the number in the control group. This argument is ignored when <code>method = "proportions"</code> .
<code>conf.level</code>	scalar, defining the level of confidence in the computed result.
<code>sided.test</code>	use a one- or two-sided test? Use a two-sided test if you wish to evaluate whether or not the treatment group is better or worse than the control group. Use a one-sided test to evaluate whether or not the treatment group is better than the control group.
<code>method</code>	a character string indicating the method to be used. Options are <code>means</code> , <code>proportions</code> , <code>survival</code> , <code>cohort.count</code> , or <code>case.control</code> .

Details

The methodologies adopted in this function follow closely the approach described in Chapter 8 of Woodward (2005).

When `method = "means"` the argument `treat` defines the mean outcome for the treatment group, `control` defines the mean outcome for the control group, and `sigma` defines the standard deviation of the outcome, assumed to be the same across the treatment and control groups (see Woodward pp 397 - 403).

When `method = "proportions"` the argument `treat` defines the proportion in the treatment group and `control` defines the proportion in the control group. The arguments `sigma` and `r` are ignored.

When `method = "survival"` the argument `treat` is the proportion of treated subjects that will have not experienced the event of interest at the end of the study period and `control` is the proportion of control subjects that will have not experienced the event of interest at the end of the study period. The argument `sigma` is ignored (see Therneau and Grambsch pp 61 - 65).

When `method = "cohort.count"` the argument `treat` defines the estimated incidence risk (cumulative incidence) of the event of interest in the treatment group and `control` defines the estimated incidence risk of the event of interest in the control group. The argument `sigma` is ignored (see Woodward pp 405 - 410).

When `method = "case.control"` the argument `treat` defines the estimated incidence risk (cumulative incidence) of the event of interest in the treatment group and `control` defines the estimated incidence risk of the event of interest in the control group. The argument `sigma` is the expected proportion of study subjects exposed to the risk factor of interest (see Woodward pp 410 - 412).

In case control studies sample size estimates are worked out on the basis of an expected odds (or risk) ratio. When `method = "case.control"` the estimated incidence risk estimates in the

treat and control groups are used to define the expected risk ratio. See example 7 below, taken from Woodward p 412.

For `method = "proportions"` it is assumed that one of the two proportions is known and we want to test the null hypothesis that the second proportion is equal to the first. In contrast, `method = "cohort.count"` relates to the two-sample problem where neither proportion is known (or assumed, at least). Thus, there is much more uncertainty in the `method = "cohort.count"` situation (compared with `method = "proportions"`) and correspondingly a requirement for a much larger sample size. Generally, `method = "cohort.count"` is more useful in practice. `method = "proportions"` is used in special situations, such as when a politician claims that at least 90% of the population use seatbelts and we want to see if the data supports this claim.

Value

A list containing one or more of the following:

<code>n.crude</code>	the crude estimated total number of subjects required for the specified level of confidence and power.
<code>n.total</code>	the total estimated number of subjects required for the specified level of confidence and power, respecting the requirement for <code>r</code> times as many individuals in the treatment group compared with the control group.
<code>delta</code>	the minimum detectable difference given the specified level of confidence and power.
<code>lambda</code>	the minimum detectable risk ratio >1 and the maximum detectable risk ratio <1 .
<code>power</code>	the power of the study given the specified number of study subjects and power.

Note

The power of a study is its ability to demonstrate an association, given that an association actually exists.

The odds ratio and the risk ratio are approximately equal when the event of interest is rare. In this function `method = "case.control"` returns the sample size required to detect an approximate risk ratio in a case-control study (see Woodward p 412).

When `method = "proportions"` values need to be entered for `control`, `n`, and `power` to return a value for `delta`. When `method = "cohort.count"` values need to be entered for `control`, `n`, and `power` to return a value for `lambda` (see example 6 below).

References

- Fleiss JL (1981). Statistical Methods for Rates and Proportions. Wiley, New York.
- Kelsey JL, Thompson WD, Evans AS (1986). Methods in Observational Epidemiology. Oxford University Press, London, pp. 254 - 284.
- Therneau TM, Grambsch PM (2000). Modelling Survival Data - Extending the Cox Model. Springer, London, pp. 61 - 65.
- Woodward M (2005). Epidemiology Study Design and Data Analysis. Chapman & Hall/CRC, New York, pp. 381 - 426.

Examples

```
## EXAMPLE 1 (from Woodward p 399)
## Supposed we wish to test, at the 5% level of significance, the hypothesis
## that cholesterol means in a population are equal in two study years against
## the one-sided alternative that the mean is higher in the second of the
## two years. Suppose that equal sized samples will be taken in each year,
## but that these will not necessarily be from the same individuals (i.e. the
## two samples are drawn independently). Our test is to have a power of 0.95
## at detecting a difference of 0.5 mmol/L. The standard deviation of serum
## cholesterol in humans is assumed to be 1.4 mmol/L.
```

```
epi.studysize(treat = 5, control = 4.5, n = NA, sigma = 1.4, power = 0.95,
  r = 1, conf.level = 0.95, sided.test = 1, method = "means")
```

```
## To satisfy the study requirements 340 individuals need to be tested: 170 in
## the first year and 170 in the second year.
```

```
## EXAMPLE 2 (from Woodward pp 399 - 400)
## Women taking oral contraceptives sometimes experience anaemia due to
## impaired iron absorption. A study is planned to compare the use of iron
## tablets against a course of placebos. Oral contraceptive users are
## randomly allocated to one of the two treatment groups and mean serum
## iron concentration compared after 6 months. Data from previous studies
## indicates that the standard deviation of the increase in iron
## concentration will be around 4 micrograms% over a 6-month period.
## The average increase in serum iron concentration without supplements is
## also thought to be 4 micrograms%. The investigators wish to be 90% sure
## of detecting when the supplement doubles the serum iron concentration using
## a two-sided 5% significance test. It is decided to allocate 4 times as many
## women to the treatment group so as to obtain a better idea of its effect.
## How many women should be enrolled in this study?
```

```
epi.studysize(treat = 8, control = 4, n = NA, sigma = 4, power = 0.90,
  r = 4, conf.level = 0.95, sided.test = 2, method = "means")
```

```
## The estimated sample size is 66. We round this up to the nearest multiple
## of 5, to 70. We allocate 70/5 = 14 women to the placebo group and four
## times as many (56) to the iron treatment group.
```

```
## EXAMPLE 3 (from Woodward pp 403 - 404)
## A government initiative has decided to reduce the prevalence of male
## smoking to, at most, 0.30. A sample survey is planned to test, at the
## 0.05 level, the hypothesis that the proportion of smokers in the male
## population is 0.30 against the one-sided alternative that it is greater.
## The survey should be able to find a prevalence of 0.32, when it is true,
## with 0.90 power. How many men need to be sampled?
```

```
epi.studysize(treat = 0.30, control = 0.32, n = NA, sigma = NA, power = 0.90,
  r = 1, conf.level = 0.95, sided.test = 1, method = "proportions")
```

```
## ## A total of 4568 men should be sampled: 2284 in the treatment group and
## 2284 in the control group.
```

```

## EXAMPLE 4 (from Therneau and Grambsch p 63)
## The 5-year survival probability of patients receiving a standard treatment
## 0.30 and we anticipate that a new treatment will increase it to 0.45.
## Assume that a study will use a two-sided test at the 0.05 level with 0.90
## power to detect this difference. How many events are required?

epi.studysize(treat = 0.45, control = 0.30, n = NA, sigma = NA, power = 0.90,
  r = 1, conf.level = 0.95, sided.test = 2, method = "survival")

## A total of 250 events are required. Assuming one event per individual,
## assign 125 individuals to the treatment group and 125 to the control group.

## EXAMPLE 5 (from Therneau and Grambsch p 63)
## What is the minimum detectable hazard in a study involving 500 subjects where
## the treatment to control ratio is 1:1, assuming a power of 0.90 and a
## 2-sided test at the 0.05 level?

epi.studysize(treat = NA, control = NA, n = 500, sigma = NA, power = 0.90,
  r = 1, conf.level = 0.95, sided.test = 2, method = "survival")

## Assuming treatment increases time to event (compared with controls), the
## minimum detectable hazard of a study involving 500 subjects (250 in the
## treatment group and 250 in the controls) is 1.33.

## EXAMPLE 6 (from Woodward p 406)
## A cohort study of smoking and coronary heart disease (CHD) in middle aged men
## is planned. A sample of men will be selected at random from the population
## and will be asked to complete a questionnaire. The follow-up period will be
## 5 years. The investigators would like to be 0.90 sure of being able to
## detect when the risk ratio of CHD is 1.4 for smokers, using a 0.05
## significance test. Previous evidence suggests that the death rate in
## non-smokers is 413 per 100000 per year. Assuming equal numbers of smokers
## and non-smokers are sampled, how many should be sampled overall?

treat = 1.4 * (5 * 413)/100000
control = (5 * 413)/100000
epi.studysize(treat = treat, control = control, n = NA, sigma = NA,
  power = 0.90, r = 1, conf.level = 0.95, sided.test = 1, method = "cohort.count")

## A total of 12130 men need to be sampled (6065 smokers and 6065 non-smokers).

## EXAMPLE 7 (from Woodward p 406)
## Say, for example, we are only able to enrol 5000 subjects into the study
## described above. What is the minimum and maximum detectable risk ratio?

control = (5 * 413)/100000
epi.studysize(treat = NA, control = control, n = 5000, sigma = NA, power = 0.90,
  r = 1, conf.level = 0.95, sided.test = 1, method = "cohort.count")

## The minimum detectable risk ratio >1 is 1.65. The maximum detectable
## risk ratio <1 is 0.50.

## EXAMPLE 8 (from Woodward p 412)

```



```
## A case-control study of the relationship between smoking and CHD is
## planned. A sample of men with newly diagnosed CHD will be compared for
## smoking status with a sample of controls. Assuming an equal number of
## cases and controls, how many are needed to detect an approximate risk
## ratio of 2.0 with 0.90 power using a two-sided 0.05 test? Previous surveys
## indicate that 0.30 of the male population are smokers.

epi.studysize(treat = 2/100, control = 1/100, n = NA, sigma = 0.30,
  power = 0.90, r = 1, conf.level = 0.95, sided.test = 2,
  method = "case.control")

## A total of 376 men need to be sampled: 188 cases and 188 controls.

## EXAMPLE 9 (from Woodward p 414)
## Suppose we wish to determine the power to detect an approximate risk
## ratio of 2.0 using a two-sided 0.05 test when 188 cases and 940 controls
## are available (that is, the ratio of cases to controls is 1:5). Assume
## a 0.30 prevalence of smoking in the male population.

n <- 188 + 940
epi.studysize(treat = 2/100, control = 1/100, n = n, sigma = 0.30,
  power = NA, r = 0.2, conf.level = 0.95, sided.test = 2,
  method = "case.control")

## The power of this study, with the given sample size allocation is 0.99.
```

epi.tests

Sensitivity, specificity and predictive value of a diagnostic test

Description

Computes true and apparent prevalence, sensitivity, specificity, positive and negative predictive values, and positive and negative likelihood ratios from count data provided in a 2 by 2 table.

Usage

```
epi.tests(a, b, c, d, conf.level = 0.95)
```

Arguments

a	number of observations where true disease status positive and test is positive.
b	number of observations where true disease status negative and test is positive.
c	number of observations where true disease status positive and test is negative.
d	number of observations where true disease status is negative and test is negative.
conf.level	magnitude of the returned confidence interval. Must be a single number between 0 and 1.

Details

Exact binomial confidence limits are calculated for test sensitivity, specificity, and positive and negative predictive value (see Collett 1999 for details).

Confidence intervals for positive and negative likelihood ratios are based on formulae provided by Simel et al. (1991).

Diagnostic accuracy is defined as the proportion of all tests that give a correct result. Diagnostic odds ratio is defined as how much more likely will the test make a correct diagnosis than an incorrect diagnosis in patients with the disease (Scott et al. 2008). The number needed to diagnose is defined as the number of patients that need to be tested to give one correct positive test. Youden's index is the difference between the true positive rate and the false positive rate. Youden's index ranges from -1 to +1 with values closer to 1 if both sensitivity and specificity are high (i.e. close to 1).

Value

A list containing the following:

<code>aprev</code>	apparent prevalence.
<code>tprev</code>	true prevalence.
<code>se</code>	test sensitivity.
<code>sp</code>	test specificity.
<code>da</code>	diagnostic accuracy.
<code>dor</code>	diagnostic odds ratio.
<code>nnd</code>	number needed to diagnose.
<code>youden</code>	Youden's index.
<code>ppv</code>	positive predictive value.
<code>npv</code>	negative predictive value.
<code>lr.pos</code>	likelihood ratio of a positive test.
<code>lr.neg</code>	likelihood ratio of a negative test.

Note

	Disease +	Disease -	Total
Test +	a	b	a + b
Test -	c	d	c + d
Total	a + c	b + d	a + b + c + d

References

- Altman DG, Machin D, Bryant TN, and Gardner MJ (2000). *Statistics with Confidence*, second edition. British Medical Journal, London, pp. 28 - 29.
- Bangdiwala SI, Haedo AS, Natal ML (2008). The agreement chart as an alternative to the receiver-operating characteristic curve for diagnostic tests. *Journal of Clinical Epidemiology* 61: 866 - 874.
- Collett D (1999). *Modelling Binary Data*. Chapman & Hall/CRC, Boca Raton Florida, p. 24.

Scott IA, Greenburg PB, Poole PJ (2008). Cautionary tales in the clinical interpretation of studies of diagnostic tests. *Internal Medicine Journal* 38: 120 - 129.

Simel D, Samsa G, Matchar D (1991). Likelihood ratios with confidence: Sample size estimation for diagnostic test studies. *Journal of Clinical Epidemiology* 44: 763 - 770.

Greg Snow (2008) Need help in calculating confidence intervals for sensitivity, specificity, PPV & NPV. *R-sig-Epi Digest* 23(1): 3March 2008.

Examples

```
## Scott et al. 2008, Table 1:
## A new diagnostic test was trialled on 1586 patients. Of 744 patients
## that were disease positive, 670 tested positive. Of 842 patients that
## were disease negative, 640 tested negative. What is the likelihood
## ratio of a positive test? What is the number needed to diagnose?

a <- 670; b <- 202; c <- 74; d <- 640
epi.tests(a = a, b = b, c = c, d = d, conf.level = 0.95)

## Test sensitivity is 0.90 (95% CI 0.88 -- 0.92). Test specificity is
## 0.76 (95% CI 0.73 -- 0.79). The likelihood ratio of a positive test
## is 3.75 (95% CI 3.32 to 4.24). The number needed to diagnose is
## 1.51 (95% CI 1.41 to 1.65). Around 15 persons need to be tested
## to return 10 positive tests.
```

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