Package ‘DALY’

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Type Package

Title The DALY Calculator - Graphical User Interface for Probabilistic DALY Calculation in R

Version 1.5.0

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BugReports `https://github.com/brechtdv/DALY/issues`

Depends R (>= 3.3.0)

Imports tcltk, grid, stats

Description The DALY Calculator is a free, open-source Graphical User Interface (GUI) for stochastic disability-adjusted life year (DALY) calculation.

License GPL (>= 2)

SystemRequirements Tcl/Tk (>= 8.5), Tktable (>= 2.9)

URL `http://daly.cbra.be`

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Contents

`DALY-package` *The DALY Calculator – Graphical User Interface for Probabilistic DALY Calculation in R*

Description

The *DALY Calculator* is a free, open-source Graphical User Interface (GUI) for probabilistic disability-adjusted life year (DALY) calculation, developed in the R environment for statistical computing.

The main goal of the *DALY Calculator* is to provide a flexible and easy-to-use tool for DALY calculation, and to promote consistency in the uncertainty analysis of DALYs.

Details

Package:	DALY
Type:	Package
Version:	1.5.0
Date:	2016-11-25
Depends:	R (>= 3.3.0)
License:	GPL (>= 2)
SystemRequirements:	Tcl/Tk (>= 8.5), Tktable (>= 2.9)
URL:	`http://daly.cbra.be`

Author(s)

Brecht Devleesschauwer, Scott McDonald, Juanita Haagsma, Nicolas Praet, Arie Havelaar, Niko Speybroeck

Maintainer: `<brechtdv@gmail.com>`

References

- `http://daly.cbra.be`
- Devleesschauwer B, et al. (2014). Calculating Disability-Adjusted Life Years to quantify burden of disease. *International Journal of Public Health 59,* 565-569. `http://dx.doi.org/10.1007/s00038-014-0552-z`
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- Praet N, et al. (2009). The disease burden of *Taenia solium* cysticercosis in Cameroon. *PLoS Neglected Tropical Diseases 3,* e406.
- Kortbeek LM, et al. (2009). Congenital toxoplasmosis and DALYs in the Netherlands. *Memorias de Instituto Oswaldo Cruz 104,* 370-373.

See Also

`DALYcalculator` (for a brief description of the *DALY Calculator*)
`DALYmanual` (for a more comprehensive overview)

`aggregate.DALY` *Aggregate method for class 'DALY'*

Description

Aggregate *DALY Calculator* output by outcome, age/sex class, or both.

Usage

```
## S3 method for class 'DALY'
aggregate(x, by = c("total", "class", "outcome"), ...)
```

Arguments

`x`	Object of class `'DALY'`
`by`	Any of `c("total", "outcome", "class")`
`...`	Additional arguments to be passed to `aggregate`

Value

For `by` = `"total"`:

`DALY`	Vector of DALYs aggregated by outcome and age/sex class
`YLD`	Vector of YLDs aggregated by outcome and age/sex class
`YLL`	Vector of YLLs aggregated by outcome and age/sex class
`cases`	Vector of cases aggregated by outcome and age/sex class
`deaths`	Vector of deaths aggregated by outcome and age/sex class
`pop`	Population matrix
`name`	Name of the disease

For `by` = `"class"`:

`DALY`	Vector of DALYs aggregated by age/sex class
`YLD`	Vector of YLDs aggregated by age/sex class
`YLL`	Vector of YLLs aggregated by age/sex class
`cases`	Vector of cases aggregated by age/sex class
`deaths`	Vector of deaths aggregated by age/sex class
`pop`	Population matrix
`name`	Name of the disease

For `by` = `"outcome"`:

`\emph{i}`	List containing vectors of DALYs, YLDs, YLLs, cases and deaths for each outcome `i`
`pop`	Population matrix
`name`	Name of the disease

Author(s)

`<brechtdv@gmail.com>`

See Also

`print.DALY`, `summary.DALY`

`DALYcalculator` (for a brief description of the *DALY Calculator*)
`DALYmanual` (for a more comprehensive overview)

Examples

```
## Not run:

##= load the NCC example ==================================
setDALYexample(1)

##= perform DALY calculation, store results in 'x' ========
x <- getDALY()

##= store simulations aggregated by =======================
##= outcome and age/sex class     =========================
y <- aggregate(x, by = "total")

summary(y$DALY)  # default summary of total DALYs =========
hist(y$deaths)   # default histogram of total deaths ======

## End(Not run)
```

`DALYcalculator` *DALY Calculator main window*

Description

This function opens the main window of the *DALY Calculator*.

After initiating the *DALY Calculator* main window, the following steps have to be followed to calculate DALYs:

1. Set the ‘Population’ table
2. Set the ‘Life Expectancy’ table - the default is the standard life expectancy table introduced in the GBD2010 study
3. Set the input parameters and corresponding distributions and stratification levels
4. Set the age weighting and time discounting rates
5. Calculate DALYs !

In order to demonstrate the calculation process of the *DALY Calculator*, two examples from the foodborne disease burden literature are built-in:

- The burden of *Taenia solium* cysticercosis in Cameroon (Praet et al., 2009)
- Congenital toxoplasmosis and DALYs in the Netherlands (Kortbeek et al., 2009)

In the following sections, a brief summary will be given of the functionalities of the *DALY Calculator*. A more comprehensive overview is provided in the **DALY Calculator manual**, which is available through the `DALYmanual` function.

Usage

```
DALYcalculator()
```

Details

The *DALY Calculator* provides the following three menu options:

File

- **Load DALY data from file. . .** reads population and epidemiological data from an .RData file (through `readDALYdata`)
- **Save DALY data to file. . .** saves the population and epidemiological data to an .RData file (through `saveDALYdata`)
- **Reset DALY calculator** clears all entered data, and resets the *DALY Calculator* to its default settings, except for the life expectancy table (through `reset`)
- **Exit** exits the *DALY Calculator*, without saving the entered data

Settings

- **Life Expectancy Table. . .** opens the life expectancy table window (through `setLifeExp`)
- **Options. . .** opens the options window (through `DALYoptions`)

Help

- **Load examples** loads one of the two built-in examples (through `setDALYexample`)
  1. The burden of Neurocysticercosis in West-Cameroon
  2. The burden of Congenital Toxoplasmosis in the Netherlands
- **Html help** opens the HTML help file for the *DALY Calculator* (cf `?DALYcalculator`)
- **DALY Calculator manual (PDF)** opens the **DALY Calculator Manual** (through `DALYmanual`)
- **Package description** opens the HTML help file for the **DALY** package (cf `?DALY`)
- **DALY Calculator Info** shows current version and developers core team

Author(s)

`<brechtdv@gmail.com>`

References

- `http://daly.cbra.be`
- Devleesschauwer B, et al. (2014). Calculating Disability-Adjusted Life Years to quantify burden of disease. *International Journal of Public Health 59,* 565-569. `http://dx.doi.org/10.1007/s00038-014-0552-z`
- Praet N, Speybroeck N, Manzanedo R, Berkvens D, Nforninwe DN, Zoli A, Quet F, Preux P-M, Carabin H, Geerts S (2009). The disease burden of *Taenia solium* cysticercosis in Cameroon. *PLoS Neglected Tropical Diseases 3(3),* e406.
- Kortbeek LM, Hofhuis A, Nijhuis CDM, Havelaar AH (2009). Congenital toxoplasmosis and DALYs in the Netherlands. *Memorias de Instituto Oswaldo Cruz 104(2),* 370-373.

See Also

A command-line interface to the *DALY Calculator* is available through the following functions:

- `setPop` opens the ‘Population’ window
- `setLifeExp` opens the ‘Life Expectancy’ window
- `setStdLE` sets the standard life expectancy
- `setData` opens a ‘Data’ window
- `getDALY` initiates the DALY calculation process and returns the simulated results
- `sensitivity` performs DALY sensitivity analysis
- `DALY_list` merges different DALY objects

See `DALYmanual` for a more comprehensive overview of the *DALY Calculator*

`DALYmanual` *Open the PDF "**DALY Calculator Manual**"*

Description

This function opens the "**DALY Calculator Manual**", which is included as PDF file in the **DALY** package.

Usage

```
DALYmanual()
```

Author(s)

`<brechtdv@gmail.com>`

See Also

`DALYcalculator` (for a brief description of the *DALY Calculator*)
`DALYmanual` (for a more comprehensive overview)

`DALYoptions` *Open the ‘Options’ window*

Description

This function opens the ‘Options’ window of the *DALY Calculator*.

Usage

```
DALYoptions()
```

Details

The following settings can be modified in the ‘options’ window:

- **Iterations:** the default number of iterations is 20,000
- **Numerical output:** the standard output contains a summary of DALYs, YLDs, YLLs, incident cases and deaths. Different options are available:
  - “Summed over age/sex classes” OR “Per age/sex class”
  - “Summed over outcomes” OR “Per outcome”
  - “Absolute” OR “Relative (per 1000 pop)”
- **Graphical output:** the user can specfiy whether or not to view a standardized DALY histogram (see `hist.DALY`).

Author(s)

`<brechtdv@gmail.com>`

See Also

The numerical output methods for class `'DALY'`: `print.DALY`, `summary.DALY`
The graphical output method for class `'DALY'`: `hist.DALY`
The aggregator method for class `'DALY'`: `aggregate.DALY`

`DALYcalculator` (for a brief description of the *DALY Calculator*)
`DALYmanual` (for a more comprehensive overview)

`DALY_list` *Make list of 'DALY' objects*

Description

This function produces a list of DALY objects and assigns class `'DALY_list'` to it. Methods are available to print and plot the resulting object.

Usage

```
DALY_list(...)

## S3 method for class 'DALY_list'
print(x, ...)

## S3 method for class 'DALY_list'
plot(x, prob = 0.95, sort = TRUE, names = NULL,
     bars = TRUE, col = c("grey90", "white"),
     error_bars = TRUE, eb_col = "black",
     grid = TRUE, ...)
```

Arguments

`...`	In `DALY_list`: Multiple objects of class `'DALY'`; In `print.DALY_list`: Additional arguments to be passed to `print.DALY`; In `plot.DALY_list`: Additional arguments to be passed to `plot.DALY`
`x`	Object of class `'DALY_list'`
`prob`	Probability span by DALY error bar; defaults to `0.95`
`sort`	Should values be sorted from high to low? defaults to `TRUE`
`names`	Vector of names to be plotted on the y-axis. If this argument is `NULL`, the default, then the names are taken from the `name` element of the constituting `DALY` objects
`bars`	Should YLL/YLD bars be plotted? defaults to `TRUE`
`col`	Color of YLL and YLD barplot; defaults to `c("grey90", "white")`
`error_bars`	Should DALY error bars be plotted? defaults to `TRUE`
`eb_col`	Color of DALY error bars; defaults to black
`grid`	Should a vertical grid be plotted? defaults to `TRUE`

Value

An object of S3 class `'DALY_list'`.

Author(s)

`<brechtdv@gmail.com>`

See Also

`getDALY`
`print.DALY`
`plot.DALY`
`scatterplot`

`DALYcalculator` (for a brief description of the *DALY Calculator*)
`DALYmanual` (for a more comprehensive overview)

Examples

```
## Not run:

##= load NCC example =====================================
setDALYexample(1)

##= calculate DALYs under different scenarios =============
ncc_00 <- getDALY(aw = FALSE, dr = 0)
ncc_03 <- getDALY(aw = FALSE, dr = 0.03)
ncc_13 <- getDALY(aw = TRUE,  dr = 0.03)

##= store results as 'DALY_list' ==========================
ncc <- DALY_list(ncc_00, ncc_03, ncc_13)

##= barplot of different scenarios ========================
par(mar = c(4, 4, 1, 1) + .5)
plot(ncc, names = c("DALY[0,0]", "DALY[0,0.03]", "DALY[1,0.03]"))

## End(Not run)
```

`DALY_Neurocysticercosis`

Example Dataset 1: Neurocysticercosis in West-Cameroon

Description

The `Neurocysticercosis` dataset consists of a nested list containing data needed to calculate DALYs due to Neurocysticercosis in West Cameroon, according to Praet et al. (2009).

Usage

```
data(DALY_Neurocysticercosis)
```

Format

`List of 3`

`$ model : List of 2`

```
..$ diseaseName : chr "Neurocysticercosis"
..$ outcomeNames : List of 8

$ settings : List of 4
..$ pop : num [1:5, 1:2] 397229 686600 1073342 210474 129081 ...
..$ LE : num [1:21, 1:2] 80 79.4 75.4 70.4 65.4 ...
..$ aw : chr "Yes"
..$ dr : num 3

$ data : List of 8
..$ : List of 8
.. ..$ inc : List of 3
.. .. ..$ dist : chr "Gamma"
.. .. ..$ strat : chr "Age and Sex"
.. .. ..$ param : num [1:5, 1:4] 47.3 47.3 47.3 47.3 47.3 ...
.. ..$ trt : List of 3
.. .. ..$ dist : chr "Beta"
.. .. ..$ strat : chr "None"
.. .. ..$ param : num [1, 1:2] 267 733
.. ..$ ons : List of 3
.. .. ..$ dist : chr "Fixed"
.. .. ..$ strat : chr "Age"
.. .. ..$ param : num [1:5, 1] 2.5 9.95 26.99 51.94 73.6
.. ..$ dur : List of 3
.. .. ..$ dist : chr "Fixed"
.. .. ..$ strat : chr "Age and Sex"
.. .. ..$ param : num [1:5, 1:2] 1.4 2 3.6 2.8 1.6 1.6 3.1 5.9 6 2.8
.. ..$ DWt : List of 3
.. .. ..$ dist : chr "Beta"
.. .. ..$ strat : chr "Age"
.. .. ..$ param : num [1:5, 1:2] 1.5 1.5 1.5 1.5 1.5 35 21.6 21.6 21.6 21.6
.. ..$ DWn : List of 3
.. .. ..$ dist : chr "Beta"
.. .. ..$ strat : chr "Age"
.. .. ..$ param : num [1:5, 1:2] 3 3 3 3 3 27.3 17 17 17 17
.. ..$ mrt : List of 3
.. .. ..$ dist : chr "Gamma"
.. .. ..$ strat : chr "None"
.. .. ..$ param : num [1, 1:2] 3.05 12.32
.. ..$ lxp : List of 3
.. .. ..$ dist : chr "Fixed"
.. .. ..$ strat : chr "Age"
.. .. ..$ param : num [1:5, 1] 2.5 10 30 52.5 77.5

[...]
```

Details

Taenia solium cysticercosis is a zoonotic disease occurring in many developing countries. A relatively high prevalence in humans and pigs has been reported in several parts of the world, but insufficient data are available on the disease burden. Disease impact assessment needs detailed information on well-defined epidemiological and economic parameters. Our work conducted in West Cameroon over several years allowed us to collect the necessary information to estimate the impact of the parasite on the human and animal populations in this area using both cost and Disability Adjusted Life Year (DALY) estimations. This study identified the professional inactivity caused by the disease as the major loss factor in comparison to the cost of health care and losses due to infected pigs. These findings should allow a simpler estimation of the global disease burden based on information on salary levels and human cysticercosis prevalence in endemic areas of the world. In addition, the number of DALYs was higher than estimates already available for some other neglected tropical diseases in sub-Saharan Africa.

The average number of DALYs was 9.0 per thousand persons per year (95% CR 2.8-20.4).

Source

Praet N, Speybroeck N, Manzanedo R, Berkvens D, Nforninwe DN, Zoli A, Quet F, Preux P-M, Carabin H, Geerts S (2009). The disease burden of *Taenia solium* cysticercosis in Cameroon. *PLoS Neglected Tropical Diseases 3(3),* e406.

See Also

`setDALYexample`

`DALYcalculator` (for a brief description of the *DALY Calculator*)
`DALYmanual` (for a more comprehensive overview)

`DALY_Toxoplasmosis` *Example Dataset 2: Congenital toxoplasmosis in the Netherlands*

Description

The `Toxoplasmosis` dataset consists of a nested list containing data needed to calculate DALYs due to congenital toxoplasmosis in the Netherlands, according to Kortbeek et al. (2009).

Usage

```
data(DALY_Toxoplasmosis)
```

Format

```
List of 3

$ model : List of 2
..$ diseaseName : chr "Toxoplasmosis"
```

```
..$ outcomeNames : List of 8

$ settings : List of 4
..$ pop : num [1:5, 1:2] 97000 NA NA NA NA 97000 NA NA NA NA
..$ LE : num [1:21, 1:2] 79 0 0 0 0 0 0 0 0 0 ...
..$ aw : chr "No"
..$ dr : num 0

$ data : List of 8
..$ : List of 8
.. ..$ inc : List of 3
.. .. ..$ dist : chr "Beta-Pert"
.. .. ..$ strat : chr "Age"
.. .. ..$ param : logi [1:5, 1:3] NA NA NA NA NA NA ...
.. ..$ trt : List of 3
.. .. ..$ dist : chr "Fixed"
.. .. ..$ strat : chr "Age"
.. .. ..$ param : logi [1:5, 1] NA NA NA NA NA
.. ..$ ons : List of 3
.. .. ..$ dist : chr "Fixed"
.. .. ..$ strat : chr "Age"
.. .. ..$ param : logi [1:5, 1] NA NA NA NA NA
.. ..$ dur : List of 3
.. .. ..$ dist : chr "Fixed"
.. .. ..$ strat : chr "Age"
.. .. ..$ param : logi [1:5, 1] NA NA NA NA NA
.. ..$ DWt : List of 3
.. .. ..$ dist : chr "Fixed"
.. .. ..$ strat : chr "Age"
.. .. ..$ param : logi [1:5, 1] NA NA NA NA NA
.. ..$ DWn : List of 3
.. .. ..$ dist : chr "Fixed"
.. .. ..$ strat : chr "Age"
.. .. ..$ param : logi [1:5, 1] NA NA NA NA NA
.. ..$ mrt : List of 3
.. .. ..$ dist : chr "Beta-Pert"
.. .. ..$ strat : chr "Age"
.. .. ..$ param : num [1:5, 1:3] 0.0323 NA NA NA NA ...
.. ..$ lxp : List of 3
.. .. ..$ dist : chr "Fixed"
.. .. ..$ strat : chr "Age"
.. .. ..$ param : num [1:5, 1] 0 NA NA NA NA

[...]
```

Details

The calculation of disability-adjusted life years (DALYs) enables public health policy makers to compare the burden of disease of a specific disease with that of other (infectious) diseases. The incidence of a disease is important for the calculation of DALYs. To estimate the incidence of congenital toxoplasmosis (CT), a random sample of 10,008 dried blood spot filter paper cards from babies born in 2006 in the Netherlands were tested for *Toxoplasma gondii*-specific IgM antibodies. Eighteen samples were confirmed as positive for IgM, resulting in an observed birth incidence of CT of 1.8 cases per 1,000 live-born children in 2006 and an adjusted incidence of 2.0 cases per 1,000. This means that 388 infected children were born in 2006. The most likely burden of disease is estimated to be 2,300 DALYs (range 820-6,710 DALYs). In the previous calculations, using data from a regional study from 1987, this estimate was 620 DALYs (range 220-1,900 DALYs). The incidence of CT in the Netherlands is much higher than previously reported; it is 10 times higher than in Denmark and 20 times higher than in Ireland, based on estimates obtained using the same methods. There is no screening program in the Netherlands; most children will be born asymptomatic and therefore will not be detected or treated.

Source

Kortbeek LM, Hofhuis A, Nijhuis CDM, Havelaar AH (2009). Congenital toxoplasmosis and DALYs in the Netherlands. *Memorias de Instituto Oswaldo Cruz 104(2),* 370-373.

See Also

`setDALYexample`

`DALYcalculator` (for a brief description of the *DALY Calculator*)
`DALYmanual` (for a more comprehensive overview)

`getDALY` *Initiate the DALY calculation process*

Description

This function initiates the Monte Carlo DALY calculation process, based on the entered data, and returns the simulated results.

Usage

```
getDALY(button.call = FALSE, aw, dr)
```

Arguments

`button.call`	Gives information on the origin of the call (i.e., through the GUI button (`TRUE`) or the R Console (`FALSE`))
`aw`	Logical flag, indicating if age weighting should be applied; if `aw` is not specified, the value from the GUI will be used
`dr`	Time discount rate (numeric value between 0 and 1); if `dr` is not specified, the value from the GUI will be used

Value

`getDALY` returns an object of class `'DALY'`, which inherits from class `'list'`.

The generic functions `print` and `summary` may be used to obtain and print the DALY calculation results. The generic function `aggregate` extracts from the `'DALY'` object results by outcome, age/sex class, or both.

An object of class `'DALY'` is a list containing the following elements:

`\emph{i}`	For each outcome `i`, an unnamed list containing simulated results (see next paragraph)
`pop`	Population
`name`	Name of the disease

For each outcome `i`, `DALY[[i]]` is a list containing the following elements:

`DALY`	Vector of simulated DALYs
`YLD`	Vector of simulated YLDs
`YLL`	Vector of simulated YLLs
`INC`	Vector of simulated incident cases
`MRT`	Vector of simulated deaths
`name`	Name of the health outcome

The vectors containing simulated DALYs, YLDs, YLLs, incident cases and deaths each have three dimensions:

`1`	Iterations
`2`	Age groups
`3`	Sex

Author(s)

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See Also

The numerical output methods for `'DALY'`: `print.DALY`, `summary.DALY`
The graphical output method for `'DALY'`: `hist.DALY`
The aggregator method for `'DALY'`: `aggregate.DALY`
DALY sensitivity analysis : `sensitivity`

`DALYcalculator` (for a brief description of the *DALY Calculator*)
`DALYmanual` (for a more comprehensive overview)

Examples

```
## Not run:

##= load the NCC example ==================================
setDALYexample(1)

##= perform DALY calculation  =============================
##= without age weighting and time discounting ============
getDALY(aw = FALSE, dr = 0)

##= perform DALY calculation, store results in 'x' ========
##= (with age weighting and a 3% time discount rate) ======
x <- getDALY(aw = TRUE, dr = 0.03)

##= view the structure of 'x' =============================
str(x)

##= view the DALY calculation results =====================
print(x)                   # absolute, total ==============
print(x, relative = TRUE)  # relative (ie, per 1000 pop) ==
print(x, outcomes = TRUE)  # outcome-wise =================

##= obtain minimum & maximum simulated DALY ===============
min(x[[1]]$DALY)
max(x[[1]]$DALY)

##= standardized DALY histogram ===========================
hist(x)

##= DALY sensitivity analysis =============================
sensitivity(x)

## End(Not run)
```

`hist.DALY` *Histogram method for class 'DALY'*

Description

Plot a standardized histogram of *DALY Calculator* output.

Usage

```
## S3 method for class 'DALY'
hist(x, xval = c("DALY", "YLD", "YLL", "cases", "deaths"),
     prob = 0.95, central = c("mean", "median"),
     breaks = 25, fill = "grey95", ...)
```

Arguments

`x`	Object of class `'DALY'`
`xval`	Value to plot on x-axis; must be any of `c("DALY", "YLD", "YLL", "cases", "deaths")`
`prob`	Probability span by plotted credibility interval; defaults to `0.95`
`central`	Plotted central value of distribution; must be any of `c("mean", "median")`
`breaks`	See `hist`; the default is 25 bars
`fill`	The colour to be used to fill the bars
`...`	Additional arguments to be passed to `gpar`

Details

This function plots a standardized histogram of *DALY Calculator* output. The histogram contains by default 25 bars. The limits of the credible interval are denoted by vertical lines; the credible interval limits and central tendency are printed above the histogram.

Author(s)

`<brechtdv@gmail.com>`

See Also

`plot.DALY`

`DALYcalculator` (for a brief description of the *DALY Calculator*)
`DALYmanual` (for a more comprehensive overview)

Examples

```
## Not run:

##= load NCC example =====================================
setDALYexample(1)

##= perform DALY calculation, store results in 'x'  =======
x <- getDALY()

##= plot histogram of total deaths ========================
##= + show 90% credible interval & median =================
hist(x, xval = "deaths", prob = 0.90, central = "median")

## End(Not run)
```

`plot.DALY` *Plot method for class 'DALY'*

Description

Plot a stacked barplot of YLLs/YLDs with a DALY error bar.

Usage

```
## S3 method for class 'DALY'
plot(x, prob = 0.95, sort = TRUE, names = NULL,
     bars = TRUE, col = c("grey90", "white"),
     error_bars = TRUE, eb_col = "black",
     grid = TRUE, ...)
```

Arguments

`x`	Object of class `'DALY'`
`prob`	Probability span by DALY error bar; defaults to `0.95`
`sort`	Should values be sorted from high to low? defaults to `TRUE`
`names`	Vector of names to be plotted on the y-axis. If this argument is `NULL`, the default, then the names are taken from the `name` elements of the outcomes
`bars`	Should YLL/YLD bars be plotted? defaults to `TRUE`
`col`	Color of YLL and YLD barplot; defaults to `c("grey90", "white")`
`error_bars`	Should DALY error bars be plotted? defaults to `TRUE`
`eb_col`	Color of DALY error bars; defaults to black
`grid`	Should a vertical grid be plotted? defaults to `TRUE`
`...`	Additional arguments to be passed to `barplot`

Details

This function plots the results of the DALY calculation aggregated by outcome. By default, both a stacked barplot of YLLs/YLDs and an error bar of total DALYs are shown.

Author(s)

`<brechtdv@gmail.com>`

See Also

`hist.DALY`

`DALYcalculator` (for a brief description of the *DALY Calculator*)
`DALYmanual` (for a more comprehensive overview)

Examples

```
## Not run:

##= load toxoplasmosis example ===========================
setDALYexample(2)

##= perform DALY calculation, store results in 'x'  =======
x <- getDALY()

##= plot results =========================================
par(mar = c(4, 7, 4, 1))
plot(x)

plot(x, bars = FALSE)        # only error bars
plot(x, error_bars = FALSE)  # only barplots

## End(Not run)
```

`print.DALY` *Print method for class 'DALY'*

Description

Print summary of *DALY Calculator* output aggregated by age/sex class.

Usage

```
## S3 method for class 'DALY'
print(x, relative = FALSE, outcomes = FALSE,
     prob = 0.95, digits = 0, ...)
```

Arguments

`x`	Object of class `'DALY'`
`relative`	Show results per 1000 population? See details below
`outcomes`	Show results per outcome? See details below
`prob`	Probability span by printed credibility intervals; defaults to `0.95`
`digits`	Number of decimals to be printed; defaults to `0`
`...`	Additional arguments to be passed to `print`

Details

The standard `print` method gives the absolute number of DALYs, YLDs, YLLs, Cases and Deaths. By specifying `relative = TRUE`, the number of DALYs, YLDs, YLLs, cases and deaths per 1,000 population will be shown.

The standard `print` method gives the number of DALYs, YLDs, YLLs, cases and deaths aggregated over all health outcomes. By specifying `outcomes = TRUE`, the number of DALYs, YLDs, YLLs, cases and deaths for each outcome will be shown as well.

Value

`print.DALY` returns a list containg the following elements:

`total`	Matrix containing mean, median and `prob` credible interval of total DALYs, YLDs, YLLs, cases and deaths
`outcomes`	Named list, containing matrices of DALYs, YLDs, YLLs, cases and deaths for each health outcome
`pct`	Vector of contribution of YLDs and YLLs to overall DALYs

Author(s)

`<brechtdv@gmail.com>`

See Also

`summary.DALY`, `aggregate.DALY`

`DALYcalculator` (for a brief description of the *DALY Calculator*)
`DALYmanual` (for a more comprehensive overview)

Examples

```
## Not run:

##= load the NCC example ==================================
setDALYexample(1)

##= perform DALY calculation, store results in 'x' ========
x <- getDALY()

##= view the DALY calculation results =====================
print(x)                   # absolute, total ==============
print(x, prob = .90)       # absolute, total (90% CrI) ====
print(x, relative = TRUE)  # relative (ie, per 1000 pop) ==
print(x, outcomes = TRUE)  # outcome-wise =================

## End(Not run)
```

`readDALYdata` *Read in DALY data stored in an .RData image file*

Description

This function loads data from an .RData image file into the *DALY Calculator*. The file can be an external file, previously saved through `saveDALYdata()`, or one of the two built-in example datasets.

Usage

```
readDALYdata(file = NULL, example = NULL)
```

Arguments

`file`	Character string, denoting the name of the .RData file
`example`	Integer, denoting the example to be loaded (any of `c(1, 2)`)

Details

NA

Author(s)

`<brechtdv@gmail.com>`

See Also

`saveDALYdata`, `setDALYexample`, `DALY_Neurocysticercosis`, `DALY_Toxoplasmosis`

`DALYcalculator` (for a brief description of the *DALY Calculator*)
`DALYmanual` (for a more comprehensive overview)

`reset` *Reset the DALY Calculator*

Description

This function resets the *DALY Calculator* to its default values, *except* for the ‘Life Expectancy’ table and the options (cf `DALYoptions`).

Usage

```
reset()
```

Author(s)

`<brechtdv@gmail.com>`

See Also

`DALYcalculator` (for a brief description of the *DALY Calculator*)
`DALYmanual` (for a more comprehensive overview)

`saveDALYdata` *Save population and epidemiological data to an .RData image file*

Description

This function saves the population and epidemiological data to an .RData image file. This file can be loaded into the *DALY Calculator* through `readDALYdata()`.

Usage

```
saveDALYdata()
```

Author(s)

`<brechtdv@gmail.com>`

See Also

`readDALYdata`

`DALYcalculator` (for a brief description of the *DALY Calculator*)
`DALYmanual` (for a more comprehensive overview)

`scatterplot` *Scatterplot method for class 'DALY' and 'DALY_list'*

Description

Generate a scatterplot of population versus patient level burden. The method is available for objects of class 'DALY' and 'DALY_list'.

Usage

```
## S3 method for class 'DALY'
scatterplot(x, plot = c("DALY", "YLD", "YLL"), outcomes = TRUE,
            per = 1000, samples = 1000, pch = 16, col = NULL, legend = NULL,
         legend_pos = c("topright", "topleft", "bottomright", "bottomleft"), ...)

## S3 method for class 'DALY_list'
scatterplot(x, plot = c("DALY", "YLD", "YLL"),
            per = 1000, samples = 1000, pch = 16, col = NULL, legend = NULL,
         legend_pos = c("topright", "topleft", "bottomright", "bottomleft"), ...)
```

Arguments

`x`	Object of class `'DALY'` or `'DALY_list'`
`plot`	Which estimates should be plotted? Must be either `"DALY"`, `"YLD"` or `"YLL"`
`outcomes`	Should different outcomes be plotted? Defaults to `TRUE`. If `FALSE`, aggregated estimates are plotted
`per`	Denominator for population level burden. Defaults to 1000
`samples`	Number of samples to plotted. Defaults to 1000
`pch`	Plotting symbol. Defaults to 16 (= solid circle). See `pch` for more info
`col`	Plotting color. Defaults to `NULL`, in which case the function tries to generate distinctive rainbow colors
`legend`	A character or `expression` vector of length ≥ 1 to appear in the legend. Defaults to `NULL`, in which case the legend names are derived from the plotted objects; if `FALSE`, no legend is plotted
`legend_pos`	The position of the legend, either `"topright"`, `"topleft"`, `"bottomright"` or `"bottomleft"`
`...`	Additional arguments to be passed to `plot`

Details

This function generates a scatterplot of the estimated burden at the population level (x-axis) versus the patient level (y-axis). Scatterplots can be generated of `'DALY'` objects, to visualize the overall or outcome-specific burden; and of `'DALY_list'` objects, to compare the overall burden of, e.g., different diseases or different DALY calculation scenarios.

Author(s)

<brechtdv@gmail.com>

See Also

`DALY_list`

`plot.DALY`, `hist.DALY`

`DALYcalculator` (for a brief description of the *DALY Calculator*)
`DALYmanual` (for a more comprehensive overview)

Examples

```
## Not run:

##= load toxoplasmosis example ============================
setDALYexample(2)

##= perform DALY calculation for different scenarios ======
toxo_00 <- getDALY(aw = FALSE, dr = 0)
toxo_03 <- getDALY(aw = FALSE, dr = 0.03)
toxo_13 <- getDALY(aw = TRUE,  dr = 0.03)

##= combine scenarios in 'DALY_list' ======================
toxo <- DALY_list(toxo_00, toxo_03, toxo_13)

##= plot YLL and YLL for toxo_00 ==========================
par(mar = c(4, 4, 1, 1) + .5)
par(mfrow = c(1, 2))
scatterplot(toxo_00, plot = "YLL",
            outcomes = FALSE, legend = FALSE)
scatterplot(toxo_00, plot = "YLD",
            outcomes = FALSE, legend = FALSE)

##= plot all three scenarios ==============================
par(mfrow = c(1, 1))
scatterplot(toxo,
            legend = c("DALY[0,0]",
                       "DALY[0,0.03]",
                       "DALY[1,0.03]"),
            legend_pos = "topleft",
            log = "xy",
            main = "Scenario analysis")

## End(Not run)
```

`sensitivity` *DALY sensitivity analysis*

Description

This function performs a probabilistic global sensitivity analysis of the overall DALY estimate, based on standardized regression coefficients (method `src`) or partial correlation coefficients (method `pcc`). Actual or ranked values may be used, and for method `src`, coefficients or mapped values may be reported. See below for more details.

Usage

```
sensitivity(x, method = c("src", "pcc"), rank = FALSE, mapped = TRUE)

## S3 method for class 'DALY_sensitivity'
print(x, digits = 3, signif_stars = getOption("show.signif.stars"), ...)

## S3 method for class 'DALY_sensitivity'
plot(x, alpha = 0.05, main = "Sensitivity analysis",
     show_values = FALSE, value_digits = 3, value_cex = 0.6, ...)
```

Arguments

`x`	Object of class `'DALY'`, typically obtained from a call to `getDALY`
`method`	Sensitivity analysis method: `"src"` or `"pcc"`. See below for details
`rank`	Should ranked values be used? Defaults to `FALSE`
`mapped`	Should mapped regression coefficients be presented? Defaults to `TRUE`
`digits`	Number of decimals to be printed; defaults to `0`
`signif_stars`	Should significance stars be printed?
`alpha`	Significance level for selecting significant variables; defaults to 0.05
`main`	Main title of tornado plot; defaults to "Sensitivity analysis"
`show_values`	Should values be plotted next to bars?; defaults to FALSE
`value_digits`	Number of significant digits for plotted values; defaults to 3
`value_cex`	Size of plotted values; defaults to 0.6
`...`	Additional arguments to be passed to methods

Details

Sensitivity analysis studies how the uncertainty in the overall DALY estimate can be apportioned to the different sources of uncertainty in the input parameters. These results can therefore help to identify those input parameters that cause significant uncertainty in the overall DALY estimate and that therefore may be the focus of further research if one wishes to reduce the uncertainty in the overall estimate.

The `sensitivity` function implements a *probabilistic global* sensitivity analysis, in which the analysis is conducted over the full range of plausible input values (hence *global*), determined by the specified uncertainty distributions (hence *probabilistic*).

Specifying `method = "src"` will perform a linear regression-based sensitivity analysis. Here, the simulated overall DALY estimates will be regressed against the simulated values for the stochastic input parameters (using `lm`). To facilitate comparison, the independent terms are standardized such that they are normally distributed with mean zero and standard deviation one (using `scale`). The resulting regression coefficients are therefore referred to as *standardized* regression coefficients.

Argument `rank` specifies whether the regression should be performed on the actual values (`rank = FALSE`; default) or on the ranked values (`rank = TRUE`). Rank-based regression may be preferred when the relation between output and inputs is non-linear. R^2 values smaller than 0.60 may be indicative of a poor fit of the default linear regression model.

If `mapped = TRUE`, the dependent term is not standardized, such that the resulting *mapped* regression coefficients correspond to the change in overall DALY given one standard deviation change in the corresponding input parameter. If `mapped = FALSE`, the dependent term is standardized, such that the resulting *standardized* regression coefficients correspond to the number of standard deviations change in overall DALY given one standard deviation change in the corresponding input parameter.

Specifying `method = "pcc"` will calculate partial correlation coefficients for each of the input variables. Partial correlation coefficients represent the correlation between two variables when adjusting for other variables. In the presence of important interactions between input variables, partial correlation coefficients may be preferred over standardized regression coefficients.

Argument `rank` specifies whether the correlation should be calculated between the actual values (`rank = FALSE`; default) or between the ranked values (`rank = TRUE`).

Method `plot` can be used to generate a tornado plot of the significant input variables.

Value

An object of S3 class `DALY_sensitivity`, containing the following two elements:

`method`	List containing the specified values for `method`, `rank` and `mapped`
`out`	Either the output of `summary.lm` (for method `src`), or a matrix with columns for the partial correlation coefficients (*rho*) and corresponding p-values (for method `pcc`).

Author(s)

`<brechtdv@gmail.com>`

References

- Vose D (2000). *Risk analysis: a quantitative guide*. John Wiley & Sons.
- Saltelli A, Chan K, Scott EM (2000). *Sensitivity analysis*. John Wiley & Sons.

See Also

Package **sensitivity** (`https://cran.r-project.org/package=sensitivity`), for more advanced sensitivity analysis methods.

`getDALY`
`lm`
`cor.test`

Examples

```
## Not run:

##= load NCC example =====================================
setDALYexample(1)
```

```
##= perform DALY calculation, store results in 'x' ========
x <- getDALY()

##= perform DALY sensitivity analysis =====================

## default sensitivity analysis
sa <- sensitivity(x)
print(sa)

## tornado plot of default sensitivity analysis
plot(sa, show_values = TRUE)

## standardized regression coefficients -------------------
sensitivity(x, method = "src", rank = FALSE, mapped = TRUE)
sensitivity(x, method = "src", rank = FALSE, mapped = FALSE)

## standardized rank regression coefficients --------------
sensitivity(x, method = "src", rank = TRUE, mapped = TRUE)
sensitivity(x, method = "src", rank = TRUE, mapped = FALSE)

## partial correlation coefficients -----------------------
sensitivity(x, method = "pcc", rank = FALSE)

## partial rank correlation coefficients ------------------
sensitivity(x, method = "pcc", rank = FALSE)

## End(Not run)
```

`setDALYexample` *Load one of the two built-in DALY calculation examples*

Description

This function resets the *DALY Calculator* (through `reset`), and loads one of the two built-in DALY calculation examples (through `readDALYdata`):

1. Neurocysticercosis in West-Cameroon
2. Congenital Toxoplasmosis in the Netherlands

Usage

```
setDALYexample(example)
```

Arguments

`example`	This argument takes value ‘1’ for the Neurocysticercosis example, and value ‘2’ for the Toxoplasmosis example

Author(s)

`<brechtdv@gmail.com>`

See Also

`DALY_Neurocysticercosis`, `DALY_Toxoplasmosis`, `readDALYdata`

`DALYcalculator` (for a brief description of the *DALY Calculator*)
`DALYmanual` (for a more comprehensive overview)

`setData` *Open a data input window*

Description

This function opens a data window where the input parameters (with corresponding distributions and stratification levels) for one of the disease categories or outcomes can be entered.

Usage

```
setData(n)
```

Arguments

`n`	Integer, corresponding to the health outcome to be set

Author(s)

`<brechtdv@gmail.com>`

See Also

`DALYcalculator` (for a brief description of the *DALY Calculator*)
`DALYmanual` (for a more comprehensive overview)

`setLifeExp` *Open the 'Life Expectancy' window*

Description

This function opens the 'Life Expectancy' window, where the life expectancy table can be customized. The default life expectancy table is the GBD2010 standard life expectancy table. Alternative standard life expectancy tables may be selected via the 'Life Expectancy' window or via function `setStdLE`.

Usage

```
setLifeExp()
```

Details

The DALY Calculator provides three standard life expectancy tables:

1. **GBD1990**: the Coale and Demeny model life-table West, level 26 and 25, which has a life expectancy at birth of 80 for males and 82.5 for females (Murray, 1994);
2. **GBD2010** (*default*): the synthetic standard life expectancy introduced for the GBD 2010 study, with a life expectancy at birth of 86 for both males and females;
3. **WHO/GHE**: the projected frontier life expectancy for the year 2050, used for the WHO Global Health Estimates, with a life expectancy at birth of 92 for both males and females.

Author(s)

`<brechtdv@gmail.com>`

See Also

`setStdLE`

`DALYcalculator` (for a brief description of the *DALY Calculator*)
`DALYmanual` (for a more comprehensive overview)

`setPop` *Open the 'Population' window*

Description

This function opens the 'Population' window, where the population under study can be entered, stratified by sex and age group.

Usage

```
setPop()
```

Author(s)

`<brechtdv@gmail.com>`

See Also

`DALYcalculator` (for a brief description of the *DALY Calculator*)
`DALYmanual` (for a more comprehensive overview)

`setStdLE` *Set the 'Life Expectancy' table to a standard life expectancy table*

Description

This function sets the 'Life Expectancy' table to a standard life expectancy for DALY calculation. The default standard life expectancy table is the synthetic life table introduced for the GBD 2010 study. Other options include the Coale and Demeny model life table West (introduced for GBD 1990 study), and the frontier life expectancy table used for the WHO Global Health Estimates.

Usage

```
setStdLE(table = NULL)
```

Arguments

`table`	The required standard life expectancy table – i.e., one of: `c("GBD2010", "GBD1990", "WHO/GHE")`; when set to `NULL`, the value is taken from the GUI.

Details

The DALY Calculator provides three standard life expectancy tables:

1. **GBD1990**: the Coale and Demeny model life-table West, level 26 and 25, which has a life expectancy at birth of 80 for males and 82.5 for females (Murray, 1994);
2. **GBD2010** (*default*): the synthetic standard life expectancy introduced for the GBD 2010 study, with a life expectancy at birth of 86 for both males and females;
3. **WHO/GHE**: the projected frontier life expectancy for the year 2050, used for the WHO Global Health Estimates, with a life expectancy at birth of 92 for both males and females.

Author(s)

`<brechtdv@gmail.com>`

References

- Devleesschauwer B, et al. (2014). Calculating Disability-Adjusted Life Years to quantify burden of disease. *International Journal of Public Health 59,* 565-569. `http://dx.doi.org/10.1007/s00038-014-0552-z`

See Also

`setLifeExp`

`DALYcalculator` (for a brief description of the *DALY Calculator*)
`DALYmanual` (for a more comprehensive overview)

`summary.DALY` *Summary method for class 'DALY'*

Description

Print summary of *DALY Calculator* output per age/sex class.

Usage

```
## S3 method for class 'DALY'
summary(object, relative = FALSE, outcomes = FALSE,
        digits = 0, ...)
```

Arguments

`object`	Object of class `'DALY'`
`relative`	Show results per 1000 population? See details below
`outcomes`	Show results per outcome? See details below
`digits`	Number of decimals to be printed; defaults to `0`
`...`	Additional arguments to be passed to `summary`

Details

The standard `summary` method gives the *absolute* number of DALYs, YLDs, YLLs, cases and deaths. By specifying `relative = TRUE`, the number of DALYs, YLDs, YLLs, cases and deaths per 1,000 population will be shown.

The standard `summary` method gives the number of DALYs, YLDs, YLLs, cases and deaths *aggregated over all health outcomes*. By specifying `outcomes = TRUE`, the number of DALYs, YLDs, YLLs, cases and deaths for each outcome will be shown as well.

Value

`summary.DALY` returns a list containg the following elements:

`total`	Matrix containing mean, median and `prob` credible interval of total DALYs, YLDs, YLLs, cases and deaths
`outcomes`	Named list, containing matrices of DALYs, YLDs, YLLs, cases and deaths for each health outcome
`pct`	Vector of contribution of YLDs and YLLs to overall DALYs

Author(s)

`<brechtdv@gmail.com>`

See Also

`print.DALY`, `aggregate.DALY`

`DALYcalculator` (for a brief description of the *DALY Calculator*)
`DALYmanual` (for a more comprehensive overview)

Examples

```
## Not run:

##= load the NCC example ==================================
setDALYexample(1)

##= perform DALY calculation, store results in 'x' ========
x <- getDALY()

##= view the DALY calculation results =====================
summary(x)                    # absolute, total ============
summary(x, relative = TRUE)  # relative (ie, per 1000) ====
summary(x, outcomes = TRUE)  # outcome-wise ===============

## End(Not run)
```

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