Package 'abie'

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Author Avery McIntosh [aut],
Eduard Grebe [cre, aut],
Petra Baumler [aut],
Reshma Kassanjee [ctb],
Hilmarie Brand [ctb],
Yuruo Li [ctb],
Simon Daniel [ctb],
Stefano Ongarello [ctb],
Alex Welte [aut]

Maintainer Eduard Grebe <eduardgrebe@sun.ac.za>

R topics documented:

abie *abie: a package for assay-based incidence estimation*

Description

The abie package uses methods described by Kassanjee, et al. 'A new general biomarker-based incidence estimator,' *Epidemiology* (2012), to implement functions to calculate incidence and tests of incidence difference between two populations, as well as power and sample size constraints for differenct study scenarios. abie also provides functions for calculation of mean duration of recent infection and false recency rates from assays for recent infection.

abie Functions

abie has functions *frr_binomial* to estimate false recency rate; *mdri_ml_binomial* to estimate mean duration or recent infection; *recencyI* to calculate estimates and confidence intervals for incidence and incidence difference, as well as other summary and inferential statistics related to the survey; *SSPower* to calculate sample size needed for a given power in a test of incidence difference, or vice versa; and *SSCprecision*, which gives sample size needed for a given precision in the incidence estimate.

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frr_binomial *Estimate subject-level false-recent rate for a given time cutoff. Each subject with any observations after the time cutoff is assigned a recency status according to the majority of observations for that subject after the cutoff. In the event of exactly half of the observations being classified as recent, the subject contributes a count of 0.5. The function performs an exact binomial test and reports the estimated probability of testing recent after the cutoff, a confidence interval for the proportion, the number of recent results ('successes'), number of subjects ('trials') and the number of data points contributing to the subject-level estimate.*

Description

Estimate subject-level false-recent rate for a given time cutoff. Each subject with any observations after the time cutoff is assigned a recency status according to the majority of observations for that subject after the cutoff. In the event of exactly half of the observations being classified as recent, the subject contributes a count of 0.5. The function performs an exact binomial test and reports the estimated probability of testing recent after the cutoff, a confidence interval for the proportion, the number of recent results ('successes'), number of subjects ('trials') and the number of data points contributing to the subject-level estimate.

Usage

```
frr_binomial(data = data, subid_var = "sid", time_var = "time",
  recency_cutoff_time = 730.5, recency_rule = "binary_data",
  recency_vars = "recency_status", recency_params = NULL, alpha = 0.05)
```

Arguments

data	A data frame containing variables for subject identifier, time (since detectable infection), and variables with biomarker readings or recency status (to be specified in recency_vars)
subid_var	The variable in the dataframe identifying subjects
time_var	The variable in the dataframe indicating time between 'time zero' (usually detectable infection) and biomarker measurement
recency_cutoff_time	Recency time cut-off ('Big T'). Default=730.5.
recency_rule	Specified rule for defining recent/non-recent outcomes from biomarker data (see Details)
recency_vars	Variables to be used in determining recency outcomes
recency_params	Vector of numeric parameters (e.g. thresholds) for determining recency according to the relevant rule
alpha	Confidence level, default=0.05.

Details

recency_rule: binary_data - supply a binary variable with 1=recent and 0=non-recent in recency_vars.

recency_rule: independent_thresholds: supply one threshold variable per biomarker in recency_vars and the relevant thresholds, as well as whether a value below or above each threshold indicates recency in recency_params.

recency_params expects a list of pairs of thresholds and thresholdtypes, with zero indicating a reading below the threshold implies recency and 1 that a reading above the threshold implies recency. (Note: two values, a threshold and a thresholdtype per variable must be specified in recency_params. For example, if you specify recency_vars = c('ODn','ViralLoad') you may specify recency_params = c(1.5,0,500,1), meaning that an ODn reading below 1.5 AND a viral load reasing above 500 indicates a recent result. Objects with missing values in its biomarker readings will be excluded from caculation.

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incBYcounts *Incidence and incidence difference statistics from trinomial counts of HIV and recency*

Description

Incidence and incidence difference statistics from trinomial counts of HIV and recency

Usage

```
incBYcounts(N, N_H, N_testR, N_R, DE_H = 1, DE_R = 1, BS_Count = 10000,
  Boot = FALSE, alpha = 0.05, BMest = "same.test", MDRI, RSE_MDRI, FRR,
  RSE_FRR, BigT = 730, Covar_HR = 0)
```

Arguments

N	Counts of total survey sample size(s) (vector/integer).
N_H	Number of HIV positive found in survey(s) (vector/integer).
N_testR	Number tested for recency in survey(s) (vector/integer).
N_R	Number of recent cases in survey(s) (vector/integer).
DE_H	Design effect of HIV prevalence test (vector/numeric), greater than or equal to 1. If multiple surveys are entered but only one design effect is specified, function assumes entered design effect is identical for both surveys.
DE_R	Design effect of recency test (vector/numeric), greater than or equal to 1. If multiple surveys are entered but only one design effect is specified, function assumes entered design effect is identical for both surveys.
BS_Count	Specifies number of bootstrap samples for bootstrapped confidence intervals of incidence.
Boot	True/False variable indicating whether variance of point estimates is to be calculated by Empirical Bootstrapping (TRUE) or Delta Method (FALSE), the default setting.
alpha	test rejection threshold.
BMest	Biomarker estimation by one the 3 options 'same.test'(=default), 'FRR.indep', 'MDRI.FRR.indep' (string).
MDRI	mean duration of recent infection [days] (vector/integer).
RSE_MDRI	Relative standard error of MDRI [days] (vector/integer).
FRR	False recent rate (vector/integer).
RSE_FRR	Relative standard error of FRR (vector/integer).
BigT	Cut point in days of recency used in biomarker assay to test recency in a given prevalence survey.
Covar_HR	Covariance of probability of being postive and being categorized recent from survey (or as a vector for multiple surveys).

Details

Implements assay-based incidence estimation through cross-sectional prevalence and recency of infection tests as described by Kassanjee, et al. "A new general biomarker-based incidence estimator," *Epidemiology* (2012). Function parameters must be specified to include assay test characteristics and survey results as proportions. Confidence intervals are computed via Delta method approximation, except when Boot=TRUE is specified, in which case confidence intervals are generated by empirical bootstrap resampling. Inputs must be in appropriate ranges for appropriate units. Extreme input values may make calculation impossible, and if entered will elicit error notices. Type vignette("Inference",package="abie") into console for more details on this function.

Implements assay-based incidence estimation through cross-sectional prevalence and recency of infection tests as described by Kassanjee, et al. 'A new general biomarker-based incidence estimator,' *Epidemiology* (2012). Function parameters must be specified to include assay test characteristics and survey results as proportions. Confidence intervals are computed via Delta method approximation, except when Boot=TRUE is specified, in which case confidence intervals are generated by empirical bootstrap resampling. Inputs must be in appropriate ranges for appropriate units. Extreme input values may make calculation impossible, and if entered will elicit error notices.

Value

Incidence estimate, annual risk of infection, confidence interval, relative standard error of estimate and of assay characteristics MDRI and FRR. If multiple surveys are entered, function returns said results, as well as estimates of incidence differences, confidence intervals of differences, difference relative standard errors, and p-values testing the hypothesis that the difference in incidence measures are zero. Theoretical relative standard error of incidence and incidence difference at infinite sample size is returned only if Boot=FALSE, as that calculation relies on the asymptotic behavior of components of the Delta method approximation, and is not calculable from bootstrapped values.

Examples

```
incBYcounts(N = c(5000) ,N_H = 1000, N_testR = 1000, N_R = 70,
Boot = FALSE, BMest = MDRI.FRR.indep, MDRI = 200, RSE_MDRI = 0.05,
FRR = 0.01, RSE_FRR = 0.2, BigT = 730)


incBYcounts(N = c(4000,4000,4050) ,N_H = c(1010,1000,900),
N_testR = c(1000,1000,880), N_R = c(60,70,50), Boot = TRUE,
BMest = same.test, MDRI = 210, RSE_MDRI = 0.05, FRR = 0.005,
RSE_FRR = 0.19, BigT = 700)


incBYcounts(N = c(4000,4000) ,N_H = c(1050,1090),
N_testR = c(1000,1000), N_R = c(60,67), Boot = FALSE, BMest = FRR.indep,
MDRI = 220, RSE_MDRI = 0.05, FRR = c(0.005,0.005), RSE_FRR = 0.19,
BigT = 610)
```

`mdri_ml_binomial` *Estimate MDRI (point estimate and confidence interval) using binomial regression and a maximum likelihood approach*

Description

Estimate MDRI (point estimate and confidence interval) using binomial regression and a maximum likelihood approach

Usage

```
mdri_ml_binomial(data = data, subid_var = "sid", time_var = "time",
  functional_forms = c("loglog_linear", "logit_cubic"),
  recency_cutoff_time = 730.5, inclusion_time_threshold = 800,
  recency_rule = "binary_data", recency_vars = "recency_status",
  recency_params = NULL, n_bootstraps = 100, alpha = 0.05, plot = TRUE,
  parallel = FALSE, cores = 4)
```

Arguments

`data`	A data frame containing variables for subject identifier, time (since detectable infection), and variables with biomarker readings or recency status (to be specified in recency_vars)
`subid_var`	The variable in the dataframe identifying subjects

`time_var` The variable in the dataframe indicating time between 'time zero' (usually detectable infection) and biomarker measurement

`functional_forms` Select functional form/link function combinations for fitting probability of testing recent as a function of time to data using binomial regression (see Details). Default=all supported functional forms.

`recency_cutoff_time` Recency time cut-off ('Big T'). Default=730.5.

`inclusion_time_threshold` Data points beyond this time are excluded from the calculation (in same unit as recency_cutoff_time, default=800).

`recency_rule` Specified rule for defining recent/non-recent outcomes from biomarker data (see Details)

`recency_vars` Variables to be used in determining recency outcomes

`recency_params` Vector of numeric parameters (e.g. thresholds) for determining recency according to the relevant rule

`n_bootstraps` Number of subject-level bootstrap resampling operations for estimating confidence intervals, default=100 (useful for testing purposes only)

`alpha` Confidence level, default=0.05.

`plot` Specifies whether a plot of the probability of testing recent over time should be produced

`parallel` Set to TRUE in order to perform bootstrapping in parallel on a multicore or multiprocessor syste. Not available on Windows.

`cores` Set number of cores for parallel processing when parallel=TRUE. This defaults to four.

Details

Expected data frame format: Before calling the function, please import your dataset into R environment.

time_var: Time since infection; Note: this package does not assume any specific time unit. It is important to specify the recency time cut-off 'T' and the time-based data exclusion rule (inclusion_time_threshold) in the same unit as the input times. The estimated MDRI will be in this unit.

Method: This function fits a function for probability of testing recent as a function of time to the supplied data using binomial regression. This requires binary outcomes (recent/non-recent) coded as 1 for recent and 0 for non-recent test resutls. Either a recency status variable must be specified, or a recency rule for determinging recency status from a biomarker or set of biomarkers must be specified. Currently only independent biomarker thresholds are supported (i.e. all biomarker criteria must be met in order for a specimen to be classified as recent).

Functional forms currently supported for the binomial regression fitting procedure: loglog_linear, logit_cubic

To be implemented in the near future: logit_spline

logit_cubic: Fits a binomial regression to probability of testing recent with a logit link on a polynomial in t of the third degree, where t is time since (detectable) infection.

loglog_linear: Fits a binomial regression to probability of testing recent with a log log link on log(t), where t is time since (detectable) infection.

recency_rule: binary_data - supply a binary variable with 1=recent and 0=non-recent in recency_vars.

recency_rule:independent_thresholds: supply one threshold variable per biomarker in recency_vars and the relevant thresholds, as well as whether a value below or above each threshold indicates recency in recency_params.

recency_params expects a list of pairs of thresholds and thresholdtypes, with zero indicating a reading below the threshold implies recency and 1 that a reading above the threshold implies recency. (Note: two values, a threshold and a thresholdtype per variable must be specified in recency_params. For example, if you specify recency_vars = c('ODn','ViralLoad') you may specify recency_params = c(1.5,0,500,1), meaning that an ODn reading below 1.5 AND a viral load reasing above 500 indicates a recent result. Objects with missing values in its biomarker readings will be excluded from caculation.

Value

MDRI Dataframe containing MDRI point estimates, CI lower and upper bounds and standard deviation of point estimates produced during bootstrapping. One row per functional form.

Plots A plot of Probability of testing recent over time for each functional form.

Models The fitted GLM models for each functional form.

Examples

```
mdri_ml_binomial(data=data, subid_var=PT_ID, time_var=DaysSinceEDDI,
 functional_forms=c(loglog_linear,logit_cubic), recency_rule=independent_thresholds,
 recency_vars=c(ODn,VL), recency_params=c(1.5,0,400,1), n_bootstraps = 10000, alpha=0.05,
 plot=TRUE, parallel=FALSE)

In this example the MDRI and 95% confidence interval would be calculated by determining
recency for each data point by evaluating whether normalised optical density (ODn) is
below 1.5 and Viral Load above 400 copies/ml. The probability of testing recent as a
function of time will be modelled using the loglog binomial (linear) and logit cubic polynomial
functional forms, the confidence interval will be estimated by means of 10,000
subject-level resampling operations and the fitted model curve will be plotted.
```

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prevBYcounts *Prevalence and Relative Standard Errors by Counts*

Description

Prevalence and Relative Standard Errors by Counts

Usage

```
prevBYcounts(N, N_H, N_testR, N_R, DE_H = 1, DE_R = 1)
```

Arguments

N	Counts of total survey sample size(s) (vector/integer).
N_H	Number of HIV positive found in survey(s) (vector/integer).
N_testR	Number tested for recency in survey(s) (vector/integer).
N_R	Number of recent cases in survey(s) (vector/integer).

DE_H	Design effect of HIV prevalence test (vector/numeric), greater than or equal to 1. If multiple surveys are entered but only one design effect is specified, function assumes entered design effect is identical for both surveys.
DE_R	Design effect of recency test (vector/numeric), greater than or equal to 1. If multiple surveys are entered but only one design effect is specified, function assumes entered design effect is identical for both surveys.

Details

Type vignette("Inference",package="abie") into console for more details on this function.

Value

Prevalences and relative standard errors. Design effects are assumed negligible unless user specifies otherwise.

Examples

```
prevBYcounts(N = 5000, N_H = 1000, N_testR = 1000, N_R = 70, DE_R = 1.1)

prevBYcounts (N = c(5000,5000), N_H = c(1000,1000), N_testR = c(1000,1000),
N_R = c(100,70), DE_H = 1, DE_R = c(1,1.1))
```

---

recencyI *Incidence and incidence difference statistics from trinomial prevalences of HIV and recency*

Description

Incidence and incidence difference statistics from trinomial prevalences of HIV and recency

Usage

```
recencyI(PrevH, RSE_PrevH, PrevR, RSE_PrevR, Boot = FALSE, BS_Count = 10000,
  alpha = 0.05, BMest = "same.test", MDRI, RSE_MDRI, FRR, RSE_FRR,
  BigT = 730, Covar_HR = 0)
```

Arguments

PrevH	Prevalence of HIV (vector/integer).
RSE_PrevH	Relative Standard Error (RSE) of estimate for population prevalence of HIV (vector/integer).
PrevR	Proportion of persons found to be 'recent' by biomarker assay among total persons found positive for HIV (vector/integer).
RSE_PrevR	Relative Standard Error (RSE) of estimate for population proportion of those testing positive for HIV who have been infected recently (vector/integer).
Boot	True/False variable indicating whether variance of point estimates is to be calculated by Empirical Bootstrapping (TRUE) or Delta Method (FALSE), the default setting.
BS_Count	Specifies number of bootstrap samples for bootstrapped confidence intervals of incidence.

alpha	test rejection threshold.
BMest	Biomarker estimation by one the 3 options 'same.test'(=default), 'FRR.indep', 'MDRI.FRR.indep' (string).
MDRI	mean duration of recent infection [days] (vector/integer).
RSE_MDRI	Relative standard error of MDRI [days] (vector/integer).
FRR	False recent rate (vector/integer).
RSE_FRR	Relative standard error of FRR (vector/integer).
BigT	post-infection time cut-off true vs false recent [days] default 730 days (integer).
Covar_HR	Covariance of probability of being positive and being categorized recent from survey (vector/integer). Note that as the variances of PrevH and PrevR are often quite small, only a suitably commensurate covariance will enable the inversion of the bootstrap covariance matrix for random number generation to proceed without error.

Details

Implements assay-based incidence estimation through cross-sectional prevalence and recency of infection tests as described by Kassanjee, et al. "A new general biomarker-based incidence estimator," *Epidemiology* (2012). Function parameters must be specified to include assay test characteristics and survey results as proportions. Confidence intervals are computed via Delta method approximation, except when Boot=TRUE is specified, in which case confidence intervals are generated by empirical bootstrap resampling. Inputs must be in appropriate ranges for appropriate units. Extreme input values may make calculation impossible, and if entered will elicit error notices. Type vignette("Inference",package="abie") into console for more details on this function.

Implements assay-based incidence estimation through cross-sectional prevalence and recency of infection tests as described by Kassanjee, et al. 'A new general biomarker-based incidence estimator,' *Epidemiology* (2012). Function parameters must be specified to include assay test characteristics and survey results as proportions. Confidence intervals are computed via Delta method approximation, except when Boot=TRUE is specified, in which case confidence intervals are generated by empirical bootstrap resampling. Inputs must be in appropriate ranges for appropriate units. Extreme input values may make calculation impossible, and if entered will elicit error notices.

Value

Incidence estimate, annual risk of infection, confidence interval, relative standard error of estimate and of assay characteristics MDRI and FRR. If multiple surveys are entered, function returns said results, as well as estimates of incidence differences, confidence intervals of differences, difference relative standard errors, and p-values testing the hypothesis that the difference in incidence measures are zero. Theoretical relative standard error of incidence and incidence difference at infinite sample size is returned only if Boot=FALSE, as that calculation relies on the asymptotic behavior of components of the Delta method approximation, and is not calculable from bootstrapped values.

Examples

```
recencyI(PrevH = 0.20, RSE_PrevH = 0.028, PrevR = 0.10, RSE_PrevR = 0.094,
BS_Count = 10000, Boot = TRUE, BMest = same.test, MDRI = 200, RSE_MDRI = 0.05,
FRR = 0.01, RSE_FRR = 0.2, BigT = 730)


recencyI(PrevH = c(0.20,0.21,0.18), RSE_PrevH = c(0.028,0.03,0.022),
PrevR = c(0.10,0.13,0.12), RSE_PrevR = c(0.094,0.095,0.05),
```

```
BS_Count = 10000, Boot = FALSE, BMest = MDRI.FRR.indep, MDRI = 200,
RSE_MDRI = 0.05, FRR = c(0.01,0.009,0.02), RSE_FRR = 0.2, BigT = 730)
```

SSCprecision *Sample size or precision calculation*

Description

Sample size or precision calculation

Usage

```
SSCprecision(I, RSE_I, PrevH, CR, MDRI, RSE_MDRI, FRR, RSE_FRR, BigT = 730,
  DE_H = 1, DE_R = 1, n = "out", step = 5)
```

Arguments

I	Expected Incidence.
RSE_I	Relative Standard Error of Incidence Estimate.
PrevH	Prevalence of HIV.
CR	Coverage rate: probability (0-1) of being tested for recency when positive for HIV.
MDRI	mean duration of recent infection in days (vector/integer).
RSE_MDRI	Relative standard error of MDRI (vector/integer).
FRR	False recent rate (vector/integer).
RSE_FRR	Relative standard error of FRR (vector/integer).
BigT	post-infection time cut-off for true vs. false recency. Default is 730 days.
DE_H	Design effect of HIV prevalence test (vector/integer).
DE_R	Design effect of recency test (vector/integer).
n	Sample Size: either a given hypothetical value, or to be determined by function, which is the default.
step	number of steps between minimum I and maximum I in the calculation of a range of output.

Details

Summarizes performance of a recent infection test (into a standard error of the incidence estimate), given estimated test properties (RSE of incidence) and the prevalence/incidence in a hypothetical context; or gives sample size necessary for a given level of estimator precision. Returns: proportion of sample categorized as HIV positive and recently infected; proportion of sample categorized as HIV positive and non-recently infected; the relative standard error of the incidence estimator at infinite sample size, which is the component of variability explained solely by the assay characteristics; the relative standard error of the estimate of prevalence; the relative standard error of the estimate of proportion of HIV positive that are recent.

Up to two parameters can be given as tuple vetors, with the input parameter 'step' giving the number of points analyzed between the endpoints of the vector. This yields output for each value in the step for the output parameters that take as argument one of the varying inputs. See the second and third example below for an instantiation of this process.

Value

Either sample size necessary for a given precision under a given set of testing characteristics and a hypothetical prevalence/incidence scenario, or precision under a particular sample size scenario, with a given hypothetical prevalence/incidence scenario.

Examples

```
SSCprecision(I = 0.015, RSE_I = 0.25, PrevH = 0.2, CR = 1,
MDRI = 200, RSE_MDRI = 0.05, FRR = 0.01, RSE_FRR = 0.2,
BigT = 730, DE_H = 1.1, DE_R = 1, n = out)

SSCprecision(I = c(0.015,0.02), RSE_I = 0.25, PrevH = c(0.10,0.20),
CR = 1, MDRI = 200, RSE_MDRI = 0.05, FRR = 0.01, RSE_FRR = 0.2,
BigT = 700, DE_H = 1, DE_R = 1, n = out, step = 5)

SSCprecision(I = 0.017, RSE_I = out, PrevH = c(0.10,0.20),
CR = 1, MDRI = 211, RSE_MDRI = 0.05, FRR = 0.009, RSE_FRR = 0.2,
BigT = 720, n = 5000, step = 5)
```

`SSPower` *Power and sample size calculation for assay-based incidence estimation*

Description

Power and sample size calculation for assay-based incidence estimation

Usage

```
SSPower(I1, I2, PrevH1, PrevH2, n1 = "both", n2 = "both", alpha = 0.05,
  Power = 0.8, SS = "out", CR = 1, DE_H = 1, DE_R = 1,
  BMest = "same.test", MDRI, RSE_MDRI, FRR, RSE_FRR, BigT = 730)
```

Arguments

`I1`	Predicted incidence of HIV in survey 1.
`I2`	Predicted incidence of HIV in survey 2.
`PrevH1`	Predicted prevalence of HIV in survey 1.
`PrevH2`	Predicted prevalence of HIV in survey 2.
`n1`	Sample size for survey 1. If equal sample sizes for both surveys are desired at a given power level, both n1 and n2 must have value "both", which is the default. If necessary sample size at a given power level for survey 1 is desired and survey 2 has been completed, n1 must be set to "out" along with SS.
`n2`	Sample size for survey 2. If equal sample sizes for both surveys are desired at a given power level, both n1 and n2 must have value "both", which is the default. If necessary sample size at a given power level for survey 2 is desired and survey 1 has been completed, n2 must be set to "out" along with SS.
`alpha`	Significance level for test (default alpha=0.05).

Power	Desired power used to calculate a sample size for the surveys. Default is 0.80, meaning the function outputs the necessary sample size to achieve stated power for a test of differences in incidence. If Power is set to "out", function will return power of detecting a difference in incidences for given sample size inputs.
SS	Sample size. Default is "out", meaning the function takes a power argument and outputs a common sample size needed to achieve power level for test of differences for incidence. If power is desired for a given sample size, parameter value is irrelevant; however, values for n1 and n2 must be specified.
CR	Coverage rate (0-1).
DE_H	Design effect of HIV prevalence test (vector/integer). If a single value is specified, that value is assumed to be the value for both surveys.
DE_R	Design effect of recency test (vector/integer). If a single value is specified, that value is assumed to be the value for both surveys.
BMest	Biomarker test parameter (MDRI, FRR, and RSE) estimation by one the 3 options "same.test"(default), "FRR.indep", "MDRI.FRR.indep" (string).
MDRI	mean duration of recent infection [days] (vector/integer). If a single value is specified, that value is assumed to be the value for both surveys.
RSE_MDRI	Relative standard error of MDRI [days] (vector/integer). If a single value is specified, that value is assumed to be the value for both surveys.
FRR	False recent rate (vector/integer). If a single value is specified, that value is assumed to be the value for both surveys.
RSE_FRR	Relative standard error of FRR (vector/integer). If a single value is specified, that value is assumed to be the value for both surveys.
BigT	Post-infection time cut-off (days). Default 730. If a single value is specified, that value is assumed to be the value for both surveys.

Value

Common sample size of two surveys–or the sample size of one survey given the other has already been completed–necessary to achieve a given power level for testing a null hypothesis that the incidence rates are identical between populations; alternatively, the power of said test under a particular sample size scenario. Function also returns implied statistics from input values on paramters, confidence limits, and population counts.

Examples

```
SSPower(I1 = 0.05, I2 = 0.03, PrevH1 = 0.20, PrevH2 = 0.20,
n1 = 5000, n2 = 5000, alpha = 0.05, Power = "out", SS = NULL,
DE_H = c(1,1.1), DE_R = 1, BMest = "same.test", MDRI = 200,
RSE_MDRI = 0.05, FRR = 0.01, RSE_FRR = 0.20, BigT = 730)


SSPower(I1 = 0.05, I2 = 0.03, PrevH1 = 0.20, PrevH2 = 0.20,
alpha = 0.05, Power = 0.80, SS = "out", DE_H = 1, DE_R = 1,
BMest = "FRR.indep", MDRI = 200, RSE_MDRI = 0.05,
FRR = c(0.01,0.009), RSE_FRR = c(0.20,0.21), BigT = 730)


SSPower(I1 = 0.05, I2 = 0.03, PrevH1 = 0.20, PrevH2 = 0.20,
n1 = 5000, n2 = "out", alpha = 0.05, Power = 0.80, SS ="out",
DE_H = 1, DE_R = 1, BMest = "MDRI.FRR.indep", MDRI = 200,
```

```
RSE_MDRI = c(0.05,0.06), FRR = c(0.01,0.009),
RSE_FRR = c(0.20,0.21), BigT = 730)
```

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