

Package ‘DiffRelRisk’

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Type Package

Title Confidence Intervals for the Difference Between Two Relative Risks

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Description Estimates and provides a confidence interval for the difference between two relative risks from data that may contain small sample sizes, stratified studies, or individual-level covariates.

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NeedsCompilation yes

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DiffRelRisk-package

Confidence Intervals for the Difference Between Two Relative Risks

Description

Estimates and provides a confidence interval for the difference between two relative risks

Details

This package contains methods to estimate the confidence interval for the difference between two relative risks. Letting p_0 , p_1 , and p_2 be the probabilities of an event in three groups (i.e. control, treatment 1, treatment 2), these methods estimate a confidence interval for $r = p_1/p_0 - p_2/p_0$. These methods can handle small sample sizes, stratified studies, and individual-level covariates. They were developed specifically for vaccine trials to estimate the difference between two vaccine efficacies (VE), where $VE_1 = 1 - p_1/p_0$, $VE_2 = 1 - p_2/p_0$ and $r = VE_2 - VE_1$.

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DRRCI_adj

Difference in Relative Risks

Description

This function estimates and provides a confidence interval for the difference between two relative risks when adjusting for covariates.

Usage

```
DRRCI_adj(trtGroup, outcome, covars, options=NULL)
```

Arguments

<code>trtGroup</code>	A vector of 3 treatment groups coded 0-2, with 0=control, 1=treatment group 1, and 2=treatment group 2.
<code>outcome</code>	A binary vector of outcomes coded as 0 and 1.
<code>covars</code>	A matrix of covariates
<code>options</code>	List of options (see options).

Details

The objects `trtGroup`, `outcome`, and `covars` must all have the same number of subjects. Subjects with missing values will be removed.

Value

A list containing:

Name	Description
<code>EST</code>	The estimated difference in relative risks
<code>LB</code>	The lower bound for <code>EST</code>
<code>UB</code>	The upper bound for <code>EST</code>
<code>beta</code>	The MLE (and asymptotic SE) for the coefficients for individual level covariates

See Also

`DRRCI_unadj`, `DRRCI_counts`

Examples

```
set.seed(1234)
n <- 100
trt <- sample(0:2, n, replace=TRUE)
Y <- sample(0:1, n, replace=TRUE)
X <- runif(n)

DRRCI_adj(trt, Y, covars=X)
```

```
DRRCI_adj(trt, Y, covars=X, options=list(alpha=0.05,LRT=0))
```

DRRCI_counts	<i>Difference in Relative Risks</i>
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Description

This function estimates and provides a confidence interval for the difference between two relative risks with count data.

Usage

```
DRRCI_counts(x1, n1, x2, n2, x0, n0, x0b=NULL, n0b=NULL, options=NULL)
```

Arguments

x1	The number of events in the first treatment group. This can also be a vector if there are strata.
n1	The number of subjects in the first treatment group. This can also be a vector if there are strata.
x2	The number of events in the second treatment group. This can also be a vector if there are strata.
n2	The number of subjects in the second treatment group. This can also be a vector if there are strata.
x0	The number of events in the (first) control group. This can also be a vector if there are strata.
n0	The number of subjects in the (first) control group. This can also be a vector if there are strata.
x0b	NULL or the number of events in the (second) control group. This can also be a vector if there are strata.
n0b	NULL or the number of subjects in the (second) control group. This can also be a vector if there are strata.
options	List of options (see options).

Details

This function estimates and provides a confidence interval for the difference between two relative risks. If `x0b` is `NULL`, then there are three populations, with one control population, and the goal to estimate the difference: $p_1/p_0 - p_2/p_0$, where p_0 , p_1 , and p_2 are the risks in each population. When `x0b` is not `NULL`, then there are four populations (two control populations), with `x0`, `n0` as the control population for the first treatment group and `x0b`, `n0b` as the control population for the second treatment group. With two control populations, the goal is to estimate the difference: $p_2/p_{0b} - p_1/p_0$.

If any group has zero events, then for the calculation of the lower and upper bounds with `options$deltaMethod = 1`, the zero will be replaced with 0.5.

Value

A list containing:

Name	Description
EST	The estimated difference in relative risks
LB	The lower bound for EST
UB	The upper bound for EST

See Also

DRRCI_adj, DRRCI_unadj

Examples

```
# No strata
DRRCI_counts(15, 29, 16, 40, 17, 31)
DRRCI_counts(15, 29, 16, 40, 17, 31,
             options=list(alpha=0.05, altParam=0))

# With 3 strata
DRRCI_counts(c(6, 4, 5), c(10, 9, 10),
             c(5, 7, 4), c(13, 15, 12),
             c(5, 7, 5), c(10, 10, 11))
DRRCI_counts(c(6, 4, 5), c(10, 9, 10),
             c(5, 7, 4), c(13, 15, 12),
             c(5, 7, 5), c(10, 10, 11),
             options=list(alpha=0.05, altParam=0))
```

DRRCI_unadj	<i>Difference in Relative Risks</i>
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Description

This function estimates and provides a confidence interval for the difference between two relative risks with no covariates.

Usage

```
DRRCI_unadj(trtGroup, outcome, strata=NULL, options=NULL)
```

Arguments

trtGroup	A vector of (3 or 4) treatment groups coded 0-2, or 1-4 (see details).
outcome	A binary vector of outcomes coded as 0 and 1.
strata	NULL or a vector of strata.
options	List of options (see options).

Details

This function is essentially `DRRCI_counts`, but with a different interface. If `trt` is coded 0-2, then it is assumed that 0 denotes the control group, 1 denotes treatment group 1, and 2 denotes treatment group 2. If there are four groups (`trt` is coded 1-4), then `trt=3` denotes the control group for treatment group 1 (`trt=1`), and `trt=4` denotes the control group for treatment group 2 (`trt=2`).

Value

A list containing:

Name	Description
EST	The estimated difference in relative risks
LB	The lower bound for EST
UB	The upper bound for EST

See Also

DRRCI_adj, DRRCI_counts

Examples

```
set.seed(1234)
n <- 100
trt <- sample(0:2, n, replace=TRUE)
Y <- sample(0:1, n, replace=TRUE)
S <- sample(1:3, n, replace=TRUE)

DRRCI_unadj(trt, Y, options=list(deltaMethod=0, LRT=0))
DRRCI_unadj(trt, Y, options=list(deltaMethod=0, LRT=1))
DRRCI_unadj(trt, Y, options=list(deltaMethod=1, LRT=0))

DRRCI_unadj(trt, Y, strata=S)
DRRCI_unadj(trt, Y, strata=S, options=list(deltaMethod=0, LRT=0, alpha=0.05))
```

options	<i>Options</i>
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Description

The list of options

Format

The format is: List of 8

- alpha** The two-sided error rate for the confidence interval. The default is 0.05.
- altParam** A binary variable (i.e. 0 or 1) indicating whether to use the full likelihood (altParam=0) or assume the log-linear model holds true (altParam=1). The default is altParam = 0. We note, altParam=1 is equivalent to using DRRCI_adj with covars set to binary indicators for strata.
- deltaMethod** A binary variable (i.e. 0 or 1) indicating whether the delta method should (deltaMethod=1) or should not (deltaMethod=0) be used. The default is deltaMethod = 0.
- estRR** A binary variable (i.e. 0 or 1) indicating whether we should calculate the confidence intervals for each relative risk (estRR=1) or the difference in relative risks (estRR=0). The default is estRR = 0.
- fast** A binary variable (i.e. 0 or 1) indicating that the optimizations should be performed over a coarser grid to speed up the analysis (fast=1). Use with caution. The default is fast = 0.

fast.c A binary variable (i.e. 0 or 1) indicating that the `c` code should be called instead of the `R` code for faster computing times. The default is `fast.c = 1`.

LRT A binary variable (i.e. 0 or 1) indicating the type of confidence interval desired: 0 = a score-based confidence interval and 1 = a likelihood-based confidence interval. The default is `LRT = 0`.

refPop NULL or a string to denote the target population when standardization is used. The choices are

Choice	Description
"All"	All subjects
"Cont"	The control population
"Ind"	Indirect standardization for the delta method
"Opt"	An optimally chosen population
"Treat"	The treated population

The default is NULL unless `deltaMethod=1`, in that case, the default is "All".

Details

Not all options are for all functions. Below is a table showing which options can be used.

Option	DRRCI_adj	DRRCI_counts	DRRCI_unadj
alpha	Yes	Yes	Yes
altParam	No	Yes (3 groups)	Yes (3 groups)
deltaMethod	No	Yes (3 groups)	Yes (3 groups)
estRR	Yes	No	No
fast	Yes	Yes	Yes
fast.c	Yes	Yes	Yes
LRT	Yes	Yes	Yes
refPop	No	Yes	Yes

Notes:

1. The option `fast` is only valid when `LRT = 0`.
2. With four treatment groups, `refPop = "Opt"` is not valid and will default to `refPop = "All"`.

See Also

`DRRCI_adj`, `DRRCI_unadj`, `DRRCI_counts`