

# Package ‘episheet’

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**Type** Package

**Title** Rothman's Episheet

**Version** 0.4.0

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**Description** A collection of R functions supporting the text book  
Modern Epidemiology, Second Edition, by Kenneth J.Rothman and Sander Greenland.  
ISBN 13: 978-0781755641 See <<http://www.krothman.org/>> for more information.

**License** GPL (>= 2)

**URL** <https://github.com/epijim/episheet>

**BugReports** <https://github.com/epijim/episheet/issues>

**Encoding** UTF-8

**LazyData** true

**RoxygenNote** 6.1.1

**Depends** R (>= 2.10.0)

**Suggests** knitr, rmarkdown, testthat

**Imports** dplyr, tidyr, ggplot2, magrittr, assertthat, rlang

**VignetteBuilder** knitr

**NeedsCompilation** no

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**Repository** CRAN

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ebola	<i>ebola data</i>
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## Description

Person-time data for death from ebola. Data from <https://datacompass.lshtm.ac.uk/599/> Marks, M. Learning Clinical Epidemiology with R. (Project). London School of Hygiene & Tropical Medicine, London, United Kingdom.

## Usage

ebola

## Format

A dataframe

**id** Unique patient identifier

**age** Age in years

**age\_group** Grouped age

**sex** Sex

**disease\_onset** Date of onset (date class)

**disease\_ended** Date of death or recovery (date class)

**days\_at\_risk** Number of days at risk of death

**status** Died or recovered (string)

**transmission** How ebola was transmitted

**died** Integer 1 = died, 0 = survived

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pvalueplot

*Plot the p-value function*


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### Description

Plot the p-value function for one or two confidence interval pairs. See following for example of the use in the literature: Is flutamide effective in patients with bilateral orchiectomy? Rothman, Kenneth J et al. The Lancet , Volume 353 , Issue 9159 , 1184

### Usage

```
pvalueplot(est1.ll, est1.ul, est2.ll = NA, est2.ul = NA,
  label1 = "Estimate 1", label2 = "Estimate 2",
  xlabel = "Relative Risk", cotype = "95%CI", labelsize = NULL,
  functionwidth = 1, referencewidth = 1)
```

### Arguments

est1.ll	Lower confidence interval of estimate 1
est1.ul	Upper confidence interval of estimate 1
est2.ll	Lower confidence interval of estimate 2 (optional)
est2.ul	Upper confidence interval of estimate 2 (optional)
label1	If using two estimates, name the 1st
label2	If using two estimates, name the 2nd
xlabel	The x axis label
cotype	Choose between '95%CI', '90%CI' or '99%CI'
labelsiz	Change size of labels
functionwidth	Change width of pvalue function line
referencewidth	Change width of reference lines

### Bugs

Code repo: <https://github.com/epijim/episheet>

### Examples

```
pvalueplot(
  est1.ll = 0.9,
  est1.ul = 12,
  xlabel = "Relative Risk"
)
```

```
pvalueplot(
  est1.ll = 0.8,
  est1.ul = 3.8,
```

```

    est2.ll = 1.2,
    est2.ul = 2,
    label1 = "Estimate 1",
    label2 = "Estimate 2",
    xlabel = "Relative Risk",
    cotype = "95%CI"
  )

```

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rate

*Calculate risk ratio and risk difference*


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### Description

Calculate risk ratios and risk differences using a Poisson distribution for person-time data. Function works on individual level data or aggregated data p244 2nd Edition

### Usage

```
rate(data, outcome, denominator, exposure, per_unit, ci_level = 95)
```

### Arguments

data	A dataframe
outcome	Variable with the outcomes as a numeric variable
denominator	Variable giving the amount of time at risk
exposure	Variable giving whether exposed or not
per_unit	Multiplier for rate values, e.g. 1000 for n outcomes per 1000 denominator
ci_level	A numeric value giving the confidence interval

### Examples

```

# Using individual level data

data(ebola)
library(dplyr)
ebola %>%
  mutate(male = ifelse(sex == "male", 1, 0)) %>%
  rate(outcome = died, denominator = days_at_risk, exposure = male,
       per_unit = 100)

# Using aggregated data
# Table 14-2
cancer_xray <- data.frame(cases = c(41, 15), pyar = c(28010, 19017),
  radiation = c(1, 0))
cancer_xray
cancer_xray %>%
  rate(outcome = cases, denominator = pyar, exposure = radiation,
       per = 100000)

```

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risk	<i>Calculate risk ratio and risk difference</i>
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**Description**

Calculate risk ratios and risk differences

**Usage**

```
risk(data, exposure, outcome, ci_level = 95)
```

**Arguments**

data	A dataframe
exposure	Variable giving the levels of the outcome
outcome	Variable giving cases (1) or non-cases (0)
ci_level	a string giving the confidence interval

**Value**

A dataframe with the risk ratio, risk difference and confidence intervals

**Examples**

```
# Data from stratum 1 of table 15-1., p260
dat <- data.frame(
  exposure_var = c(rep(1, 8), rep(0, 5), rep(1, 98), rep(0, 115)),
  outcome_var = c(rep(1, 8), rep(1, 5), rep(0, 98), rep(0, 115)),
  stringsAsFactors = FALSE
)
risk(data = dat, exposure = exposure_var, outcome = outcome_var)
```

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stratified_risk	<i>Stratified risk</i>
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**Description**

Calculate stratified risk estimates as per Chapter 15,

**Usage**

```
stratified_risk(data, exposure, outcome, stratifier, ci_level = 95)
```

**Arguments**

<code>data</code>	A dataframe providing the exposure, outcome and stratifying variable
<code>exposure</code>	binary variable giving the exposure status
<code>outcome</code>	binary variable giving the outcome status
<code>stratifier</code>	stratifying variable
<code>ci_level</code>	variable giving the limits for the confidence interval

**Value**

A dataframe giving an MH-adjusted risk ratio

**Examples**

```
data(tolbutamide)
stratified_risk(tolbutamide, exposure = tolbutamide, outcome = dead,
  stratifier = age)
```

---

tolbutamide                      *tolbutamide data - chapter 15-1, p260*

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**Description**

Age-specific comparison of death from all causes for Tolbutamide and placebo treatment groups, University Group Diabetes Program (1970)

**Usage**

```
tolbutamide
```

**Format**

An object of class `data.frame` with 409 rows and 3 columns.

**Details**

**@format** A dataframe with 409 observations and 3 variables

**tolbutamide** Given Tolbutamide (1) or placebo (0)

**dead** Died (1) or surviving (0)

**age** Less than 55 (<55) or 55 and over (ge55)

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