

# Package ‘popEpi’

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**Title** Functions for Epidemiological Analysis using Population Data

**Author** Joonas Miettinen [cre, aut] (<<https://orcid.org/0000-0001-8624-6754>>),  
Matti Rantanen [aut],  
Karri Seppa [ctb]

**Maintainer** Joonas Miettinen <[joonas.miettinen@cancer.fi](mailto:joonas.miettinen@cancer.fi)>

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**Description** Enables computation of epidemiological statistics, including those where counts or mortality rates of the reference population are used. Currently supported: excess hazard models (Dickman, Sloggett, Hills, and Hakulinen (2012) <[doi:10.1002/sim.1597](https://doi.org/10.1002/sim.1597)>), rates, mean survival times, relative/net survival (in particular the Ederer II (Ederer and Heise (1959)) and Pohar Perme (Pohar Perme, Stare, and Esteve (2012) <[doi:10.1111/j.1541-0420.2011.01640.x](https://doi.org/10.1111/j.1541-0420.2011.01640.x)>) estimators), and standardized incidence and mortality ratios, all of which can be easily adjusted for by covariates such as age. Fast splitting and aggregation of 'Lexis' objects (from package 'Epi') and other computations achieved using 'data.table'.

**Depends** R (>= 3.2.0)

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adjust	<i>Adjust Estimates by Categorical Variables</i>
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**Description**

This function is only intended to be used within a formula when supplied to e.g. `survtab_ag` and should not be used elsewhere.

**Usage**

```
adjust(...)
```

**Arguments**

```
...          variables to adjust by, e.g. adjust(factor(v1), v2, v3)
```

**Value**

Returns a list of promises of the variables supplied which can be evaluated.

## Examples

```
y ~ x + adjust(z)
```

---

aggre

*Aggregation of split Lexis data*

---

## Description

Aggregates a split Lexis object by given variables and / or expressions into a long-format table of person-years and transitions / end-points. Automatic aggregation over time scales by which data has been split if the respective time scales are mentioned in the aggregation argument to e.g. intervals of calendar time, follow-up time and/or age.

## Usage

```
aggre(
  lex,
  by = NULL,
  type = c("unique", "full"),
  sum.values = NULL,
  subset = NULL,
  verbose = FALSE
)
```

## Arguments

lex	a Lexis object split with e.g. <a href="#">splitLexis</a> or <a href="#">splitMulti</a>
by	variables to tabulate (aggregate) by. <a href="#">Flexible input</a> , typically e.g. <code>by = c("V1", "V2")</code> . See Details and Examples.
type	determines output levels to which data is aggregated varying from returning only rows with <code>pyrs &gt; 0</code> ("unique") to returning all possible combinations of variables given in <code>aggre</code> even if those combinations are not represented in data ("full"); see Details
sum.values	optional: additional variables to sum by argument by. <a href="#">Flexible input</a> , typically e.g. <code>sum.values = c("V1", "V2")</code>
subset	a logical condition to subset by before computations; e.g. <code>subset = area %in% c("A", "B")</code>
verbose	logical; if TRUE, the function returns timings and some information useful for debugging along the aggregation process

## Details

### Basics

aggre is intended for aggregation of split Lexis data only. See [Lexis](#) for forming Lexis objects by hand and e.g. [splitLexis](#), [splitLexisDT](#), and [splitMulti](#) for splitting the data. [lexpand](#) may be used for simple data sets to do both steps as well as aggregation in the same function call.

Here aggregation refers to computing person-years and the appropriate events (state transitions and end points in status) for the subjects in the data. Hence, it computes e.g. deaths (end-point and state transition) and censorings (end-point) as well as events in a multi-state setting (state transitions).

The result is a long-format data.frame or data.table (depending on options("popEpi.datatable")); see ?popEpi) with the columns pyrs and the appropriate transitions named as fromXtoY, e.g. from0to0 and from0to1 depending on the values of lex.Cst and lex.Xst.

### The by argument

The by argument determines the length of the table, i.e. the combinations of variables to which data is aggregated. by is relatively flexible, as it can be supplied as

- a character string vector, e.g. `c("sex", "area")`, naming variables existing in lex
- an expression, e.g. `factor(sex, 0:1, c("m", "f"))` using any variable found in lex
- a list (fully or partially named) of expressions, e.g. `list(gender = factor(sex, 0:1, c("m", "f")), area)`

Note that expressions effectively allow a variable to be supplied simply as e.g. `by = sex` (as a symbol/name in R lingo).

The data is then aggregated to the levels of the given variables or expression(s). Variables defined to be time scales in the supplied Lexis are processed in a special way: If any are mentioned in the by argument, intervals of them are formed based on the breaks used to split the data: e.g. if age was split using the breaks `c(0, 50, Inf)`, mentioning age in by leads to creating the age intervals `[0, 50)` and `[50, Inf)` and aggregating to them. The intervals are identified in the output as the lower bounds of the appropriate intervals.

The order of multiple time scales mentioned in by matters, as the last mentioned time scale is assumed to be a survival time scale for when computing event counts. E.g. when the data is split by the breaks `list(FUT = 0:5, CAL = c(2008, 2010))`, time lines cut short at `CAL = 2010` are considered to be censored, but time lines cut short at `FUT = 5` are not. See [Return](#).

### Aggregation types (styles)

It is almost always enough to aggregate the data to variable levels that are actually represented in the data (default `aggre = "unique"`; alias "non-empty"). For certain uses it may be useful to have also "empty" levels represented (resulting in some rows in output with zero person-years and events); in these cases supplying `aggre = "full"` (alias "cartesian") causes aggre to determine the Cartesian product of all the levels of the supplied by variables or expressions and aggregate to them. As an example of a Cartesian product, try

```
merge(1:2, 1:5).
```

## Value

A long data.frame or data.table of aggregated person-years (pyrs), numbers of subjects at risk (`at.risk`), and events formatted fromXtoY, where X and X are states transitioning from and to states at the end of each lex.id's follow-up (implying  $X = Y$ ). Subjects at risk are computed in the

beginning of an interval defined by any Lexis time scales and mentioned in by, but events occur at any point within an interval.

When the data has been split along multiple time scales, the last time scale mentioned in by is considered to be the survival time scale with regard to computing events. Time lines cut short by the extrema of non-survival-time-scales are considered to be censored ("transitions" from the current state to the current state).

### Author(s)

Joonas Miettinen

### See Also

[aggregate](#) for a similar base R solution, and [ltable](#) for a data.table based aggregator. Neither are directly applicable to split Lexis data.

Other aggregation functions: [as.aggre\(\)](#), [lexpand\(\)](#), [setaggre\(\)](#), [summary.aggre\(\)](#)

### Examples

```
## form a Lexis object
library(Epi)
data(sibr)
x <- sibr[1:10,]
x[1:5,]$sex <- 0 ## pretend some are male
x <- Lexis(data = x,
           entry = list(AGE = dg_age, CAL = get.yrs(dg_date)),
           exit = list(CAL = get.yrs(ex_date)),
           entry.status=0, exit.status = status)
x <- splitMulti(x, breaks = list(CAL = seq(1993, 2013, 5),
                                AGE = seq(0, 100, 50)))

## these produce the same results (with differing ways of determining aggre)
a1 <- aggre(x, by = list(gender = factor(sex, 0:1, c("m", "f")),
                        agegroup = AGE, period = CAL))

a2 <- aggre(x, by = c("sex", "AGE", "CAL"))

a3 <- aggre(x, by = list(sex, agegroup = AGE, CAL))

## returning also empty levels
a4 <- aggre(x, by = c("sex", "AGE", "CAL"), type = "full")

## computing also expected numbers of cases
x <- lexpand(sibr[1:10,], birth = bi_date, entry = dg_date,
            exit = ex_date, status = status %in% 1:2,
            pophaz = popmort, fot = 0:5, age = c(0, 50, 100))
x$d.exp <- with(x, lex.dur*pop.haz)
## these produce the same result
a5 <- aggre(x, by = c("sex", "age", "fot"), sum.values = list(d.exp))
a5 <- aggre(x, by = c("sex", "age", "fot"), sum.values = "d.exp")
```

```
a5 <- aggre(x, by = c("sex", "age", "fot"), sum.values = d.exp)
## same result here with custom name
a5 <- aggre(x, by = c("sex", "age", "fot"),
            sum.values = list(expCases = d.exp))

## computing pohar-perme weighted figures
x$d.exp.pp <- with(x, lex.dur*pop.haz*pp)
a6 <- aggre(x, by = c("sex", "age", "fot"),
            sum.values = c("d.exp", "d.exp.pp"))
## or equivalently e.g. sum.values = list(expCases = d.exp, expCases.p = d.exp.pp).
```

---

all\_names\_present      *Check if all names are present in given data*

---

## Description

Given a character vector, checks if all names are present in names(data). Throws error if stops=TRUE, else returns FALSE if some variable name is not present.

## Usage

```
all_names_present(data, var.names, stops = TRUE, msg = NULL)
```

## Arguments

data	dataset where the variable names should be found
var.names	a character vector of variable names, e.g. c("var1", "var2")
stops	logical, stop returns exception
msg	Custom message to return instead of default message. Special: include %%VARs%% in message string and the missing variable names will be inserted there (quoted, separated by comma, e.g. 'var1', 'var2' — no leading or trailing white space).

## Value

'TRUE' if all 'var.names' are in 'data', else 'FALSE'.

## Author(s)

Joonas Miettinen

## See Also

[robust\\_values](#)

---

array\_df\_ratetable\_utils

*'array's, 'data.frame's and 'ratetable's*

---

## Description

Utilities to transform objects between 'array', 'data.frame', and [survival::ratetable].

## Usage

```
long_df_to_array(x, stratum.col.nms, value.col.nm)
```

```
long_df_to_ratetable(  
  x,  
  stratum.col.nms,  
  value.col.nm,  
  dim.types,  
  cut.points = NULL  
)
```

```
long_dt_to_array(x, stratum.col.nms, value.col.nm)
```

```
long_dt_to_ratetable(  
  x,  
  stratum.col.nms,  
  value.col.nm,  
  dim.types,  
  cut.points = NULL  
)
```

```
array_to_long_df(x)
```

```
array_to_long_dt(x)
```

```
array_to_ratetable(x, dim.types, cut.points = NULL)
```

```
ratetable_to_array(x)
```

```
ratetable_to_long_df(x)
```

```
ratetable_to_long_dt(x)
```

## Arguments

x                    '[data.frame, data.table, array, ratetable]' (mandatory, no default)



- 'long\_df\_to\_array': a 'data.frame' - 'long\_df\_to\_ratetable': a 'data.frame' -  
 'long\_dt\_to\_array': a 'data.table' - 'long\_dt\_to\_ratetable': a 'data.table' - 'array\_to\_long\_df': an 'array' - 'array\_to\_long\_dt': an 'array' - 'array\_to\_ratetable': an 'array' - 'ratetable\_to\_array': a [survival::ratetable] - 'ratetable\_to\_long\_df': a [survival::ratetable] - 'ratetable\_to\_long\_dt': a [survival::ratetable]

stratum.col.nms  
 '[character]' (mandatory, no default)  
 a vector of column names in 'x' by which values are stratified

value.col.nm  
 '[character]' (mandatory, no default)  
 name of column in 'x' containing values (these will be contents of the array)

dim.types  
 '[integer]' (mandatory, no default)  
 see 'type' under **Details** in [survival::ratetable]

cut.points  
 '[NULL, list]' (optional, default 'NULL')  
 see 'cutpoints' under **Details** in [survival::ratetable]  
 - 'NULL': automatically set using 'dimnames(x)' and 'dim.types' - 'list': one element for each dimensions of 'x'

## Details

- 'long\_df\_to\_array': converts a long-format 'data.frame' to an 'array' with one or more dimensions
- 'long\_df\_to\_ratetable': calls 'long\_df\_to\_array' and then 'array\_to\_ratetable'
- 'long\_dt\_to\_array': simply asserts that 'x' is a 'data.table' and calls 'long\_df\_to\_array'
- 'long\_dt\_to\_ratetable': calls 'long\_dt\_to\_array' and then 'array\_to\_ratetable'
- 'array\_to\_long\_df': converts an array with one or more dimensions into a long-format 'data.frame'; any [dimnames] are used to name and fill the stratifying columns; for dimensions without a name, ".dX" is used for stratifying column number 'X'; for each 'k', if there are no contents in 'dimnames(x)[[k]]', the elements of 'seq(dim(x)[k])' are used to fill the corresponding stratifying column; the value column always has the name "value"
- 'array\_to\_long\_dt': calls 'array\_to\_long\_df' and converts result to a 'data.table' for convenience
- 'array\_to\_ratetable': converts an array to a [survival::ratetable]
- 'ratetable\_to\_array': converts a [survival::ratetable] to an array
- 'ratetable\_to\_long\_df': calls 'ratetable\_to\_array' and then 'array\_to\_long\_df'
- 'ratetable\_to\_long\_dt': calls 'ratetable\_to\_array' and then 'array\_to\_long\_dt'

## Value

- 'long\_df\_to\_array': an 'array' - 'long\_df\_to\_ratetable': a [survival::ratetable] - 'long\_dt\_to\_array': an 'array' - 'long\_dt\_to\_ratetable': a [survival::ratetable] - 'array\_to\_long\_df': a 'data.frame' - 'array\_to\_long\_dt': a 'data.table' - 'array\_to\_ratetable': a [survival::ratetable] - 'ratetable\_to\_array': an 'array' - 'ratetable\_to\_long\_df': a 'data.frame' - 'ratetable\_to\_long\_dt': a 'data.table'

**Examples**

```

long_dt <- popEpi::popmort
arr <- long_df_to_array(long_dt, c("agegroup", "year", "sex"), "haz")
rt <- array_to_ratetable(arr, dim.types = c(2L, 4L, 1L))

arr2 <- ratetable_to_array(rt)
long_df2 <- array_to_long_df(arr2)

identical(sort(long_dt[["haz"]]), sort(long_df2[["value"]]))

```

---

as.aggre

*Coercion to Class aggre*


---

**Description**

Coerces an R object to an aggre object, identifying the object as one containing aggregated counts, person-years and other information.

**Usage**

```

as.aggre(x, values = NULL, by = NULL, breaks = NULL, ...)

## S3 method for class 'data.frame'
as.aggre(x, values = NULL, by = NULL, breaks = NULL, ...)

## S3 method for class 'data.table'
as.aggre(x, values = NULL, by = NULL, breaks = NULL, ...)

## Default S3 method:
as.aggre(x, ...)

```

**Arguments**

x	a data.frame or data.table
values	a character string vector; the names of value variables
by	a character string vector; the names of variables by which values have been tabulated
breaks	a list of breaks, where each element is a breaks vector as usually passed to e.g. <a href="#">splitLexisDT</a> . The list must be fully named, with the names corresponding to time scales at the aggregate level in your data. Every unique value in a time scale variable in data must also exist in the corresponding vector in the breaks list.
...	arguments passed to or from methods

**Value**

Returns a copy of 'x' with attributes set to those of an object of class "aggre".

**Methods (by class)**

- data.frame: Coerces a data.frame to an aggre object
- data.table: Coerces a data.table to an aggre object
- default: Default method for as.aggre (stops computations if no class-specific method found)

**Author(s)**

Joonas Miettinen

**See Also**

Other aggregation functions: [aggre\(\)](#), [lexpand\(\)](#), [setaggre\(\)](#), [summary.aggre\(\)](#)

**Examples**

```
library("data.table")
df <- data.frame(sex = rep(c("male", "female"), each = 5),
                obs = rpois(10, rep(7,5, each=5)),
                pyrs = rpois(10, lambda = 10000))
dt <- as.data.table(df)

df <- as.aggre(df, values = c("pyrs", "obs"), by = "sex")
dt <- as.aggre(dt, values = c("pyrs", "obs"), by = "sex")

class(df)
class(dt)

BL <- list(fot = 0:5)
df <- data.frame(df)
df <- as.aggre(df, values = c("pyrs", "obs"), by = "sex", breaks = BL)
```

---

as.Date.yrs

*Coerce Fractional Year Values to Date Values*


---

**Description**

Coerces an yrs object to a Date object. Some loss of information comes if year.length = "approx" was set when using [get.yrs](#), so the transformation back to Date will not be perfect there. With year.length = "actual" the original values are perfectly retrieved.

**Usage**

```
## S3 method for class 'yrs'
as.Date(x, ...)
```

**Arguments**

x                    an yrs object created by `get.yrs`  
...                   unused, included for compatibility with other `as.Date` methods

**Value**

A vector of 'Date' values based on the input fractional years.

**Author(s)**

Joonas Miettinen

**See Also**

[get.yrs](#)

**Examples**

```
data("sire", package = "popEpi")

## approximate year lengths: here 20 % have an extra day added
sire$dg_yrs <- get.yrs(sire$dg_date)
summary(sire$dg_yrs)
dg_date2 <- as.Date(sire$dg_yrs)
summary(as.numeric(dg_date2 - as.Date(sire$dg_date)))

## using actual year lengths
sire$dg_yrs <- get.yrs(sire$dg_date, year.length = "actual")
summary(sire$dg_yrs)
dg_date2 <- as.Date(sire$dg_yrs)
summary(as.numeric(dg_date2 - as.Date(sire$dg_date)))
```

---

cast\_simple

*Cast data.table/data.frame from long format to wide format*

---

**Description**

Convenience function for using [dcast.data.table](#); inputs are character strings (names of variables) instead of a formula.

**Usage**

```
cast_simple(data = NULL, columns = NULL, rows = NULL, values = NULL)
```

**Arguments**

data	a <code>data.table</code> or <code>data.frame</code>
columns	a character string vector; the (unique combinations of the) levels of these variable will be different rows
rows	a character string vector; the (unique combinations of the) levels of these variable will be different columns
values	a character string; the variable which will be represented on rows and columns as specified by columns and rows

**Details**

This function is just a small interface for `dcast` / `dcast.data.table` and less flexible than the originals.

Note that all `data.table` objects are also `data.frame` objects, but that each have their own `dcast` method. `dcast.data.table` is faster.

If any values in `value.vars` need to be aggregated, they are aggregated using `sum`. See `?dcast`.

**Value**

A `'data.table'` just like `'[data.table::dcast]'`.

**Author(s)**

Matti Rantanen, Joonas Miettinen

**Examples**

```
library("data.table")
## e.g. silly counts from a long-format table to a wide format
test <- data.table::copy(popEpi::sire)
test$dg_y <- year(test$dg_date)
test$ex_y <- year(test$ex_date)
tab <- ltable(test, c("dg_y", "ex_y"))
cast_simple(tab, columns='dg_y', rows="ex_y", values="obs")
```

---

cut\_bound

*Change output values from cut(..., labels = NULL) output*

---

**Description**

Selects lowest values of each factor after `cut()` based on the assumption that the value starts from index 2 and end in comma ",".

**Usage**

```
cut_bound(t, factor = TRUE)
```

**Arguments**

t is a character vector of elements, e.g. "(20,60)"  
factor logical; TRUE returns informative character string, FALSE numeric (left value)

**Details**

type = 'factor': "[50,52)" -> "50-51" OR "[50,51)" -> "50"  
type = 'numeric': lowest bound in numeric.

**Value**

If 'factor = TRUE', returns a character vector; else returns a numeric vector.

**Author(s)**

Matti Rantanen

**Examples**

```
cut_bound("[1900, 1910)") ## "1900-1909"
```

---

direct\_standardization

*Direct Adjusting in **popEpi** Using Weights*

---

**Description**

Several functions in **popEpi** have support for direct standardization of estimates. This document explains the usage of weighting with those functions.

**Details**

Direct standardization is performed by computing estimates of E by the set of adjusting variables A, to which a set of weights W is applicable. The weighted average over A is then the direct-adjusted estimate of E ( $E^*$ ).

To enable both quick and easy as well as more rigorous usage of direct standardization with weights, the weights arguments in **popEpi** can be supplied in several ways. Ability to use the different ways depends on the number of adjusting variables.

The weights are always handled internally to sum to 1, so they do not need to be scaled in this manner when they are supplied. E.g. counts of subjects in strata may be passed.

### Basic usage - one adjusting variable

In the simple case where we are adjusting by only one variable (e.g. by age group), one can simply supply a vector of weights:

```
FUN(weights = c(0.1, 0.25, 0.25, 0.2, 0.2))
```

which may be stored in advance:

```
w <- c(0.1, 0.25, 0.25, 0.2, 0.2)
```

```
FUN(weights = w)
```

The order of the weights matters. **popEpi** functions with direct adjusting enabled match the supplied weights to the adjusting variables as follows: If the adjusting variable is a factor, the order of the levels is used. Otherwise, the alphabetic order of the unique values is used (try `sort` to see how it works). For clarity and certainty we recommend using factor or numeric variables when possible. character variables should be avoided: to see why, try `sort(15:9)` and `sort(as.character(15:9))`.

It is also possible to supply a character string corresponding to one of the age group standardization schemes integrated into **popEpi**:

- 'europe\_1976\_18of5' - European std. population (1976), 18 age groups
- 'nordic\_2000\_18of5' - Nordic std. population (2000), 18 age groups
- 'world\_1966\_18of5' - world standard (1966), 18 age groups
- 'world\_2000\_18of5' - world standard (2000), 18 age groups
- 'world\_2000\_20of5' - world standard (2000), 20 age groups
- 'world\_2000\_101of1' - world standard (2000), 101 age groups

Additionally, [ICSS](#) contains international weights used in cancer survival analysis, but they are not currently usable by passing a string to weights and must be supplied by hand.

You may also supply `weights = "internal"` to use internally computed weights, i.e. usually simply the counts of subjects / person-time experienced in each stratum. E.g.

```
FUN(weights = "world_2000_18of5")
```

will use the world standard population from 2000 as weights for 18 age groups, that your adjusting variable is assumed to contain. The adjusting variable must be coded in this case as a numeric variable containing 1:18 or as a factor with 18 levels (coded from the youngest to the oldest age group).

### More than one adjusting variable

In the case that you employ more than one adjusting variable, separate weights should be passed to match to the levels of the different adjusting variables. When supplied correctly, "grand" weights are formed based on the variable-specific weights by multiplying over the variable-specific weights (e.g. if men have  $w = 0.5$  and the age group 0-4 has  $w = 0.1$ , the "grand" weight for men aged 0-4 is  $0.5 \times 0.1$ ). The "grand" weights are then used for adjusting after ensuring they sum to one.

When using multiple adjusting variables, you are allowed to pass either a named list of weights or a data.frame of weights. E.g.

```
WL <- list(agegroup = age_w, sex = sex_w)
```

```
FUN(weights = WL)
```

where `age_w` and `sex_w` are numeric vectors. Given the conditions explained in the previous section are satisfied, you may also do e.g.

```
WL <-list(agegroup = "world_2000_18of", sex = sex_w)
```

```
FUN(weights = WL)
```

and the world standard pop is used as weights for the age groups as outlined in the previous section.

Sometimes using a `data.frame` can be clearer (and it is fool-proof as well). To do this, form a `data.frame` that repeats the levels of your adjusting variables by each level of every other adjusting variable, and assign the weights as a column named "weights". E.g.

```
wdf <-data.frame(sex = rep(0:1, each = 18), agegroup = rep(1:18, 2))
```

```
wdf$weights <-rbinom(36, size = 100, prob = 0.25)
```

```
FUN(weights = wdf)
```

If you want to use the counts of subjects in strata as the weights, one way to do this is by e.g.

```
wdf <-as.data.frame(x$V1, x$V2, x$V3) names(wdf) <-c("V1", "V2", "V3", "weights")
```

### Author(s)

Joonas Miettinen

### References

Source of the Nordic standard population in 5-year age groups (also contains European & 1966 world standards): <https://www-dep.iarc.fr/NORDCAN/english/glossary.htm>

Source of the 1976 European standard population:

Waterhouse, J.,Muir, C.S.,Correa, P.,Powell, J., eds (1976). Cancer Incidence in Five Continents, Vol. III. IARC Scientific Publications, No. 15, Lyon, IARC. ISBN: 9789283211150

Source of 2000 world standard population in 1-year age groups: <https://seer.cancer.gov/stdpopulations/stdpop.singleages.html>

### See Also

Other weights: [ICSS](#), [stdpop101](#), [stdpop18](#)

Other popEpi argument evaluation docs: [flexible\\_argument](#)

---

fac2num

*Convert factor variable to numeric*

---

### Description

Convert factor variable with numbers as levels into a numeric variable

### Usage

```
fac2num(x)
```



## Arguments

x a factor variable with numbers as levels

## Details

For example, a factor with levels `c("5", "7")` is converted into a numeric variable with values `c(5, 7)`.

## Value

A numeric vector based on the levels of 'x'.

## Source

[Stackoverflow thread](#)

## See Also

[robust\\_values](#)

## Examples

```
## this is often not intended
as.numeric(factor(c(5,7))) ## result: c(1,2)
## but this
fac2num(factor(c(5,7))) ## result: c(5,7)

## however
as.numeric(factor(c("5", "7", "a"))) ## 1:3

suppressWarnings(
  fac2num(factor(c("5", "7", "a"))) ## c(5,7,NA)
)
```

---

flexible\_argument

*Flexible Variable Usage in **popEpi** Functions*

---

## Description

Certain arguments in **popEpi** can be passed in multiple ways. This document shows the usage and a pitfall in the usage of such flexible arguments.

## Details

Flexible arguments in **popEpi** are used to pass variables existing in your data or in the environment where the function is used (for everyday users this is the global environment - in simple terms, where your data is / your work space). The flexible arguments are modelled after the `by` argument in `data.tables` - see `?data.table`. There are many ways to supply the same information to certain functions in **popEpi**, but the possible ways listed below may be limited in some of them to only allow for using only a part of them.

## Everyday usage

Most commonly you may pass variable names as character strings, e.g.

```
FUN(arg = c("V1", "V2"), data = x)
```

which may be stored in advance:

```
vars <-c("V1", "V2")
```

```
FUN(arg = vars, data = x)
```

where `x` contains those variables. You may also supply variable names as symbols:

```
FUN(arg = V1, data = x)
```

Or as a list of symbols (similarly to as in [aggregate](#)):

```
FUN(arg = list(V1, V2), data = x)
```

Or as a list of expressions:

```
FUN(arg = list(V1 + 1, factor(V2)), data = x)
```

A formula without a left-hand-side specified is sometimes allowed as well:

```
FUN(arg = ~ I(V1 + 1) + factor(V2), data = x)
```

Using a symbol or a list of symbols/expressions typically causes the function to look for the variable(s) first in the supplied data (if any) and then where the function was called. For everyday users this means you might define e.g.

```
V3 <-factor(letters)
```

and do e.g.

```
FUN(arg = list(V1 + 1, factor(V2), V3), data = x)
```

provided `V1` and `V2` exist in `x` or in the function calling environment.

## A pitfall

There is one way to use flexible arguments incorrectly: By supplying the name of a variable which exists both in the supplied data and the calling environment, and intending the latter to be used. E.g.

```
vars <-c("V2")
```

```
FUN(arg = V3, data = x)
```

where `x` has a column named `vars`. This causes the function to use `x$vars` and NOT `x$V2`.

**Advanced**

Function programmers are advised to pass character strings whenever possible. To fool-proof against conflicts as described in the section above, refer to the calling environment explicitly when passing the variable containing the character strings:

```
TF <-environment() ## current env to refer to
vars <-c("V1", "V2")
FUN(arg = TF$vars, data = x)
```

Even if `x` has columns named `vars` and `TF`, using `TF$vars` does not use those columns but only evaluates `TF$vars` in the calling environment. This is made possible by the fact that data is always passed as a `data.frame`, within which evaluation of expressions using the dollar operator is not possible. Therefore it is safe to assume the data should not be used. However, lists of expressions will not be checked for dollar use and will fail in conflict situations:

```
TF <-environment() ## current env to refer to
vars <-letters[1:5]
x <-data.frame(vars = 1:5, TF = 5:1, V1 = 10:6)
FUN(arg = list(TF$vars, V1), data = x)
```

On the other hand you may typically also pass quoted ([quote](#)) or substituted [substitute](#) expressions etc., where the `env$object` trick will work as well:

```
q <-quote(list(vars, V1))
FUN(arg = TF$q, data = x)
```

This works even with

```
a <-1:5
V1 <-quote(TF$a)
FUN(arg = TF$V1, data = x)
```

So no conflicts should occur.

**Author(s)**

Joonas Miettinen

**See Also**

Other `popEpi` argument evaluation docs: [direct\\_standardization](#)

**Examples**

```
data(sire)
## prepare data for e.g. 5-year "period analysis" for 2008-2012
## note: sire is a simulated cohort integrated into popEpi.
BL <- list(fot=seq(0, 5, by = 1/12))
x <- leexpand(sire, birth = bi_date, entry = dg_date, exit = ex_date,
             status = status %in% 1:2,
             breaks = BL)
```

```

x <- aggre(x, by = fot)

## silly example of referring to pyrs data by fixed character string;
## its possible that the real name wont be fixed in a real-life application.
pyrs <- "actual_pyr"
TF <- environment()
x$actual_pyr <- as.numeric(x$pyrs)
x$pyrs <- 1

## this works (uses actual_pyr eventually)
st <- survtab_ag(fot ~ 1, data = x, surv.type = "surv.obs",
                pyrs = TF$pyrs, d = from0to1,
                surv.method = "hazard")
## this would be wrong (sees expression 'pyrs' and uses that column,
## which is not what is intended here)
st <- survtab_ag(fot ~ 1, data = x, surv.type = "surv.obs",
                pyrs = pyrs, d = from0to1,
                surv.method = "hazard")

```

---

get.yrs

---

*Convert date objects to fractional years*


---

## Description

Using Date objects, calculates given dates as fractional years.

## Usage

```
get.yrs(x, year.length = "approx", ...)
```

## Arguments

x	a Date object, or anything that link{as.Date} accepts
year.length	character string, either 'actual' or 'approx'; can be abbreviated; see Details
...	additional arguments passed on to <a href="#">as.Date</a> ; typically format when x is a character string variable, and origin when x is numeric

## Details

x should preferably be a date, Date or IDate object, although it can also be a character string variable which is coerced internally to Date format using [as.Date.character](#).

When year.length = 'actual', fractional years are calculated as  $\text{year} + (\text{day\_in\_year} - 1) / 365$  for non-leap-years and as  $\text{year} + (\text{day\_in\_year} - 1) / 366$  for leap years. If year.length = 'approx', fractional years are always calculated as  $\text{year} + (\text{day\_in\_year} - 1) / 365.242199$ .

There is a slight difference, then, between the two methods when calculating durations between fractional years. For meticulous accuracy one might instead want to calculate durations using dates (days) and convert the results to fractional years.

Note that dates are effectively converted to fractional years at 00:00:01 o'clock:

`get.yrs("2000-01-01") = 2000` , and `get.yrs("2000-01-02") = 2000 + 1/365.242199` .

### Value

A numeric vector of fractional years.

### Author(s)

Joonas Miettinen

### See Also

[cal.yr](#), [as.Date.yrs](#), [as.Date](#)

### Examples

```
data("sire")
sire$dg_yrs <- get.yrs(sire$dg_date)
summary(sire$dg_yrs)

## see: ?as.Date.yrs
dg_date2 <- as.Date(sire$dg_yrs)
summary(as.numeric(dg_date2 - as.Date(sire$dg_date)))

## Epi's cal.yr versus get.yrs
d <- as.Date("2000-01-01")
Epi::cal.yr(d) ## 1999.999
get.yrs(d) ## 2000

## "..." passed on to as.Date, so character / numeric also accepted as input
## (and whatever else as.Date accepts)
get.yrs("2000-06-01")
get.yrs("20000601", format = "%Y%m%d")
get.yrs("1/6/00", format = "%d/%m/%y")

get.yrs(100, origin = "1970-01-01")
```

### Description

Contains three sets age-standardisation weights for age-standardized survival (net, relative or observed).

**Format**

data.table with columns

- age - lower bound of the age group
- ICSS1 - first set of weights, sums to 100 000
- ICSS2 - second set of weights, sums to 100 000
- ICSS3 - third set of weights, sums to 100 000

**Source**

[ICSS weights \(US National Cancer Institute website\)](#)

Corazziari, Isabella, Mike Quinn, and Riccardo Capocaccia. "Standard cancer patient population for age standardising survival ratios." *European Journal of Cancer* 40.15 (2004): 2307-2316.

**See Also**

Other popEpi data: [meanpop\\_fi](#), [popmort](#), [sibr](#), [sire](#), [stdpop101](#), [stdpop18](#)

Other weights: [direct\\_standardization](#), [stdpop101](#), [stdpop18](#)

**Examples**

```
## aggregate weights to a subset of age groups
data(ICSS)
cut <- c(0, 30, 50, 70, Inf)
agegr <- cut(ICSS$age, cut, right = FALSE)
aggregate(ICSS1~agegr, data = ICSS, FUN = sum)
```

---

is.Date

*Test if object is a Date object*

---

**Description**

Tests if an object is a Date object and returns a logical vector of length 1. IDate objects are also Date objects, but date objects from package **date** are not.

**Usage**

```
is.Date(obj)
```

**Arguments**

obj                    object to test on

**Value**

‘TRUE’ if ‘obj’ is of class “Date” or “IDate”.

**Author(s)**

Joonas Miettinen

**See Also**[get.yrs](#), [is\\_leap\\_year](#), [as.Date](#)**Examples**

```
## the base "capital Date" format
da <- as.Date("2000-01-01")
is.Date(da) ## TRUE
date::is.date(da) ## FALSE

## IDate format from data.table
library("data.table")
da <- as.IDate("2000-01-01")
is.Date(da) ## TRUE
date::is.date(da) ## FALSE

## from package "date"
da <- date::as.date("1jan2000")
is.Date(da) ## FALSE
date::is.date(da) ## TRUE
```

---

is_leap_year	<i>Detect leap years</i>
--------------	--------------------------

---

**Description**

Given a vector or column of year values (numeric or integer), [is\\_leap\\_year](#) returns a vector of equal length of logical indicators, i.e. a vector where corresponding leap years have value TRUE, and FALSE otherwise.

**Usage**

```
is_leap_year(years)
```

**Arguments**

years            a vector or column of year values (numeric or integer)

**Value**

A 'logical' vector where 'TRUE' indicates a leap year.

**Author(s)**

Joonas Miettinen

**Examples**

```
## can be used to assign new columns easily, e.g. a dummy indicator column
df <- data.frame(yrs=c(1900,1904,2005,1995))
df$lyd <- as.integer(is_leap_year(df$yrs))

## mostly it is useful as a condition or to indicate which rows have leap years
which(is_leap_year(df$yrs)) # 2
df[is_leap_year(df$yrs),] # 2nd row
```

---

Lexis_fpa	<i>Create a Lexis Object with Follow-up Time, Period, and Age Time Scales</i>
-----------	---

---

**Description**

This is a simple wrapper around [Lexis](#) for creating a Lexis object with the time scales fot, per, and age.

**Usage**

```
Lexis_fpa(
  data,
  birth = NULL,
  entry = NULL,
  exit = NULL,
  entry.status = NULL,
  exit.status = NULL,
  subset = NULL,
  ...
)
```

**Arguments**

data	a data.frame; mandatory
birth	the time of birth; A character string naming the variable in data or an expression to evaluate - see <a href="#">Flexible input</a>
entry	the time at entry to follow-up; supplied the same way as birth
exit	the time at exit from follow-up; supplied the same way as birth
entry.status	passed on to <a href="#">Lexis</a> if not NULL; supplied the same way as birth
exit.status	passed on to <a href="#">Lexis</a> if not NULL; supplied the same way as birth
subset	a logical condition to subset by before passing data and arguments to <a href="#">Lexis</a>
...	additional optional arguments passed on to <a href="#">Lexis</a>



**Value**

A Lexis object with the usual columns that Lexis objects have, with time scale columns fot, per, and age. They are calculated as

```
fot = entry -entry (to ensure correct format, e.g. difftime)
```

```
per = entry
```

```
and
```

```
age = entry -birth
```

**Examples**

```
data("sire", package = "popEpi")

lex <- Lexis_fpa(sire,
                birth = "bi_date",
                entry = dg_date,
                exit = ex_date + 1L,
                exit.status = "status")

## some special cases
myVar <- "bi_date"
l <- list(myVar = "bi_date")
sire$l <- sire$myVar <- l

## conflict: myVar taken from data when "bi_date" was intended
lex <- Lexis_fpa(sire,
                birth = myVar,
                entry = dg_date,
                exit = ex_date + 1L,
                exit.status = "status")

## no conflict with names in data
lex <- Lexis_fpa(sire,
                birth = l$myVar,
                entry = dg_date,
                exit = ex_date + 1L,
                exit.status = "status")
```

---

lexpand

*Split case-level observations*


---

**Description**

Given subject-level data, data is split by calendar time (per), age, and follow-up time (fot, from 0 to the end of follow-up) into subject-time-interval rows according to given breaks and additionally processed if requested.

**Usage**

```

lexpand(
  data,
  birth = NULL,
  entry = NULL,
  exit = NULL,
  event = NULL,
  status = status != 0,
  entry.status = NULL,
  breaks = list(fot = c(0, Inf)),
  id = NULL,
  overlapping = TRUE,
  aggre = NULL,
  aggre.type = c("unique", "cartesian"),
  drop = TRUE,
  pophaz = NULL,
  pp = TRUE,
  subset = NULL,
  merge = TRUE,
  verbose = FALSE,
  ...
)

```

**Arguments**

<code>data</code>	dataset of e.g. cancer cases as rows
<code>birth</code>	birth time in date format or fractional years; string, symbol or expression
<code>entry</code>	entry time in date format or fractional years; string, symbol or expression
<code>exit</code>	exit from follow-up time in date format or fractional years; string, symbol or expression
<code>event</code>	advanced: time of possible event differing from exit; typically only used in certain SIR/SMR calculations - see Details; string, symbol or expression
<code>status</code>	variable indicating type of event at exit or event; e.g. <code>status = status != 0</code> ; expression or quoted variable name
<code>entry.status</code>	input in the same way as <code>status</code> ; status at entry; see Details
<code>breaks</code>	a named list of vectors of time breaks; e.g. <code>breaks = list(fot=0:5, age=c(0, 45, 65, Inf))</code> ; see Details
<code>id</code>	optional; an id variable; e.g. <code>id = my_id</code> ; string, symbol or expression
<code>overlapping</code>	advanced, logical; if FALSE AND if data contains multiple rows per subject, ensures that the timelines of id-specific rows do not overlap; this ensures e.g. that person-years are only computed once per subject in a multi-state paradigm
<code>aggre</code>	e.g. <code>aggre = list(sex, fot)</code> ; a list of unquoted variables and/or expressions thereof, which are interpreted as factors; data events and person-years will be aggregated by the unique combinations of these; see Details
<code>aggre.type</code>	one of <code>c("unique", "cartesian")</code> ; can be abbreviated; see Details

drop	logical; if TRUE, drops all resulting rows after splitting that reside outside the time window as defined by the given breaks (all time scales)
pophaz	a dataset of population hazards to merge with split data; see Details
pp	logical; if TRUE, computes Pohar-Perme weights using pophaz; adds variable with reserved name pp; see Details for computing method
subset	a logical vector or any logical condition; data is subsetted before splitting accordingly
merge	logical; if TRUE, retains all original variables from the data
verbose	logical; if TRUE, the function is chatty and returns some messages along the way
...	e.g. fot = 0:5; instead of specifying a breaks list, correctly named breaks vectors can be given for fot, age, and per; these override any breaks in the breaks list; see Examples

## Details

### Basics

`lexpand` splits a given data set (with e.g. cancer diagnoses as rows) to subintervals of time over calendar time, age, and follow-up time with given time breaks using `splitMulti`.

The dataset must contain appropriate Date / IDate / date format or other numeric variables that can be used as the time variables.

You may take a look at a simulated cohort `sire` as an example of the minimum required information for processing data with `lexpand`.

Many arguments can be supplied as a character string naming the appropriate variable (e.g. "sex"), as a symbol (e.g. `sex`) or as an expression (e.g. `factor(sex, 0:1, c("m", "f"))`) for flexibility.

### Breaks

You should define all breaks as left inclusive and right exclusive time points (e.g. `[a, b)`) for 1-3 time dimensions so that the last member of a breaks vector is a meaningful "final upper limit", e.g. `per = c(2002, 2007, 2012)` to create a last subinterval of the form `[2007, 2012)`.

All breaks are explicit, i.e. if `drop = TRUE`, any data beyond the outermost breaks points are dropped. If one wants to have unspecified upper / lower limits on one time scale, use `Inf`: e.g. `breaks = list(fot = 0:5, age = c(0, 45, Inf))`. Breaks for `per` can also be given in Date/IDate/date format, whereupon they are converted to fractional years before used in splitting.

The age time scale can additionally be automatically split into common age grouping schemes by naming the scheme with an appropriate character string:

- "18of5": age groups 0-4, 5-9, 10-14, ..., 75-79, 80-84, 85+
- "20of5": age groups 0-4, 5-9, 10-14, ..., 85-89, 90-94, 95+
- "101of1": age groups 0, 1, 2, ..., 98, 99, 100+

### Time variables

If any of the given time variables (`birth`, `entry`, `exit`, `event`) is in any kind of date format, they are first coerced to fractional years before splitting using `get.yrs` (with `year.length = "actual"`).

Sometimes in e.g. SIR/SMR calculation one may want the event time to differ from the time of exit from follow-up, if the subject is still considered to be at risk of the event. If event is specified, the transition to status is moved to event from exit using `cutLexis`. See Examples.

### The status variable

The statuses in the expanded output (`lex.Cst` and `lex.Xst`) are determined by using either only `status` or both `status` and `entry.status`. If `entry.status = NULL`, the status at entry is guessed according to the type of variable supplied via `status`: For numeric variables it will be zero, for factors the first level (`levels(status)[1]`) and otherwise the first unique value in alphabetical order (`sort(unique(status))[1]`).

Using numeric or factor status variables is strongly recommended. Logical expressions are also allowed (e.g. `status = my_status != 0L`) and are converted to integer internally.

### Merging population hazard information

To enable computing relative/net survivals with `survtab` and `relpois`, `lexpand` merges an appropriate population hazard data (`pophaz`) to the expanded data before dropping rows outside the specified time window (if `drop = TRUE`). `pophaz` must, for this reason, contain at a minimum the variables named `agegroup`, `year`, and `haz`. `pophaz` may contain additional variables to specify different population hazard levels in different strata; e.g. `popmort` includes `sex`. All the strata-defining variables must be present in the supplied data. `lexpand` will automatically detect variables with common names in the two datasets and merge using them.

Currently `year` must be an integer variable specifying the appropriate year. `agegroup` must currently also specify one-year age groups, e.g. `popmort` specifies 101 age groups of length 1 year. In both `year` and `agegroup` variables the values are interpreted as the lower bounds of intervals (and passed on to a `cut` call). The mandatory variable `haz` must specify the appropriate average rate at the person-year level; e.g. `haz = -log(survProb)` where `survProb` is a one-year conditional survival probability will be the correct hazard specification.

The corresponding `pophaz` population hazard value is merged by using the mid points of the records after splitting as reference values. E.g. if `age=89.9` at the start of a 1-year interval, then the reference age value is `90.4` for merging. This way we get a "typical" population hazard level for each record.

### Computing Pohar-Perme weights

If `pp = TRUE`, Pohar-Perme weights (the inverse of cumulative population survival) are computed. This will create the new `pp` variable in the expanded data. `pp` is a reserved name and `lexpand` throws exception if a variable with that name exists in data.

When a survival interval contains one or several rows per subject (e.g. due to splitting by the `per` scale), `pp` is cumulated from the beginning of the first record in a survival interval for each subject to the mid-point of the remaining time within that survival interval, and that value is given for every other record that a given person has within the same survival interval.

E.g. with 5 rows of duration `1/5` within a survival interval `[0, 1]`, `pp` is determined for all records by a cumulative population survival from `0` to `0.5`. The existing accuracy is used, so that the weight is cumulated first up to the end of the second row and then over the remaining distance to the mid-point (first to `0.4`, then to `0.5`). This ensures that more accurately merged population hazards are fully used.

### Event not at end of follow-up & overlapping time lines

`event` may be used if the event indicated by `status` should occur at a time differing from `exit`. If `event` is defined, `cutLexis` is used on the data set after coercing it to the `Lexis` format and before

splitting. Note that some values of event are allowed to be NA as with `cutLexis` to accommodate observations without an event occurring.

Additionally, setting `overlapping = FALSE` ensures that (irrespective of using event) the each subject defined by `id` only has one continuous time line instead of possibly overlapping time lines if there are multiple rows in data by `id`.

### Aggregating

Certain analyses such as SIR/SMR calculations require tables of events and person-years by the unique combinations (interactions) of several variables. For this, `aggre` can be specified as a list of such variables (preferably factor variables but not mandatory) and any arbitrary functions of the variables at one's disposal. E.g.

```
aggre = list(sex, agegr = cut(dg_age, 0:100))
```

would tabulate events and person-years by sex and an ad-hoc age group variable. Every ad-hoc-created variable should be named.

`fot`, `per`, and `age` are special reserved variables which, when present in the `aggre` list, are output as categories of the corresponding time scale variables by using e.g.

```
cut(fot, breaks$fot, right=FALSE).
```

This only works if the corresponding breaks are defined in `breaks` or via "...". E.g.

```
aggre = list(sex, fot.int = fot) with
```

```
breaks = list(fot=0:5).
```

The output variable `fot.int` in the above example will have the lower limits of the appropriate intervals as values.

`aggre` as a named list will output numbers of events and person-years with the given new names as categorizing variable names, e.g. `aggre = list(follow_up = fot, gender = sex, agegroup = age)`.

The output table has person-years (`pyrs`) and event counts (e.g. `from0to1`) as columns. Event counts are the numbers of transitions (`lex.Cst != lex.Xst`) or the `lex.Xst` value at a subject's last record (subject possibly defined by `id`).

If `aggre.type = "unique"` (alias "non-empty"), the above results are computed for existing combinations of expressions given in `aggre`, but also for non-existing combinations if `aggre.type = "cartesian"` (alias "full"). E.g. if a factor variable has levels "a", "b", "c" but the data is limited to only have levels "a", "b" present (more than zero rows have these level values), the former setting only computes results for "a", "b", and the latter also for "c" and any combination with other variables or expression given in `aggre`. In essence, "cartesian" forces also combinations of variables used in `aggre` that have no match in data to be shown in the result.

If `aggre` is not NULL and `pophaz` has been supplied, `lexpand` also aggregates the expected counts of events, which appears in the output data by the reserved name `d.exp`. Additionally, having `pp = TRUE` causes `lexpand` to also compute various Pohar-Perme weighted figures necessary for computing Pohar-Perme net survivals with `survtab_ag`. This can be slow, so consider what is really needed. The Pohar-Perme weighted figures have the suffix `.pp`.

### Value

If `aggre = NULL`, returns a `data.table` or `data.frame` (depending on `options("popEpi.datatable")`; see `?popEpi`) object expanded to accommodate split observations with time scales as fractional

years and pophaz merged in if given. Population hazard levels in new variable pop.haz, and Pohar-Perme weights as new variable pp if requested.

If `aggre` is defined, returns a long-format data.table/data.frame with the variable `pyrs` (person-years), and variables for the counts of transitions in state or state at end of follow-up formatted from `XtoY`, where `X` and `Y` are the states transitioned from and to, respectively. The data may also have the columns `d.exp` for expected numbers of cases and various Pohar-Perme weighted figures as identified by the suffix `.pp`; see Details.

### Author(s)

Joonas Miettinen

### See Also

[Lexis](#), [popmort](#)

Other splitting functions: [splitLexisDT\(\)](#), [splitMulti\(\)](#)

Other aggregation functions: [aggre\(\)](#), [as.aggre\(\)](#), [setaggre\(\)](#), [summary.aggre\(\)](#)

### Examples

```
## prepare data for e.g. 5-year cohort survival calculation
x <- lexpand(sire, breaks=list(fot=seq(0, 5, by = 1/12)),
            birth = bi_date, entry = dg_date, exit = ex_date,
            status = status != 0, pophaz=popmort)

## prepare data for e.g. 5-year "period analysis" for 2008-2012
BL <- list(fot = seq(0, 5, by = 1/12), per = c("2008-01-01", "2013-01-01"))
x <- lexpand(sire, breaks = BL,
            birth = bi_date, entry = dg_date, exit = ex_date,
            pophaz=popmort, status = status != 0)

## aggregating
BL <- list(fot = 0:5, per = c("2003-01-01", "2008-01-01", "2013-01-01"))
ag <- lexpand(sire, breaks = BL, status = status != 0,
            birth = bi_date, entry = dg_date, exit = ex_date,
            aggre=list(sex, period = per, surv.int = fot))

## aggregating even more
ag <- lexpand(sire, breaks = BL, status = status != 0,
            birth = bi_date, entry = dg_date, exit = ex_date,
            aggre=list(sex, period = per, surv.int = fot),
            pophaz = popmort, pp = TRUE)

## using "...
x <- lexpand(sire, fot=0:5, status = status != 0,
            birth = bi_date, entry = dg_date, exit = ex_date,
            pophaz=popmort)

x <- lexpand(sire, fot=0:5, status = status != 0,
            birth = bi_date, entry = dg_date, exit = ex_date,
```

```

    aggre=list(sex, surv.int = fot))

## using the "event" argument: it just places the transition to given "status"
## at the "event" time instead of at the end, if possible using cutLexis
x <- leexpand(sire, status = status, event = dg_date,
             birth = bi_date, entry = dg_date, exit = ex_date,)

## aggregating with custom "event" time
## (the transition to status is moved to the "event" time)
x <- leexpand(sire, status = status, event = dg_date,
             birth = bi_date, entry = dg_date, exit = ex_date,
             per = 1970:2014, age = c(0:100,Inf),
             aggre = list(sex, year = per, agegroup = age))

```

---

lines.sirspline      *lines method for sirspline-object*

---

### Description

Plot SIR spline lines with R base graphics

### Usage

```

## S3 method for class 'sirspline'
lines(x, conf.int = TRUE, print.levels = NA, select.spline, ...)

```

### Arguments

x	an object returned by function sirspline
conf.int	logical; default TRUE draws also the 95 confidence intervals
print.levels	name(s) to be plotted. Default plots all levels.
select.spline	select which spline variable (a number or a name) is plotted.
...	arguments passed on to lines()

### Details

In lines.sirspline most of graphical parameters is user adjustable. Desired spline variable can be selected with select.spline and only one can be plotted at a time. The spline variable can include several levels, e.g. gender (these are the levels of print from sirspline). All levels are printed by default, but a specific level can be selected using argument print.levels. Printing the levels separately enables e.g. to give different colours for each level.

### Value

Always returns 'NULL' invisibly. This function is called for its side effects.

**Author(s)**

Matti Rantanen

**See Also**

Other sir functions: [plot.sirspline\(\)](#), [sir\\_exp\(\)](#), [sir\\_ratio\(\)](#), [sirspline\(\)](#), [sir\(\)](#)

---

lines.survmean

*Graphically Inspect Curves Used in Mean Survival Computation*

---

**Description**

Plots the observed (with extrapolation) and expected survival curves for all strata in an object created by [survmean](#)

**Usage**

```
## S3 method for class 'survmean'  
lines(x, ...)
```

**Arguments**

x	a survmean object
...	arguments passed (ultimately) to <code>matlines</code> ; you may, therefore, supply e.g. <code>lwd</code> through this, though arguments such as <code>lty</code> and <code>col</code> will not work

**Details**

This function is intended to be a workhorse for [plot.survmean](#). If you want finer control over the plotted curves, extract the curves from the `survmean` output using

```
attr(x, "curves")
```

where `x` is a `survmean` object.

**Value**

Always returns 'NULL' invisibly. This function is called for its side effects.

**Author(s)**

Joonas Miettinen

**See Also**

Other `survmean` functions: [Surv\(\)](#), [plot.survmean\(\)](#), [survmean\(\)](#)



---

lines.survtab	lines <i>method for survtab objects</i>
---------------	---

---

**Description**

Plot lines from a survtab object

**Usage**

```
## S3 method for class 'survtab'
lines(x, y = NULL, subset = NULL, conf.int = TRUE, col = NULL, lty = NULL, ...)
```

**Arguments**

x	a survtab output object
y	a variable to plot; a quoted name of a variable in x; e.g. y = "surv.obs"; if NULL, picks last survival variable column in order in x
subset	a logical condition; obj is subset accordingly before plotting; use this for limiting to specific strata, e.g. subset = sex == "male"
conf.int	logical; if TRUE, also plots any confidence intervals present in obj for variables in y
col	line colour passed to matlines
lty	line type passed to matlines
...	additional arguments passed on to to a matlines call; e.g. lwd can be defined this way

**Value**

Always returns 'NULL' invisibly. This function is called for its side effects.

**Author(s)**

Joonas Miettinen

**See Also**

Other survtab functions: [Surv\(\)](#), [plot.survtab\(\)](#), [print.survtab\(\)](#), [summary.survtab\(\)](#), [survtab\\_ag\(\)](#), [survtab\(\)](#)

**Examples**

```
data(sire)
data(sibr)
si <- rbind(sire, sibr)
si$period <- cut(si$dg_date, as.Date(c("1993-01-01", "2004-01-01", "2013-01-01")), right = FALSE)
si$cancer <- c(rep("rectal", nrow(sire)), rep("breast", nrow(sibr)))
```

```
x <- leexpand(si, birth = bi_date, entry = dg_date, exit = ex_date,
             status = status %in% 1:2,
             fot = 0:5, aggre = list(cancer, period, fot))
st <- survtab_ag(fot ~ cancer + period, data = x,
               surv.method = "lifetable", surv.type = "surv.obs")

plot(st, "surv.obs", subset = cancer == "breast", ylim = c(0.5, 1), col = "blue")
lines(st, "surv.obs", subset = cancer == "rectal", col = "red")

## or
plot(st, "surv.obs", col = c(2,2,4,4), lty = c(1, 2, 1, 2))
```

---

lower_bound	<i>Return lower_bound value from char string (20,30]</i>
-------------	--

---

### Description

selects lowest values of each factor after cut() based on that the value starts from index 2 and end in comma ",".

### Usage

```
lower_bound(cut)
```

### Arguments

cut is a character vector of elements "(20,60]"

### Value

A numeric vector.

### Author(s)

Matti Rantanen

---

ltable	<i>Tabulate Counts and Other Functions by Multiple Variables into a Long-Format Table</i>
--------	---

---

### Description

ltable makes use of data.table capabilities to tabulate frequencies or arbitrary functions of given variables into a long format data.table/data.frame. expr.by.cj is the equivalent for more advanced users.

**Usage**

```

ltable(
  data,
  by.vars = NULL,
  expr = list(obs = .N),
  subset = NULL,
  use.levels = TRUE,
  na.rm = FALSE,
  robust = TRUE
)

expr.by.cj(
  data,
  by.vars = NULL,
  expr = list(obs = .N),
  subset = NULL,
  use.levels = FALSE,
  na.rm = FALSE,
  robust = FALSE,
  .SDcols = NULL,
  enclos = parent.frame(1L),
  ...
)

```

**Arguments**

<code>data</code>	a <code>data.table</code> / <code>data.frame</code>
<code>by.vars</code>	names of variables that are used for categorization, as a character vector, e.g. <code>c('sex', 'agegroup')</code>
<code>expr</code>	object or a list of objects where each object is a function of a variable (see: details)
<code>subset</code>	a logical condition; data is limited accordingly before evaluating <code>expr</code> - but the result of <code>expr</code> is also returned as NA for levels not existing in the subset. See Examples.
<code>use.levels</code>	logical; if TRUE, uses factor levels of given variables if present; if you want e.g. counts for levels that actually have zero observations but are levels in a factor variable, use this
<code>na.rm</code>	logical; if TRUE, drops rows in table that have NA as values in any of <code>by.vars</code> columns
<code>robust</code>	logical; if TRUE, runs the output data's <code>by.vars</code> columns through <code>robust_values</code> before outputting
<code>.SDcols</code>	advanced; a character vector of column names passed to inside the <code>data.table</code> 's brackets <code>DT[, , ...]</code> ; see <a href="#">data.table</a> ; if NULL, uses all appropriate columns. See Examples for usage.
<code>enclos</code>	advanced; an environment; the enclosing environment of the data.
<code>...</code>	advanced; other arguments passed to inside the <code>data.table</code> 's brackets <code>DT[, , ...]</code> ; see <a href="#">data.table</a>

## Details

Returns `expr` for each unique combination of given by `.vars`.

By default makes use of any and all `levels` present for each variable in `by.vars`. This is useful, because even if a subset of the data does not contain observations for e.g. a specific age group, those age groups are nevertheless presented in the resulting table; e.g. with the default `expr = list(obs = .N)` all age group levels are represented by a row and can have `obs = 0`.

The function differs from the vanilla `table` by giving a long format table of values regardless of the number of `by.vars` given. Make use of e.g. `cast_simple` if data needs to be presented in a wide format (e.g. a two-way table).

The rows of the long-format table are effectively Cartesian products of the levels of each variable in `by.vars`, e.g. with `by.vars = c("sex", "area")` all levels of `area` are repeated for both levels of `sex` in the table.

The `expr` allows the user to apply any function(s) on all levels defined by `by.vars`. Here are some examples:

- `.N` or `list(.N)` is a function used inside a `data.table` to calculate counts in each group
- `list(obs = .N)`, same as above but user assigned variable name
- `list(sum(obs), sum(pyr), mean(dg_age))`, multiple objects in a list
- `list(obs = sum(obs), pyr = sum(pyr))`, same as above with user defined variable names

If use `levels = FALSE`, no `levels` information will be used. This means that if e.g. the `agegroup` variable is a factor and has 18 levels defined, but only 15 levels are present in the data, no rows for the missing levels will be shown in the table.

`na.rm` simply drops any rows from the resulting table where any of the `by.vars` values was `NA`.

## Value

A `'data.table'` of statistics (e.g. counts) stratified by the columns defined in `'by.vars'`.

## Functions

- `expr.by.cj`: Somewhat more streamlined `ltable` with defaults for speed. Explicit determination of enclosing environment of data.

## Author(s)

Joonas Miettinen, Matti Rantanen

## See Also

`table`, `cast_simple`, `melt`

**Examples**

```

data("sire", package = "popEpi")
sr <- sire
sr$agegroup <- cut(sr$dg_age, breaks=c(0,45,60,75,85,Inf))
## counts by default
ltable(sr, "agegroup")

## any expression can be given
ltable(sr, "agegroup", list(mage = mean(dg_age)))
ltable(sr, "agegroup", list(mage = mean(dg_age), vage = var(dg_age)))

## also returns levels where there are zero rows (expressions as NA)
ltable(sr, "agegroup", list(obs = .N,
                           minage = min(dg_age),
                           maxage = max(dg_age)),
       subset = dg_age < 85)

#### expr.by.cj
expr.by.cj(sr, "agegroup")

## any arbitrary expression can be given
expr.by.cj(sr, "agegroup", list(mage = mean(dg_age)))
expr.by.cj(sr, "agegroup", list(mage = mean(dg_age), vage = var(dg_age)))

## only uses levels of by.vars present in data
expr.by.cj(sr, "agegroup", list(mage = mean(dg_age), vage = var(dg_age)),
          subset = dg_age < 70)

## .SDcols trick
expr.by.cj(sr, "agegroup", lapply(.SD, mean),
          subset = dg_age < 70, .SDcols = c("dg_age", "status"))

```

---

meanpop\_fi

*Mean population counts in Finland year, sex, and age group.*


---

**Description**

Mean population counts in Finland year, sex, and age group.

**Format**

data.table with columns

- sex gender coded as male, female (0, 1)
- year calendar year 1981-2016
- agegroup - coded 0 to 100; one-year age groups
- meanpop the mean population count; that is, the mean of the annual population counts of two consecutive years; e.g. for 1990 meanpop is the mean of population counts for 1990 and 1991 (counted at 1990-01-01 and 1991-01-01, respectively)

**Source**

Statistics Finland

**See Also**

Other popEpi data: [ICSS](#), [popmort](#), [sibr](#), [sire](#), [stdpop101](#), [stdpop18](#)

---

na2zero

*Convert NA's to zero in data.table*

---

**Description**

Given a data.table DT, replaces any NA values in the variables given in vars in DT. Takes a copy of the original data and returns the modified copy.

**Usage**

```
na2zero(DT, vars = NULL)
```

**Arguments**

DT	data.table object
vars	a character string vector of variables names in DT; if NULL, uses all variable names in DT

**Details**

Given a data.table object, converts NA values to numeric (double) zeros for all variables named in vars or all variables if vars = NULL.

**Value**

A copy of 'DT' where 'NA' values have been replaced with zero.

**Author(s)**

Joonas Miettinen

---

plot.rate	<i>plot method for rate object</i>
-----------	------------------------------------

---

### Description

Plot rate estimates with confidence intervals lines using R base graphics

### Usage

```
## S3 method for class 'rate'  
plot(x, conf.int = TRUE, eps = 0.2, left.margin, xlim, ...)
```

### Arguments

x	a rate object (see <a href="#">rate</a> )
conf.int	logical; default TRUE draws the confidence intervals
eps	is the height of the ending of the error bars
left.margin	set a custom left margin for long variable names. Function tries to do it by default.
xlim	change the x-axis location
...	arguments passed on to graphical functions points and segment (e.g. col, lwd, pch and cex)

### Details

This is limited explanatory tool but most graphical parameters are user adjustable.

### Value

Always returns 'NULL' invisibly. This function is called for its side effects.

### Author(s)

Matti Rantanen

---

`plot.sir`*Plot method for sir-object*

---

**Description**

Plot SIR estimates with error bars

**Usage**

```
## S3 method for class 'sir'
plot(
  x,
  conf.int = TRUE,
  ylab,
  xlab,
  xlim,
  main,
  eps = 0.2,
  abline = TRUE,
  log = FALSE,
  left.margin,
  ...
)
```

**Arguments**

<code>x</code>	an object returned by function <code>sir</code>
<code>conf.int</code>	default TRUE draws confidence intervals
<code>ylab</code>	overwrites default y-axis label
<code>xlab</code>	overwrites default x-axis label
<code>xlim</code>	x-axis minimum and maximum values
<code>main</code>	optional plot title
<code>eps</code>	error bar vertical bar height (works only in 'model' or 'univariate')
<code>abline</code>	logical; draws a grey line in $SIR = 1$
<code>log</code>	logical; SIR is not in log scale by default
<code>left.margin</code>	adjust left marginal of the plot to fit long variable names
<code>...</code>	arguments passed on to <code>plot()</code> , <code>segment</code> and <code>lines()</code>

**Details**

Plot SIR estimates and confidence intervals

- univariate - plots SIR with univariate confidence intervals
- model - plots SIR with Poisson modelled confidence intervals



**Customize** Normal plot parameters can be passed to plot. These can be a vector when plotting error bars:

- pch - point type
- lty - line type
- col - line/point colour
- lwd - point/line size

**Tips for plotting splines** It's possible to use plot to first draw the confidence intervals using specific line type or colour and then plotting again the estimate using lines(..., conf.int = FALSE) with different settings. This works only when plot.type is 'splines'.

### Value

Always returns 'NULL' invisibly. This function is called for its side effects.

### Author(s)

Matti Rantanen

### See Also

[sir](#), [sirspline](#)

### Examples

```
# Plot SIR estimates
# plot(sir.by.gender, col = c(4,2), log=FALSE, eps=0.2, lty=1, lwd=2, pch=19,
#      main = 'SIR by gender', abline=TRUE)
```

---

plot.sirspline

plot *method for sirspline-object*

---

### Description

Plot SIR splines using R base graphics.

### Usage

```
## S3 method for class 'sirspline'
plot(x, conf.int = TRUE, abline = TRUE, log = FALSE, type, ylab, xlab, ...)
```

**Arguments**

x	an object returned by function <code>sirspline</code>
<code>conf.int</code>	logical; default TRUE draws also the 95 confidence intervals
<code>abline</code>	logical; draws a reference line where $SIR = 1$
<code>log</code>	logical; default FALSE. Should the y-axis be in log scale
<code>type</code>	select <code>type = 'n'</code> to plot only figure frames
<code>ylab</code>	overwrites default y-axis label; can be a vector if multiple splines fitted
<code>xlab</code>	overwrites default x-axis label; can be a vector if multiple splines fitted
...	arguments passed on to <code>plot()</code>

**Details**

In `plot.sirspline` almost every graphical parameter are user adjustable, such as `ylim`, `xlim`. `plot.sirsplines` calls `lines.splines` to add lines.

The plot axis without lines can be plotted using option `type = 'n'`. On top of the frame it's then possible to add a grid, `abline` or text before plotting the lines (see: `sirspline`).

**Value**

Always returns 'NULL' invisibly. This function is called for its side effects.

**Author(s)**

Matti Rantanen

**See Also**

Other sir functions: [lines.sirspline\(\)](#), [sir\\_exp\(\)](#), [sir\\_ratio\(\)](#), [sirspline\(\)](#), [sir\(\)](#)

---

plot.survmean

*Graphically Inspect Curves Used in Mean Survival Computation*

---

**Description**

Plots the observed (with extrapolation) and expected survival curves for all strata in an object created by [survmean](#)

**Usage**

```
## S3 method for class 'survmean'
plot(x, ...)
```

**Arguments**

x a survmean object  
... arguments passed (ultimately) to matlines; you may, therefore, supply e.g. xlab through this, though arguments such as lty and col will not work

**Details**

For examples see [survmean](#). This function is intended only for graphically inspecting that the observed survival curves with extrapolation and the expected survival curves have been sensibly computed in survmean.

If you want finer control over the plotted curves, extract the curves from the survmean output using `attr(x, "curves")` where x is a survmean object.

**Value**

Always returns 'NULL' invisibly. This function is called for its side effects.

**Author(s)**

Joonas Miettinen

**See Also**

Other survmean functions: [Surv\(\)](#), [lines.survmean\(\)](#), [survmean\(\)](#)

---

plot.survtab	plot method for survtab objects
--------------	---------------------------------

---

**Description**

Plotting for survtab objects

**Usage**

```
## S3 method for class 'survtab'  
plot(  
  x,  
  y = NULL,  
  subset = NULL,  
  conf.int = TRUE,  
  col = NULL,  
  lty = NULL,  
  ylab = NULL,  
  xlab = NULL,  
  ...  
)
```

**Arguments**

x	a survtab output object
y	survival a character vector of a variable names to plot; e.g. y = "r.e2"
subset	a logical condition; obj is subset accordingly before plotting; use this for limiting to specific strata, e.g. subset = sex == "male"
conf.int	logical; if TRUE, also plots any confidence intervals present in obj for variables in y
col	line colour; one value for each stratum; will be recycled
lty	line type; one value for each stratum; will be recycled
ylab	label for Y-axis
xlab	label for X-axis
...	additional arguments passed on to plot and lines.survtab; e.g. ylim can be defined this way

**Value**

Always returns 'NULL' invisibly. This function is called for its side effects.

**Author(s)**

Joonas Miettinen

**See Also**

Other survtab functions: [Surv\(\)](#), [lines.survtab\(\)](#), [print.survtab\(\)](#), [summary.survtab\(\)](#), [survtab\\_ag\(\)](#), [survtab\(\)](#)

**Examples**

```
data(sire)
data(sibr)
si <- rbind(sire, sibr)
si$period <- cut(si$dg_date, as.Date(c("1993-01-01", "2004-01-01", "2013-01-01")), right = FALSE)
si$cancer <- c(rep("rectal", nrow(sire)), rep("breast", nrow(sibr)))
x <- leexpand(si, birth = bi_date, entry = dg_date, exit = ex_date,
             status = status %in% 1:2,
             fot = 0:5, aggre = list(cancer, period, fot))
st <- survtab_ag(fot ~ cancer + period, data = x,
                surv.method = "lifetable", surv.type = "surv.obs")

plot(st, "surv.obs", subset = cancer == "breast", ylim = c(0.5, 1), col = "blue")
lines(st, "surv.obs", subset = cancer == "rectal", col = "red")

## or
plot(st, "surv.obs", col = c(2,2,4,4), lty = c(1, 2, 1, 2))
```

---

`poisson.ci`*Get rate and exact Poisson confidence intervals*

---

**Description**

Computes confidence intervals for Poisson rates

**Usage**

```
poisson.ci(x, pt = 1, conf.level = 0.95)
```

**Arguments**

<code>x</code>	observed
<code>pt</code>	expected
<code>conf.level</code>	alpha level

**Value**

A data.frame with columns

- `x`: arg `x`
- `pt`: arg `pt`
- `rate`: result of `x / pt`
- `lower`: lower bound of CI
- `upper`: upper bound of CI
- `conf.level`: arg `conf.level`

**Author(s)**

epitools

**Examples**

```
poisson.ci(x = 4, pt = 5, conf.level = 0.95)
```

popEpi

*popEpi: Functions for large-scale epidemiological analysis***Description**

**popEpi** is built for the needs of registry-based (large-scale) epidemiological analysis. This is in most part enabled by the efficient **data.table** package for handling and aggregating large data sets.

**popEpi** currently supplies some utility functions such as `splitMulti` and `get.yrs` for preparing large data sets for epidemiological analysis. Included are also a few functions that can be used in epidemiological analysis such as `sir` for estimating standardized incidence/mortality ratios (SIRs/SMRs) and `survtab` for estimating observed and relative/net survival as well as cumulative incidence functions (CIFs). In particular, `survtab` implements the Ederer II (Ederer and Heise (1959)) and Pohar Perme estimators (Pohar Perme, Stare, and Esteve (2012) doi: [10.1111/j.1541-0420.2011.01640.x](https://doi.org/10.1111/j.1541-0420.2011.01640.x)) and allows for easy age-standardisation.

Since there are many benefits to using `data.tables`, **popEpi** returns outputs by default in the `data.table` format where appropriate. Since `data.table` objects are usually modified by reference, this may have surprising side effects for users uninitiated in using `data.table`. To ensure that appropriate outputs are in the `data.frame` format, set `options("popEpi.datatable" = FALSE)`. However, `data.table` usage is recommended due to better performance and testing coverage. `data.table` is used by most functions internally in both cases.

**Details**

popEpi

pophaz

*Expected / Population Hazard Data Sets Usage in popEpi***Description**

Several functions in **popEpi** make use of population or expected hazards in computing the intended estimates (e.g. `survtab`). This document explains using such data sets in this package.

**Details**

Population hazard data sets (pophaz for short) in **popEpi** should be `data.frames` in the "long" format where one of the columns must be named `haz` (for hazard), and other columns define the values or levels in variables relating to subjects in your data. For example, `popmort` contains Finnish population mortality hazards by sex, calendar year, and 1-year age group.

sex	year	agegroup	haz
0	1951	0	0.036363176
0	1951	1	0.003616547
0	1951	2	0.002172384
0	1951	3	0.001581249
0	1951	4	0.001180690
0	1951	5	0.001070595

The names of the columns should match to the names of the variables that you have in your subject-level data. Time variables in your pophaz may also correspond to Lexis time scales; see [survtab](#).

Any time variables (as they usually have) should be coded consistently: When using fractional years in your data, the time variables in your pophaz must also be coded in fractional years. When using e.g. Dates in your data, ensure that the pophaz time variables are coded at the level of days (or Dates for calendar time).

The haz variable in your pophaz should also be coded consistently with the used time variables. E.g. haz values in life-tables reported as deaths per person-year should be multiplied by 365.25 when using day-level time variables. Typically you'll have calendar time and age expressed in years, which means haz should be expressed as the number of deaths per person-year.

If you have your population hazards in a `ratetable` object usable by functions in **survival** and **rehsurv**, you may transform them to long-format data.frames using [ratetable\\_to\\_long\\_dt](#). Ensure, however, that the created haz column is coded at the right level (events per days or years typically).

National statistical institutions, the WHO, and e.g. the Human Life-Table Database supply life-table data.

#### Author(s)

Joonas Miettinen

---

popmort

*Population mortality rates in Finland 1951 - 2013 in 101 age groups and by gender. This is an example of a population hazard table as used in **popEpi**; for the general help page, see [pophaz](#).*

---

#### Description

Population mortality rates in Finland 1951 - 2013 in 101 age groups and by gender. This is an example of a population hazard table as used in **popEpi**; for the general help page, see [pophaz](#).

#### Format

data.table with columns

- sex gender coded as male, female (0, 1)
- year calendar year
- agegroup - coded 0 to 100; one-year age groups
- haz the average population mortality rate per person-year ( $d/(\text{pyrs})$ , where  $d$  is the number of deaths and  $\text{pyrs}$  is the person-years)

#### Source

Statistics Finland

**See Also**[pophaz](#)Other popEpi data: [ICSS](#), [meanpop\\_fi](#), [sibr](#), [sire](#), [stdpop101](#), [stdpop18](#)

---

`prepExpo`*Prepare Exposure Data for Aggregation*

---

**Description**

`prepExpo` uses a `Lexis` object of periods of exposure to fill gaps between the periods and overall entry and exit times without accumulating exposure time in periods of no exposure, and splits the result if requested.

**Usage**

```
prepExpo(
  lex,
  freezeScales = "work",
  cutScale = "per",
  entry = min(get(cutScale)),
  exit = max(get(cutScale)),
  by = "lex.id",
  breaks = NULL,
  freezeDummy = NULL,
  subset = NULL,
  verbose = FALSE,
  ...
)
```

**Arguments**

<code>lex</code>	a <code>Lexis</code> object with ONLY periods of exposure as rows; one or multiple rows per subject allowed
<code>freezeScales</code>	a character vector naming <code>Lexis</code> time scales of exposure which should be frozen in periods where no exposure occurs (in the gap time periods)
<code>cutScale</code>	the <code>Lexis</code> time scale along which the subject-specific ultimate entry and exit times are specified
<code>entry</code>	an expression; the time of entry to follow-up which may be earlier, at, or after the first time of exposure in <code>freezeScales</code> ; evaluated separately for each unique combination of <code>by</code> , so e.g. with <code>entry = min(Var1)</code> and <code>by = "lex.id"</code> it sets the <code>lex.id</code> -specific minima of <code>Var1</code> to be the original times of entry for each <code>lex.id</code>
<code>exit</code>	the same as <code>entry</code> but for the ultimate exit time per unique combination of <code>by</code>



by	a character vector indicating variable names in <code>lex</code> , the unique combinations of which identify separate subjects for which to fill gaps in the records from entry to exit; for novices of <code>{data.table}</code> , this is passed to a <code>data.table</code> 's <code>by</code> argument.
breaks	a named list of breaks; e.g. <code>list(work = 0:20, per = 1995:2015)</code> ; passed on to <code>splitMulti</code> so see that function's help for more details
freezeDummy	a character string; specifies the name for a dummy variable that this function will create and add to output which identifies rows where the <code>freezeScales</code> are frozen and where not (0 implies not frozen, 1 implies frozen); if NULL, no dummy is created
subset	a logical condition to subset data by before computations; e.g. <code>subset = sex == "male"</code>
verbose	logical; if TRUE, the function is chatty and returns some messages and timings during its run.
...	additional arguments passed on to <code>splitMulti</code>

### Details

`prepExpo` is a convenience function for the purpose of eventually aggregating person-time and events in categories of not only normally progressing Lexis time scales but also some time scales which should not progress sometimes. For example a person may work at a production facility only intermittently, meaning exposure time (to work-related substances for example) should not progress outside of periods of work. This allows for e.g. a correct aggregation of person-time and events by categories of cumulative time of exposure.

Given a Lexis object containing rows (time lines) where a subject is exposed to something (and NO periods without exposure), fills any gaps between exposure periods for each unique combination of `by` and the subject-specific "ultimate" entry and exit times, "freezes" the cumulative exposure times in periods of no exposure, and splits data using breaks passed to `splitMulti` if requested. Results in a (split) Lexis object where `freezeScales` do not progress in time periods where no exposure was recorded in `lex`.

This function assumes that entry and exit arguments are the same for each row within a unique combination of variables named in `by`. E.g. with `by = "lex.id"` only each `lex.id` has a unique value for entry and exit at most.

The supplied breaks split the data using `splitMulti`, with the exception that breaks supplied concerning any frozen time scales ONLY split the rows where the time scales are not frozen. E.g. with `freezeScales = "work"`, `breaks = list(work = 0:10, cal = 1995:2010)` splits all rows over "cal" but only non-frozen rows over "work".

Only supports frozen time scales that advance and freeze contemporaneously: e.g. it would not currently be possible to take into account the cumulative time working at a facility and the cumulative time doing a single task at the facility, if the two are not exactly the same. On the other hand one might use the same time scale for different exposure types, supply them as separate rows, and identify the different exposures using a dummy variable.

### Value

Returns a Lexis object that has been split if breaks is specified. The resulting time is also a `data.table` if `options("popEpi.datatable") == TRUE` (see: `?popEpi`)

---

print.aggre                      *Print an aggre Object*

---

### Description

Print method function for aggre objects; see [as.aggre](#) and [aggre](#).

### Usage

```
## S3 method for class 'aggre'  
print(x, subset = NULL, ...)
```

### Arguments

x	an aggre object
subset	a logical condition to subset results table by before printing; use this to limit to a certain stratum. E.g. subset = sex == "male"
...	arguments passed to print.data.table; try e.g. top = 2 for numbers of rows in head and tail printed if the table is large, nrow = 100 for number of rows to print, etc.

### Value

Always returns 'NULL' invisibly. This function is called for its side effects.

### Author(s)

Joonas Miettinen

---

print.rate                      *Print an rate object*

---

### Description

Print method function for rate objects; see [rate](#).

### Usage

```
## S3 method for class 'rate'  
print(x, subset = NULL, ...)
```

**Arguments**

x                    an rate object  
 subset                a logical condition to subset results table by before printing; use this to limit to a certain stratum. E.g. subset = sex == "female"  
 ...                    arguments for data.tables print method, e.g. row.names = FALSE suppresses row numbers.

**Value**

Always returns 'NULL' invisibly. This function is called for its side effects.

**Author(s)**

Matti Rantanen

---

print.survtab                    *Print a survtab Object*

---

**Description**

Print method function for survtab objects; see [survtab\\_ag](#).

**Usage**

```
## S3 method for class 'survtab'
print(x, subset = NULL, ...)
```

**Arguments**

x                    a survtab object  
 subset                a logical condition to subset results table by before printing; use this to limit to a certain stratum. E.g. subset = sex == "male"  
 ...                    arguments passed to print.data.table; try e.g. top = 2 for numbers of rows in head and tail printed if the table is large, nrow = 100 for number of rows to print, etc.

**Value**

Always returns 'NULL' invisibly. This function is called for its side effects.

**Author(s)**

Joonas Miettinen

**See Also**

Other survtab functions: [Surv\(\)](#), [lines.survtab\(\)](#), [plot.survtab\(\)](#), [summary.survtab\(\)](#), [survtab\\_ag\(\)](#), [survtab\(\)](#)

---

rate	<i>Direct-Standardised Incidence/Mortality Rates</i>
------	--

---

### Description

rate calculates adjusted rates using preloaded weights data or user specified weights.

### Usage

```
rate(
  data,
  obs = NULL,
  pyrs = NULL,
  print = NULL,
  adjust = NULL,
  weights = NULL,
  subset = NULL
)
```

### Arguments

data	aggregated data (see e.g. <a href="#">lexpand</a> , <a href="#">aggre</a> if you have subject-level data)
obs	observations variable name in data. <a href="#">Flexible input</a> , typically e.g. obs = obs.
pyrs	person-years variable name in data. <a href="#">Flexible input</a> , typically e.g. pyrs = pyrs.
print	variable name to stratify the rates. <a href="#">Flexible input</a> , typically e.g. print = sex or print = list(sex, area).
adjust	variable for adjusting the rates. <a href="#">Flexible input</a> , typically e.g. adjust = agegroup.
weights	typically a list of weights or a character string specifying an age group standardization scheme; see the <a href="#">dedicated help page</a> and examples.
subset	a logical expression to subset data.

### Details

Input data needs to be in aggregated format with observations and person-years. For individual data use [lexpand](#), or [ltable](#) and merge person-years manually.

The confidence intervals are based on the normal approximation of the logarithm of the rate. The variance of the log rate that is used to derive the confidence intervals is derived using the delta method.

### Value

Returns a `data.table` with observations, person-years, rates and adjusted rates, if available. Results are stratified by `print`. Adjusted rates are identified with suffix `.adj` and `.lo` and `.hi` are for confidence intervals lower and upper 95% bounds, respectively. The prefix `SE.` stands for standard error.

**Author(s)**

Matti Rantanen, Joonas Miettinen

**See Also**

[lexpand](#), [ltable](#)

Other main functions: [Surv\(\)](#), [relpois\\_ag\(\)](#), [relpois\(\)](#), [sirspline\(\)](#), [sir\(\)](#), [survmean\(\)](#), [survtab\\_ag\(\)](#), [survtab\(\)](#)

Other rate functions: [rate\\_ratio\(\)](#)

**Examples**

```
## Prepare data with lexpand and then reformat agegroup.
data(sibr)
x <- lexpand(sibr, birth = bi_date, entry = dg_date, exit = ex_date,
             breaks = list(per = c(1990,2000,2010,2020), age = c(0:17*5,Inf)),
             aggre = list(agegroup = age, year.cat = per),
             status = status != 0)

x$agegroup <- cut(x$agegroup, c(0:17*5,Inf), right = FALSE)

## calculate rates for selected periods with Nordic 2000 weights:
r1 <- rate( data = x, obs = from0to1, pyrs = pyrs, print = year.cat,
            adjust = agegroup, weights = 'nordic')
r1

## use total person-years by stratum as weights (some have zero)
w <- ltable(x, by.vars = "agegroup", expr = sum(pyrs))
w[is.na(w$V1),]$V1 <- 0

r2 <- rate( data = x, obs = from0to1, pyrs = pyrs, print = year.cat,
            adjust = agegroup,
            weights = w$V1)
r2

## use data.frame of weights:
names(w) <- c("agegroup", "weights")
r2 <- rate( data = x, obs = from0to1, pyrs = pyrs, print = year.cat,
            adjust = agegroup,
            weights = w)
r2

## internal weights (same result as above)
r3 <- rate( data = x, obs = from0to1, pyrs = pyrs, print = year.cat,
            adjust = agegroup,
            weights = "internal")
r3
```

---

`rate_ratio`*Confidence intervals for the rate ratios*

---

**Description**

Calculate rate ratio with confidence intervals for rate objects or observations and person-years.

**Usage**

```
rate_ratio(x, y, crude = FALSE, SE.method = TRUE)
```

**Arguments**

<code>x</code>	a rate-object, vector of two; rate and standard error or observed and person-years.
<code>y</code>	a rate-object, vector of two; rate and standard error or observed and person-years.
<code>crude</code>	set TRUE to use crude rates; default is FALSE.
<code>SE.method</code>	default TRUE; if <code>x</code> and <code>y</code> are vectors of observed and person-years, this must be changed to FALSE.

**Details**

Calculate rate ratio of two age standardized rate objects (see [rate](#)). Multiple rates for each objects is supported if there are an equal number of rates. Another option is to set `x` and `y` as a vector of two.

1. rate and its standard error, and set `SE.method = TRUE`.
2. observations and person-year, and set `SE.method = FALSE`.

See examples.

**Value**

A vector length of three: `rate_ratio`, and lower and upper confidence intervals.

**Author(s)**

Matti Rantanen

**See Also**

[rate](#)

Other rate functions: [rate\(\)](#)

**Examples**

```

# two rate ratios; silly example with female rectal / breast cancer
## mortality rates
data("sire", package = "popEpi")
data("sibr", package = "popEpi")

BL <- list(per = 2000:2005)

re <- lexpand(sire, birth = "bi_date", entry = "dg_date", exit = "ex_date",
             status = status == 1, breaks = BL, aggre = list(per))
br <- lexpand(sibr, birth = "bi_date", entry = "dg_date", exit = "ex_date",
             status = status == 1, breaks = BL, aggre = list(per))

r_re <- rate(re, obs = "from0to1", pyrs = "pyrs")
r_br <- rate(br, obs = "from0to1", pyrs = "pyrs")

rate_ratio(r_re, r_br, SE.method = TRUE)

# manually set rates (0.003 and 0.005) and SEs (0.001 and 0.002)
# so that x = y = c('rate', 'SE')
rate_ratio(x= c(0.003, 0.001), y= c(0.005, 0.002), SE.method = TRUE)

# observed numbers (10 and 20) and person-years (30000 and 40000):
rate_ratio(x = c(10, 30000), y = c(20, 40000), SE.method = FALSE)

```

---

relpois

*Excess hazard Poisson model*


---

**Description**

Estimate a Poisson piecewise constant excess hazards model

**Usage**

```
relpois(data, formula, fot.breaks = NULL, subset = NULL, check = TRUE, ...)
```

**Arguments**

data	a dataset split with e.g. <code>lexpand</code> ; must have expected hazard merged within
formula	a formula which is passed on to <code>glm</code> ; see Details
fot.breaks	optional; a numeric vector of [a,b) breaks to specify survival intervals over the follow-up time; if NULL, the existing breaks along the mandatory fot time scale in data are used (e.g. the breaks for fot supplied to <code>lexpand</code> )
subset	a logical vector or condition; e.g. <code>subset = sex == 1</code> ; limits the data before estimation

check	logical; if TRUE, tabulates excess cases by all factor variables in the formula to check for negative / NA excess cases before fitting the GLM
...	any argument passed on to glm

## Details

### Basics

relpois employs a custom link function of the Poisson variety to estimate piecewise constant parametric excess hazards. The pieces are determined by `fot.breaks`. A `log(person-years)` offset is passed automatically to the `glm` call.

### Formula usage

The formula can be used like any ordinary `glm` formula. The user must define the outcome in some manner, which is usually `lex.Xst` after splitting with e.g. `lexpand`. The exception is the possibility of including the baseline excess hazard terms by including the reserved term `FOT` in the formula.

For example, `lex.Xst != 0 ~ FOT + agegr` estimates a model with constant excess hazards at the follow-up intervals as specified by the pertinent breaks used in splitting data, as well as for the different age groups. `FOT` is created ad hoc if it is used in the formula. If you leave out `FOT`, the hazard is effectively assumed to be constant across the whole follow-up time.

You can also simply use your own follow-up time interval variable that you have created before calling `relpois`. However, when using `FOT`, `relpois` automatically checks for e.g. negative excess cases in follow-up intervals, allowing for quickly finding splitting breaks where model estimation is possible. It also drops any data outside the follow-up time window.

### Splitting and merging population hazard

The easiest way to both split and to include population hazard information is by using `lexpand`. You may also fairly easily do it by hand by splitting first and then merging in your population hazard information.

### Data requirements

The population hazard information must be available for each record and named `pop.haz`. The follow-up time variable must be named `"fot"` e.g. as a result of using `lexpand`. The `lex.dur` variable must also be present, containing person-year information.

## Value

A `glm` object created using a custom Poisson family construct. Some `glm` methods are applicable.

## Author(s)

Joonas Miettinen, Karri Seppa

## References

Paul W Dickman, Andy Sloggett, Michael Hills, and Timo Hakulinen. Regression models for relative survival. *Stat Med.* 2004 Jan 15;23(1):51-64. doi: [10.1002/sim.1597](https://doi.org/10.1002/sim.1597)



**See Also**

[lexpand](#), [poisson](#), [glm](#)

Other main functions: [Surv\(\)](#), [rate\(\)](#), [relpois\\_ag\(\)](#), [sirspline\(\)](#), [sir\(\)](#), [survmean\(\)](#), [survtab\\_ag\(\)](#), [survtab\(\)](#)

Other relpois functions: [RPL](#), [relpois\\_ag\(\)](#), [rpcurve\(\)](#)

**Examples**

```
## use the simulated rectal cancer cohort
data("sire", package = "popEpi")
sire$agegr <- cut(sire$dg_age, c(0,45,60,Inf), right=FALSE)

## usable straight away after splitting
fb <- c(0,3/12,6/12,1,2,3,4,5)
x <- lexpand(sire, birth = bi_date, entry = dg_date,
            exit = ex_date, status=status,
            breaks = list(fot=fb), pophaz=popmort)
rpm <- relpois(x, formula = lex.Xst %in% 1:2 ~ FOT + agegr)

## some methods for glm work. e.g. test for interaction

rpm2 <- relpois(x, formula = lex.Xst %in% 1:2 ~ FOT*agegr)
anova(rpm, rpm2, test="LRT")
AIC(rpm, rpm2)
## update() won't work currently
```

---

relpois\_ag

*Excess hazard Poisson model*


---

**Description**

Estimate a Poisson Piecewise Constant Excess Hazards Model

**Usage**

```
relpois_ag(
  formula,
  data,
  d.exp,
  offset = NULL,
  breaks = NULL,
  subset = NULL,
  piecewise = TRUE,
  check = TRUE,
  ...
)
```

**Arguments**

formula	a formula with the counts of events as the response. Passed on to <code>glm</code> . May contain usage of the <code>offset()</code> function instead of supplying the offset for the Poisson model via the argument <code>offset</code> .
data	an <code>aggre</code> object (an aggregated data set; see <a href="#">as.aggre</a> and <a href="#">aggre</a> )
d.exp	the counts of expected cases. Mandatory. E.g. <code>d.exp = EXC_CASES</code> , where <code>EXC_CASES</code> is a column in <code>data</code> .
offset	the offset for the Poisson model, supplied as e.g. <code>offset = log(PTIME)</code> , where <code>PTIME</code> is a subject-time variable in <code>data</code> . Not mandatory, but almost always should be supplied.
breaks	optional; a numeric vector of [a,b) breaks to specify survival intervals over the follow-up time; if <code>NULL</code> , the existing breaks along the mandatory time scale mentioned in <code>formula</code> are used
subset	a logical vector or condition; e.g. <code>subset = sex == 1</code> ; limits the data before estimation
piecewise	logical; if <code>TRUE</code> , and if any time scale from <code>data</code> is used (mentioned) in the formula, the time scale is transformed into a factor variable indicating intervals on the time scale. Otherwise the time scale left as it is, usually a numeric variable. E.g. if <code>formula = counts ~ TS1*VAR1</code> , <code>TS1</code> is transformed into a factor before fitting model.
check	logical; if <code>TRUE</code> , performs check on the negativity excess cases by factor-like covariates in formula - negative excess cases will very likely lead to non-converging model
...	any other argument passed on to <a href="#">glm</a> such as <code>control</code> or <code>weights</code>

**Value**

A `relpois` object created using a custom Poisson family construct.

**Author(s)**

Joonas Miettinen, Karri Seppa

**See Also**

[lexpand](#), [poisson](#), [glm](#)

Other main functions: [Surv\(\)](#), [rate\(\)](#), [relpois\(\)](#), [sirspline\(\)](#), [sir\(\)](#), [survmean\(\)](#), [survtab\\_ag\(\)](#), [survtab\(\)](#)

Other `relpois` functions: [RPL](#), [relpois\(\)](#), [rpcurve\(\)](#)

**Examples**

```
## use the simulated rectal cancer cohort
data(sire, package = "popEpi")
sire$agegr <- cut(sire$dg_age, c(0,45,60,Inf), right=FALSE)
```

```

## create aggregated example data
fb <- c(0,3/12,6/12,1,2,3,4,5)
x <- leexpand(sire, birth = bi_date, entry = dg_date,
             exit = ex_date, status=status %in% 1:2,
             breaks = list(fot=fb),
             pophaz=popmort, pp = FALSE,
             aggre = list(agegr, fot))

## fit model using aggregated data
rpm <- relpois_ag(formula = from0to1 ~ fot + agegr, data = x,
                 d.exp = d.exp, offset = log(pyrs))
summary(rpm)

## the usual functions for handling glm models work
rpm2 <- update(rpm, . ~ fot*agegr)
anova(rpm, rpm2, test="LRT")
AIC(rpm, rpm2)

## other features such as residuals or predicting are not guaranteed
## to work as intended.

```

---

robust\_values

*Convert values to numeric robustly*


---

### Description

Brute force solution for ensuring a variable is numeric by coercing a variable of any type first to factor and then to numeric

### Usage

```
robust_values(num.values, force = FALSE, messages = TRUE)
```

### Arguments

num.values	values to convert to numeric
force	logical; if TRUE, returns a vector of values where values that cannot be interpreted as numeric are set to NA; if FALSE, returns the original vector and gives a warning if any value cannot be interpreted as numeric.
messages	logical; if TRUE, returns a message of what was done with the num.values

### Value

A numeric vector.

### Note

Returns NULL if given num.values is NULL.

**Author(s)**

Joonas Miettinen

**Examples**

```
## this works
values <- c("1", "3", "5")
values <- robust_values(values)

## this works
values <- c("1", "3", "5", NA)
values <- robust_values(values)

## this returns originals and throws warnings
values <- c("1", "3", "5", "a")
suppressWarnings(
  values <- robust_values(values)
)

## this forces "a" to NA and works otherwise; throws warning about NAs
values <- c("1", "3", "5", "a")
suppressWarnings(
  values <- robust_values(values, force=TRUE)
)
```

---

rpcurve

*Marginal piecewise parametric relative survival curve*

---

**Description**

Fit a marginal relative survival curve based on a relpois fit

**Usage**

```
rpcurve(object)
```

**Arguments**

object            a relpois object

**Details**

Estimates a marginal curve, i.e. the average of all possible individual curves.

Only supported when the reserved FOT variable was used in relpois. Computes a curve for each unique combination of covariates (e.g. 4 sets) and returns a weighted average curve based on the counts of subjects for each combination (e.g. 1000, 125, 50, 25 respectively). Fairly fast when only categorical variables have been used, otherwise go get a cup of coffee.

If delayed entry is present in data due to period analysis limiting, the marginal curve is constructed only for those whose follow-up started in the respective period.

### Value

A ‘data.table’ of relative survival curves.

### Author(s)

Joonas Miettinen

### See Also

Other relpois functions: [RPL](#), [relpois\\_ag\(\)](#), [relpois\(\)](#)

### Examples

```
## use the simulated rectal cancer cohort
data("sire", package = "popEpi")
ab <- c(0,45,55,65,70,Inf)
sire$agegr <- cut(sire$dg_age, breaks = ab, right = FALSE)

BL <- list(fot= seq(0,10,1/12))
pm <- data.frame(popEpi::popmort)
x <- leexpand(sire, breaks=BL, pophaz=pm,
             birth = bi_date,
             entry = dg_date, exit = ex_date,
             status = status %in% 1:2)

rpm <- relpois(x, formula = lex.Xst %in% 1:2 ~ -1+ FOT + agegr,
              fot.breaks=c(0,0.25,0.5,1:8,10))
pmc <- rpcurve(rpm)

## compare with non-parametric estimates
names(pm) <- c("sex", "per", "age", "haz")
x$agegr <- cut(x$dg_age, c(0,45,55,65,75,Inf), right = FALSE)
st <- survtab(fot ~ adjust(agegr), data = x, weights = "internal",
             pophaz = pm)

plot(st, y = "r.e2.as")
lines(y = pmc$est, x = pmc$Tstop, col="red")
```

---

RPL	<i>Relative Poisson family object</i>
-----	---------------------------------------

---

**Description**

A family object for GLM fitting of relative Poisson models

**Usage**

RPL

**Format**

A list very similar to that created by `poisson()`.

**Author(s)**

Karri Seppa

**See Also**

Other relpois functions: [relpois\\_ag\(\)](#), [relpois\(\)](#), [rpcurve\(\)](#)

---

setaggre	<i>Set aggre attributes to an object by modifying in place</i>
----------	--

---

**Description**

Coerces an R object to an aggre object, identifying the object as one containing aggregated counts, person-years and other information. `setaggre` modifies in place without taking any copies. Retains all other attributes.

**Usage**

```
setaggre(x, values = NULL, by = NULL, breaks = NULL)
```

**Arguments**

<code>x</code>	a <code>data.frame</code> or <code>data.table</code>
<code>values</code>	a character string vector; the names of value variables
<code>by</code>	a character string vector; the names of variables by which values have been tabulated
<code>breaks</code>	a list of breaks, where each element is a breaks vector as usually passed to e.g. <a href="#">splitlexisDT</a> . The list must be fully named, with the names corresponding to time scales at the aggregate level in your data. Every unique value in a time scale variable in data must also exist in the corresponding vector in the breaks list.

**Details**

setaggre sets `x` to the `aggre` class in place without taking a copy as e.g. `as.data.frame.XXX` functions do; see e.g. [setDT](#).

**Value**

Returns ‘`x`’ invisibly after setting attributes to it without taking a copy. This function is called for its side effects.

**Author(s)**

Joonas Miettinen

**See Also**

Other aggregation functions: [aggre\(\)](#), [as.aggre\(\)](#), [lexpand\(\)](#), [summary.aggre\(\)](#)

**Examples**

```
df <- data.frame(sex = rep(c("male", "female"), each = 5),
                obs = rpois(10, rep(7,5, each=5)),
                pyrs = rpois(10, lambda = 10000))
## without any breaks
setaggre(df, values = c("obs", "pyrs"), by = "sex")
df <- data.frame(df)
df$FUT <- 0:4
## with breaks list
setaggre(df, values = c("obs", "pyrs"), by = "sex", breaks = list(FUT = 0:5))
```

---

setclass	<i>Set the class of an object (convenience function for <code>setattr(obj, "class", CLASS)</code>); can add instead of replace</i>
----------	--

---

**Description**

Sets the class of an object in place to `cl` by replacing or adding

**Usage**

```
setclass(obj, cl, add = FALSE, add.place = "first")
```

**Arguments**

<code>obj</code>	and object for which to set class
<code>cl</code>	class to set
<code>add</code>	if TRUE, adds <code>cl</code> to the classes of the <code>obj</code> ; otherwise replaces the class information
<code>add.place</code>	"first" or "last"; adds <code>cl</code> to the front or to the back of the <code>obj</code> 's class vector

**Author(s)**

Joonas Miettinen

---

`setcolsnull`*Delete data.table columns if there*

---

**Description**

Deletes columns in a `data.table` conveniently. May only delete columns that are found silently. Sometimes useful in e.g. `on.exit` expressions.

**Usage**

```
setcolsnull(  
  DT = NULL,  
  delete = NULL,  
  keep = NULL,  
  colorder = FALSE,  
  soft = TRUE  
)
```

**Arguments**

<code>DT</code>	a <code>data.table</code>
<code>delete</code>	a character vector of column names to be deleted
<code>keep</code>	a character vector of column names to keep; the rest will be removed; <code>keep</code> overrides <code>delete</code>
<code>colorder</code>	logical; if <code>TRUE</code> , also does <code>setcolorder</code> using <code>keep</code>
<code>soft</code>	logical; if <code>TRUE</code> , does not cause an error if any variable name in <code>keep</code> or <code>delete</code> is missing; <code>soft = FALSE</code> useful for programming sometimes

**Value**

Always returns `'NULL'` invisibly. This function is called for its side effects.

**Author(s)**

Joonas Miettinen



---

sibr

*sibr - a simulated cohort of Finnish female breast cancer patients*

---

### Description

sibr is a simulated cohort pertaining female Finnish breast cancer patients diagnosed between 1993-2012. Instead of actual original dates, the dates are masked via modest randomization within several time windows. The dataset is additionally a random sample of 10 000 cases from the pertaining time window.

### Format

data.table with columns

- sex - gender of the patient (1 = female)
- bi\_date - date of birth
- dg\_date - date of cancer diagnosis
- ex\_date - date of exit from follow-up (death or censoring)
- status - status of the person at exit; 0 alive; 1 dead due to pertinent cancer; 2 dead due to other causes
- dg\_age - age at diagnosis expressed as fractional years

### Details

The closing date for the pertinent data was 2012-12-31, meaning status information was available only up to that point — hence the maximum possible ex\_date is 2012-12-31.

### Author(s)

Karri Seppa

### Source

The Finnish Cancer Registry

### See Also

Other popEpi data: [ICSS](#), [meanpop\\_fi](#), [popmort](#), [sire](#), [stdpop101](#), [stdpop18](#)

Other survival data: [sire](#)

sir

*Calculate SIR or SMR***Description**

Poisson modelled standardised incidence or mortality ratios (SIRs / SMRs) i.e. indirect method for calculating standardised rates. SIR is a ratio of observed and expected cases. Expected cases are derived by multiplying the strata-specific population rate with the corresponding person-years of the cohort.

**Usage**

```

sir(
  coh.data,
  coh.obs,
  coh.pyrs,
  ref.data = NULL,
  ref.obs = NULL,
  ref.pyrs = NULL,
  ref.rate = NULL,
  subset = NULL,
  print = NULL,
  adjust = NULL,
  mstate = NULL,
  test.type = "homogeneity",
  conf.type = "profile",
  conf.level = 0.95,
  EAR = FALSE
)

```

**Arguments**

coh.data	aggregated cohort data, see e.g. <a href="#">lexpand</a>
coh.obs	variable name for observed cases; quoted or unquoted. A vector when using <code>mstata</code> .
coh.pyrs	variable name for person years in cohort data; quoted (as a string 'myvar') or unquoted (AKA as a name; myvar)
ref.data	population data. Can be left NULL if coh.data is stratified in print. See <a href="#">pophaz</a> for details.
ref.obs	variable name for observed cases; quoted or unquoted
ref.pyrs	variable name for person-years in population data; quoted or unquoted
ref.rate	population rate variable (cases/person-years). Overwrites arguments ref.pyrs and ref.obs. Quoted or unquoted
subset	logical condition to select data from coh.data before any computations

<code>print</code>	variable names to stratify results; quoted vector or unquoted named list with functions
<code>adjust</code>	variable names for adjusting without stratifying output; quoted vector or unquoted list
<code>mstate</code>	set column names for cause specific observations; quoted or unquoted. Relevant only when <code>coh.obs</code> length is two or more. See details.
<code>test.type</code>	Test for equal SIRs. Test available are 'homogeneity' and 'trend'.
<code>conf.type</code>	Confidence interval type: 'profile'(=default), 'wald' or 'univariate'.
<code>conf.level</code>	Level of type-I error in confidence intervals, default 0.05 is 95% CI.
<code>EAR</code>	logical; TRUE calculates Excess Absolute Risks for univariate SIRs. (see details)

## Details

`sir` is a comprehensive tool for modelling SIRs/SMRs with flexible options to adjust and print SIRs, test homogeneity and utilize multi-state data. The cohort data and the variable names for observation counts and person-years are required. The reference data is optional, since the cohort data can be stratified (`print`) and compared to total.

### Adjust and print

A SIR can be adjusted or standardised using the covariates found in both `coh.data` and `ref.data`. Variable to adjust are given in `adjust`. Variable names needs to match in both `coh.data` and `ref.data`. Typical variables to adjust by are gender, age group and calendar period.

`print` is used to stratify the SIR output. In other words, the variables assigned to `print` are the covariates of the Poisson model. Variable levels are treated as categorical. Variables can be assigned in both `print` and `adjust`. This means the output it adjusted and printed by these variables.

`print` can also be a list of expressions. This enables changing variable names or transforming variables with functions such as `cut` and `round`. For example, the existing variables `agegroup` and `year` could be transformed to new levels using `cut` by

```
print = list( age.category = cut(agegroup,breaks = c(0,50,75,100)),year.cat = cut(year,seq(1950,2010,20))
```

### ref.rate or ref.obs & ref.pyrs

The population rate variable can be given to the `ref.rate` parameter. That is, when using e.g. the `popmort` or a comparable data file, one may supply `ref.rate` instead of `ref.obs` and `ref.pyrs`, which will be ignored if `ref.rate` is supplied.

Note that if all the stratifying variables in `ref.data` are not listed in `adjust`, or when the categories are otherwise combined, the (unweighted) mean of rates is used for computing expected cases. This might incur a small bias in comparison to when exact numbers of observations and person-years are available.

### mstate

E.g. using `lexpand` it's possible to compute counts for several outcomes so that the population at risk is same for each outcome such as a certain kind of cancer. The transition counts are in wide data format, and the relevant columns can be supplied to `sir` in a vector via the `coh.obs` argument. The name of the corresponding new column in `ref.data` is given in `mstate`. It's recommended to include the `mstate` variable in `adjust`, so the corresponding information should also be available in `ref.data`. More examples in `sir-vignette`.

This approach is analogous to where SIRs are calculated separately their own function calls.

### Other parameters

univariate confidence intervals are calculated using exact Poisson intervals (`poisson.ci`). The options `profile` and `wald` are based on a Poisson regression model: profile-likelihood confidence intervals or Wald's normal-approximation. P-value is Poisson model based `conf.type` or calculated using the method described by Breslow and Day. Function automatically switches to another `conf.type` if calculation is not possible with a message. Usually model fit fails if there is print stratum with zero expected values.

The LRT p-value tests the levels of `print`. The test can be either "homogeneity", a likelihood ratio test where the model variables defined in `print` (factor) is compared to the constant model. Option "trend" tests if the linear trend of the continuous variable in `print` is significant (using model comparison).

### EAR: Excess Absolute Risk

Excess Absolute Risk is a simple way to quantify the absolute difference between cohort risk and population risk. Make sure that the person-years are calculated accordingly before using EAR. (when using `mstate`)

Formula for EAR:

$$EAR = \frac{\text{observed} - \text{expected}}{\text{personyears}} \times 1000.$$

### Data format

The data should be given in tabulated format. That is the number of observations and person-years are represented for each stratum. Note that also individual data is allowed as long as each observations, person-years, and `print` and `adjust` variables are presented in columns. The extra variables and levels are reduced automatically before estimating SIRs. Example of data format:

sex	age	period	obs	pyrs
0	1	2010	0	390
0	2	2010	5	385
1	1	2010	3	308
1	2	2010	12	315

### Value

A `sir`-object that is a `data.table` with meta information in the attributes.

### Author(s)

Matti Rantanen, Joonas Miettinen

### See Also

[lexpand A SIR calculation vignette](#)

Other `sir` functions: `lines.sirspline()`, `plot.sirspline()`, `sir_exp()`, `sir_ratio()`, `sirspline()`

Other main functions: `Surv()`, `rate()`, `relpois_ag()`, `relpois()`, `sirspline()`, `survmean()`, `survtab_ag()`, `survtab()`

## Examples

```

data(popmort)
data(sire)
c <- leexpand( sire, status = status, birth = bi_date, exit = ex_date, entry = dg_date,
              breaks = list(per = 1950:2013, age = 1:100, fot = c(0,10,20,Inf)),
              aggre = list(fot, agegroup = age, year = per, sex) )
## SMR due other causes: status = 2
se <- sir( coh.data = c, coh.obs = 'from0to2', coh.pyrs = 'pyrs',
          ref.data = popmort, ref.rate = 'haz',
          adjust = c('agegroup', 'year', 'sex'), print = 'fot')
se
## for examples see: vignette('sir')

```

---

sire

*sire - a simulated cohort of Finnish female rectal cancer patients*


---

## Description

sire is a simulated cohort pertaining female Finnish rectal cancer patients diagnosed between 1993-2012. Instead of actual original dates, the dates are masked via modest randomization within several time windows.

## Format

data.table with columns

- sex - gender of the patient (1 = female)
- bi\_date - date of birth
- dg\_date - date of cancer diagnosis
- ex\_date - date of exit from follow-up (death or censoring)
- status - status of the person at exit; 0 alive; 1 dead due to pertinent cancer; 2 dead due to other causes
- dg\_age - age at diagnosis expressed as fractional years

## Details

The closing date for the pertinent data was 2012-12-31, meaning status information was available only up to that point — hence the maximum possible ex\_date is 2012-12-31.

## Author(s)

Karri Seppa

## Source

The Finnish Cancer Registry

**See Also**

Other popEpi data: [ICSS](#), [meanpop\\_fi](#), [popmort](#), [sibr](#), [stdpop101](#), [stdpop18](#)

Other survival data: [sibr](#)

---

 sir spline

---

*Estimate splines for SIR or SMR*


---

**Description**

Splines for standardised incidence or mortality ratio. A useful tool to e.g. check whether a constant SIR can be assumed for all calendar periods, age groups or follow-up intervals. Splines can be fitted for these time dimensions separately or in the same model.

**Usage**

```

sir spline(
  coh.data,
  coh.obs,
  coh.pyrs,
  ref.data = NULL,
  ref.obs = NULL,
  ref.pyrs = NULL,
  ref.rate = NULL,
  subset = NULL,
  print = NULL,
  adjust = NULL,
  mstate = NULL,
  spline,
  knots = NULL,
  reference.points = NULL,
  dependent.splines = TRUE
)

```

**Arguments**

coh.data	cohort data with observations and at risk time variables
coh.obs	variable name for observed cases
coh.pyrs	variable name for person-years in cohort data
ref.data	aggregated population data
ref.obs	variable name for observed cases
ref.pyrs	variable name for person-years in population data
ref.rate	population rate observed/expected. This overwrites the parameters ref.pyrs and ref.obs.
subset	logical condition to subset coh.data before any computations

<code>print</code>	variable names for which to estimate SIRs/SMRs and associated splines separately
<code>adjust</code>	variable names for adjusting the expected cases
<code>mstate</code>	set column names for cause specific observations. Relevant only when <code>coh.obs</code> length is two or more. See help for <code>sir</code> .
<code>spline</code>	variable name(s) for the splines
<code>knots</code>	number knots (vector), pre-defined knots (list of vectors) or for optimal number of knots left NULL
<code>reference.points</code>	fixed reference values for rate ratios. If left NULL the smallest value is the reference point (where SIR = 1). Ignored if <code>dependent.splines = FALSE</code>
<code>dependent.splines</code>	logical; if TRUE, all splines are fitted in same model.

## Details

See [sir](#) for help on SIR/SMR estimation in general; usage of splines is discussed below.

### The spline variables

The model can include one, two or three splines variables. Variables can be included in the same model selecting `dependent.splines = TRUE` and SIR ratios are calculated (first one is the SIR, others SIR ratios). Reference points vector can be set via `reference.points` where first element of the vector is the reference point for first ratio.

Variable(s) to fit splines are given as a vector in argument `spline`. Order will affect the results.

### dependent.splines

By default `dependent.splines` is FALSE and all splines are fitted in separate models. If TRUE, the first variable in `spline` is a function of a SIR and other(s) are ratios.

### knots

There are three options to set knots to splines:

Set the number of knots for each spline variable with a **vector**. The knots are automatically placed to the quantiles of observed cases in cohort data. The first and last knots are always the maximum and minimum values, so knot value needs to be at least two.

Predefined knot places can be set with a **list** of vectors. The vector for each spline in the list specifies the knot places. The lowest and the largest values are the boundary knots and these should be checked beforehand.

If `knots` is left **NULL**, the model searches the optimal number of knots by model AIC by fitting models iteratively from 2 to 15 knots and the one with smallest AIC is selected. If `dependent.splines = TRUE`, the number of knots is searched by fitting each spline variable separately.

### print

Splines can be stratified by the levels of variable given in `print`. If `print` is a vector, only the first variable is accounted for. The knots are placed globally for all levels of `print`. This also ensures that the likelihood ratio test is valid. Splines are also fitted independently for each level of `print`. This allows for searching interactions, e.g. by fitting spline for period (`splines='period'`) for each age group (`print = 'agegroup'`).

**p-values**

The output p-value is a test of whether the splines are equal (homogenous) at different levels of print. The test is based on the likelihood ratio test, where the full model includes print and is compared to a null model without it. When (dependent.splines = TRUE) the p-value returned is a global p-value. Otherwise the p-value is spline-specific.

**Value**

A list of data.frames and vectors. Three spline estimates are named as spline.est.A/B/C and the corresponding values in spline.seq.A/B/C for manual plotting

**Author(s)**

Matti Rantanen, Joonas Miettinen

**See Also**

[splitMulti](#) [A SIR calculation vignette](#)

Other sir functions: [lines.sirspline\(\)](#), [plot.sirspline\(\)](#), [sir\\_exp\(\)](#), [sir\\_ratio\(\)](#), [sir\(\)](#)

Other main functions: [Surv\(\)](#), [rate\(\)](#), [relpois\\_ag\(\)](#), [relpois\(\)](#), [sir\(\)](#), [survmean\(\)](#), [survtab\\_ag\(\)](#), [survtab\(\)](#)

**Examples**

```
## for examples see: vignette('sir')
```

---

sir\_exp

*Calculate SMR*

---

**Description**

Calculate Standardized Mortality Ratios (SMRs) using a single data set that includes observed and expected cases and additionally person-years.

sir\_lex solves SMR from a [Lexis](#) object calculated with [lexpand](#).

sir\_ag solves SMR from a [aggre](#) object calculated using [lexpand](#).

**Usage**

```
sir_exp(  
  x,  
  obs,  
  exp,  
  pyrs = NULL,  
  print = NULL,
```



```

    conf.type = "profile",
    test.type = "homogeneity",
    conf.level = 0.95,
    subset = NULL
  )

sir_lex(x, print = NULL, breaks = NULL, ...)

sir_ag(
  x,
  obs = "from0to1",
  print = attr(x, "aggre.meta")$by,
  exp = "d.exp",
  pyrs = "pyrs",
  ...
)

```

### Arguments

x	Data set e.g. aggre or Lexis object (see: <a href="#">lexpand</a> )
obs	Variable name of the observed cases in the data set
exp	Variable name or expression for expected cases
pyrs	Variable name for person-years (optional)
print	Variables or expression to stratify the results
conf.type	select confidence interval type: (default=) 'profile', 'wald', 'univariate'
test.type	Test for equal SIRs. Test available are 'homogeneity' and 'trend'
conf.level	Level of type-I error in confidence intervals, default 0.05 is 95% CI
subset	a logical vector for subsetting data
breaks	a named list to split age group (age), period (per) or follow-up (fot).
...	pass arguments to sir_exp

### Details

These functions are intended to calculate SMRs from a single data set that includes both observed and expected number of cases. For example utilizing the argument `pop.haz` of the [lexpand](#).

`sir_lex` automatically exports the transition from X to Y using the first state in `lex.Str` as 0 and all other as 1. No missing values is allowed in observed, `pop.haz` or person-years.

### Value

A sir object

### Functions

- `sir_lex`:
- `sir_ag`:

**Author(s)**

Matti Rantanen

**See Also**[lexpand A SIR calculation vignette](#)Other sir functions: [lines.sirspline\(\)](#), [plot.sirspline\(\)](#), [sir\\_ratio\(\)](#), [sirspline\(\)](#), [sir\(\)](#)**Examples**

```
BL <- list(fot = 0:5, per = c("2003-01-01", "2008-01-01", "2013-01-01"))

## Aggregated data
x1 <- lexpand(sire, breaks = BL, status = status != 0,
             birth = bi_date, entry = dg_date, exit = ex_date,
             pophaz=popmort,
             aggre=list(sex, period = per, surv.int = fot))
sir_ag(x1, print = 'period')

# no aggregate or breaks
x2 <- lexpand(sire, status = status != 0,
             birth = bi_date, entry = dg_date, exit = ex_date,
             pophaz=popmort)
sir_lex(x2, breaks = BL, print = 'per')
```

---

`sir_ratio`*Confidence intervals for the ratio of two SIRs/SMRs*

---

**Description**

Calculate ratio of two SIRs/SMRs and the confidence intervals of the ratio.

**Usage**

```
sir_ratio(
  x,
  y,
  digits = 3,
  alternative = "two.sided",
  conf.level = 0.95,
  type = "exact"
)
```

**Arguments**

x	a sir-object or a vector of two; observed and expected cases.
y	a sir-object or a vector of two; observed and expected cases.
digits	number of digits in the output
alternative	The null-hypothesis test: (default:) two.sided, less, greater
conf.level	the type-I error in confidence intervals, default 0.95 for 95% CI.
type	How the binomial confidence intervals are calculated (default:) exact or asymptotic.

**Details**

Function works with pooled sir-objects i.e. the print argument in sir is ignored. Also x and y can be a vector of two where first index is the observed cases and second is expected cases (see examples). Note that the ratio of two SIR's is only applicable when the age distributions are similar in both populations.

**Formula**

The observed number of first sir  $O_1$  is considered as a Binomial variable with sample size of  $O_1+O_2$ . The confidence intervals for Binomial proportion A is solved using exact or asymptotic method. Now the CI for ratio  $O_1/O_2$  is  $B = A/(1 - A)$ . And further the CI for SIR/SMR is  $B * E_2/E_1$ . (Ederer and Mantel)

**Value**

A vector length of three: sir\_ratio, and lower and upper confidence intervals.

**Note**

Parameter alternative is always two.sided when parameter type is set to asymptotic.

**Author(s)**

Matti Rantanen

**References**

Statistics with Confidence: Confidence Intervals and Statistical Guidelines, Douglas Altman, 2000. ISBN: 978-0-727-91375-3

**See Also**

[sir](#) [A SIR calculation vignette](#)

Other sir functions: [lines.sirspline\(\)](#), [plot.sirspline\(\)](#), [sir\\_exp\(\)](#), [sirspline\(\)](#), [sir\(\)](#)

## Examples

```
## Ratio for sir-object and the same values given manually:

## create example dataset
dt1 <- data.frame(obs = rep(c(5,7), 10),
                  pyrs = rep(c(250,300,350,400), 5),
                  var = 1:20)
Ref <- data.frame(obs = rep(c(50,70,80,100), 5),
                  pyrs = rep(c(2500,3000,3500,4000), 5),
                  var = 1:20)
## sir using the function
s1 <- sir(coh.data = dt1, coh.obs = obs, coh.pyrs = pyrs,
          ref.data = Ref, ref.obs = obs, ref.pyrs = pyrs,
          adjust = var)

## Ratio is simply 1:
sir_ratio(s1, c(120, 150))
```

---

splitLexisDT

*Split case-level observations*

---

## Description

Split a Lexis object along one time scale (as [splitLexis](#)) with speed

## Usage

```
splitLexisDT(lex, breaks, timeScale, merge = TRUE, drop = TRUE)
```

## Arguments

lex	a Lexis object, split or not
breaks	a vector of [a,b) breaks to split data by
timeScale	a character string; name of the time scale to split by
merge	logical; if TRUE, retains all variables from the original data - i.e. original variables are repeated for all the rows by original subject
drop	logical; if TRUE, drops all resulting rows after expansion that reside outside the time window defined by the given breaks

## Details

splitLexisDT is in essence a **data.table** version of [splitLexis](#) or [survSplit](#) for splitting along a single time scale. It requires a Lexis object as input, which may have already been split along some time scale.

Unlike `splitLexis`, `splitLexisDT` drops observed time outside the roof and floor of breaks by default - with `drop = FALSE` the functions have identical behaviour.

The Lexis time scale variables can be of any arbitrary format, e.g. Date, fractional years (see `cal.yr`) and `get.yrs`, or other. However, using date variables (from package **date**) are not recommended, as date variables are always stored as integers, whereas Date variables (see `?as.Date`) are typically stored in double ("numeric") format. This allows for breaking days into fractions as well, when using e.g. hypothetical years of 365.25 days.

### Value

A `data.table` or `data.frame` (depending on options(`"popEpi.datatable"`)); see `?popEpi` object expanded to accommodate split observations.

### Author(s)

Joonas Miettinen

### See Also

Other splitting functions: `lexpand()`, `splitMulti()`

### Examples

```
library(Epi)
data("sire", package = "popEpi")
x <- Lexis(data=sire[1000:1100, ],
           entry = list(fot=0, per=get.yrs(dg_date), age=dg_age),
           exit=list(per=get.yrs(ex_date)), exit.status=status)
BL <- list(fot=seq(0, 5, by = 3/12), per=c(2008, 2013))

x2 <- splitMulti(x, breaks = BL, drop = FALSE)

x3 <- splitLexisDT(x, breaks = BL$fot, timeScale = "fot", drop = FALSE)
x3 <- splitLexisDT(x3, breaks = BL$per, timeScale = "per", drop = FALSE)

x4 <- splitLexis(x, breaks = BL$fot, time.scale = "fot")
x4 <- splitLexis(x4, breaks = BL$per, time.scale = "per")
## all produce identical results

## using Date variables
x <- Lexis(data=sire[1000:1100, ],
           entry = list(fot=0, per=dg_date, age=dg_date-bi_date),
           exit=list(per=ex_date), exit.status=status)
BL <- list(fot = 0:5*365.25, per = as.Date(c("2008-01-01", "2013-01-01")))

x2 <- splitMulti(x, breaks = BL, drop = FALSE)

x3 <- splitLexisDT(x, breaks = BL$fot, timeScale = "fot", drop = FALSE)
x3 <- splitLexisDT(x3, breaks = BL$per, timeScale = "per", drop = FALSE)

## splitLexis may not work when using Dates
```

splitMulti

*Split case-level observations***Description**

Split a Lexis object along multiple time scales with speed and ease

**Usage**

```
splitMulti(
  data,
  breaks = NULL,
  ...,
  drop = TRUE,
  merge = TRUE,
  verbose = FALSE
)
```

**Arguments**

data	a Lexis object with event cases as rows
breaks	a list of named numeric vectors of breaks; see Details and Examples
...	alternate way of supplying breaks as named vectors; e.g. fot = 0:5 instead of breaks = list(fot = 0:5); if breaks is not NULL, breaks is used and any breaks passed through ... are NOT used; note also that due to partial matching of argument names in R, if you supply e.g. dat = my_breaks and you do not pass argument data explicitly (data = my_data), then R interprets this as data = my_breaks — so choose the names of your time scales wisely
drop	logical; if TRUE, drops all resulting rows after expansion that reside outside the time window defined by the given breaks
merge	logical; if TRUE, retains all variables from the original data - i.e. original variables are repeated for all the rows by original subject
verbose	logical; if TRUE, the function is chatty and returns some messages along the way

**Details**

splitMulti is in essence a **data.table** version of splitLexis or survSplit for splitting along multiple time scales. It requires a Lexis object as input.

The breaks must be a list of named vectors of the appropriate type. The breaks are fully explicit and left-inclusive and right exclusive, e.g. fot=c(0, 5) forces the data to only include time between [0, 5) for each original row (unless drop = FALSE). Use Inf or -Inf for open-ended intervals, e.g. per=c(1990, 1995, Inf) creates the intervals [1990, 1995), [1995, Inf).

Instead of specifying breaks, one may make use of the ... argument to pass breaks: e.g.

```
splitMulti(x, breaks = list(fot = 0:5))
```

is equivalent to

```
splitMulti(x, fot = 0:5).
```

Multiple breaks can be supplied in the same manner. However, if both breaks and ... are used, only the breaks in breaks are utilized within the function.

The Lexis time scale variables can be of any arbitrary format, e.g. Date, fractional years (see [cal.yr](#)) and [get.yrs](#), or other. However, using date variables (from package **date**) are not recommended, as date variables are always stored as integers, whereas Date variables (see `?as.Date`) are typically stored in double ("numeric") format. This allows for breaking days into fractions as well, when using e.g. hypothetical years of 365.25 days.

### Value

A data.table or data.frame (depending on options("popEpi.datatable")); see `?popEpi` object expanded to accommodate split observations.

### Author(s)

Joonas Miettinen

### See Also

[splitLexis](#), [Lexis](#), [survSplit](#)

Other splitting functions: [lexexpand\(\)](#), [splitLexisDT\(\)](#)

### Examples

```
#### let's prepare data for computing period method survivals
#### in case there are problems with dates, we first
#### convert to fractional years.

library("Epi")
library("data.table")
data("sire", package = "popEpi")
x <- Lexis(data=sire[dg_date < ex_date, ],
           entry = list(fot=0, per=get.yrs(dg_date), age=dg_age),
           exit=list(per=get.yrs(ex_date)), exit.status=status)
x2 <- splitMulti(x, breaks = list(fot=seq(0, 5, by = 3/12), per=c(2008, 2013)))
# equivalently:
x2 <- splitMulti(x, fot=seq(0, 5, by = 3/12), per=c(2008, 2013))

## using dates; note: breaks must be expressed as dates or days!
x <- Lexis(data=sire[dg_date < ex_date, ],
           entry = list(fot=0, per=dg_date, age=dg_date-bi_date),
           exit=list(per=ex_date), exit.status=status)
BL <- list(fot = seq(0, 5, by = 3/12)*365.242199,
           per = as.Date(paste0(c(1980:2014), "-01-01")),
           age = c(0,45,85,Inf)*365.242199)
x2 <- splitMulti(x, breaks = BL, verbose=TRUE)
```

```

## multistate example (healthy - sick - dead)
sire2 <- data.frame(sire)
sire2 <- sire2[sire2$dg_date < sire2$ex_date, ]

set.seed(1L)
not_sick <- sample.int(nrow(sire2), 6000L, replace = FALSE)
sire2$dg_date[not_sick] <- NA
sire2$status[!is.na(sire2$dg_date) & sire2$status == 0] <- -1

sire2$status[sire2$status==2] <- 1
sire2$status <- factor(sire2$status, levels = c(0, -1, 1),
                      labels = c("healthy", "sick", "dead"))

xm <- Lexis(data = sire2,
            entry = list(fot=0, per=get.yrs(bi_date), age=0),
            exit = list(per=get.yrs(ex_date)), exit.status=status)
xm2 <- cutLexis(xm, cut = get.yrs(xm$dg_date),
               timescale = "per",
               new.state = "sick")
xm2[xm2$lex.id == 6L, ]

xm2 <- splitMulti(xm2, breaks = list(fot = seq(0,150,25)))
xm2[xm2$lex.id == 6L, ]

```

---

stdpop101	<i>World standard population by 1 year age groups from 1 to 101. Sums to 100 000.</i>
-----------	---

---

## Description

World standard population by 1 year age groups from 1 to 101. Sums to 100 000.

## Format

data.table with columns

- world\_std weight that sums to 100000 (numeric)
- agegroup age group from 1 to 101 (numeric)

## Source

Standard population is from: [world standard population "101of1"](#)

## See Also

Other popEpi data: [ICSS](#), [meanpop\\_fi](#), [popmort](#), [sibr](#), [sire](#), [stdpop18](#)

Other weights: [ICSS](#), [direct\\_standardization](#), [stdpop18](#)



---

stdpop18	<i>Standard populations from 2000: world, Europe and Nordic.</i>
----------	--

---

**Description**

World, European, and Nordic standard populations by 18 age categories. Sums to 100000.

**Format**

data.table with columns

- agegroup, age group in 18 categories (character)
- world, World 2000 standard population (numeric)
- europe, European standard population (numeric)
- nordic, Nordic standard population (numeric)

**Source**

Nordcan, 2000

**See Also**

Other popEpi data: [ICSS](#), [meanpop\\_fi](#), [popmort](#), [sibr](#), [sire](#), [stdpop101](#)

Other weights: [ICSS](#), [direct\\_standardization](#), [stdpop101](#)

---

summary.aggre	<i>Summarize an aggre Object</i>
---------------	----------------------------------

---

**Description**

summary method function for aggre objects; see [as.aggre](#) and [aggre](#).

**Usage**

```
## S3 method for class 'aggre'
summary(object, by = NULL, subset = NULL, ...)
```

**Arguments**

object	an aggre object
by	list of columns to summarize by - e.g. <code>list(V1,V2)</code> where V1 and V2 are columns in the data.
subset	a logical condition to subset results table by before summarizing; use this to limit to a certain stratum. E.g. <code>subset = sex == "male"</code>
...	unused

**Value**

Returns a ‘data.table’ — a further aggregated version of ‘object’.

**Author(s)**

Joonas Miettinen

**See Also**

Other aggregation functions: [aggre\(\)](#), [as.aggre\(\)](#), [lexpand\(\)](#), [setaggre\(\)](#)

---

summary.survtab	<i>Summarize a survtab Object</i>
-----------------	-----------------------------------

---

**Description**

Summary method function for survtab objects; see [survtab\\_ag](#). Returns estimates at given time points or all time points if `t` and `q` are both NULL.

**Usage**

```
## S3 method for class 'survtab'
summary(object, t = NULL, subset = NULL, q = NULL, ...)
```

**Arguments**

<code>object</code>	a survtab object
<code>t</code>	a vector of times at which time points (actually intervals that contain <code>t</code> ) to print summary table of survival function estimates by strata; values not existing in any interval cause rows containing only NAs to be returned.
<code>subset</code>	a logical condition to subset results table by before printing; use this to limit to a certain stratum. E.g. <code>subset = sex == "male"</code>
<code>q</code>	a named list of quantiles to include in returned data set, where names must match to estimates in <code>object</code> ; returns intervals where the quantiles are reached first; e.g. <code>list(surv.obs = 0.5)</code> finds the interval where <code>surv.obs</code> is 0.45 and 0.55 at the beginning and end of the interval, respectively; returns rows with NA values for quantiles not reached in estimates (e.g. if <code>q = list(surv.obs = 0.5)</code> but lowest estimate is 0.6); see Examples.
<code>...</code>	unused; required for congruence with other summary methods

**Details**

Note that this function returns the intervals and NOT the time points corresponding to quantiles / estimates corresponding to time points. If you want precise estimates at time points that are not interval breaks, add the time points as breaks and re-estimate the survival time function. In interval-based estimation, the estimates denote e.g. probability of dying *during* the interval, so time points within the intervals are not usually considered at all. See e.g. Seppa, Dyba, and Hakulinen (2015).

**Value**

A 'data.table': a slice from 'object' based on 't', 'subset', and 'q'.

**Author(s)**

Joonas Miettinen

**References**

Seppa K., Dyba T. and Hakulinen T.: Cancer Survival, Reference Module in Biomedical Sciences. Elsevier. 08-Jan-2015. doi: [10.1016/B9780128012383.027458](https://doi.org/10.1016/B9780128012383.027458)

**See Also**

Other survtab functions: [Surv\(\)](#), [lines.survtab\(\)](#), [plot.survtab\(\)](#), [print.survtab\(\)](#), [survtab\\_ag\(\)](#), [survtab\(\)](#)

**Examples**

```
library(Epi)

## NOTE: recommended to use factor status variable
x <- Lexis(entry = list(FUT = 0, AGE = dg_age, CAL = get.yrs(dg_date)),
          exit = list(CAL = get.yrs(ex_date)),
          data = sire[sire$dg_date < sire$ex_date, ],
          exit.status = factor(status, levels = 0:2,
                               labels = c("alive", "canD", "othD")),
          merge = TRUE)
## pretend some are male
set.seed(1L)
x$sex <- rbinom(nrow(x), 1, 0.5)
## observed survival
st <- survtab(Surv(time = FUT, event = lex.Xst) ~ sex, data = x,
              surv.type = "cif.obs",
              breaks = list(FUT = seq(0, 5, 1/12)))

## estimates at full years of follow-up
summary(st, t = 1:5)

## interval estimate closest to 75th percentile, i.e.
## first interval where surv.obs < 0.75 at end
## (just switch 0.75 to 0.5 for median survival, etc.)
summary(st, q = list(surv.obs = 0.75))
## multiple quantiles
summary(st, q = list(surv.obs = c(0.75, 0.90), CIF_canD = 0.20))

## if you want all estimates in a new data.frame, you can also simply do
x <- as.data.frame(st)
```

**Description**

Wrapper for [survival::Surv](#).

**Usage**

```
Surv(
  time,
  time2,
  event,
  type = c("right", "left", "interval", "counting", "interval2", "mstate"),
  origin = 0
)
```

**Arguments**

time	see <a href="#">survival::Surv</a>
time2	see <a href="#">survival::Surv</a>
event	see <a href="#">survival::Surv</a>
type	see <a href="#">survival::Surv</a>
origin	see <a href="#">survival::Surv</a>

**Value**

See [[survival::Surv](#)].

**Surv in survival vs. in popEpi**

`popEpi::Surv` is a wrapper for [survival::Surv](#). Therefore you don't need to do `library("survival")` when using `Surv` with e.g. [survtab](#). Remember that if you do `library("survival")` after `library("popEpi")`, the `Surv` from **survival** is used instead of from **popEpi** (R throws a warning about this) when an expression such as `Surv(my_times,my_events)` is evaluated. You can avoid such conflicts by writing e.g. `popEpi::Surv(my_times,my_events)` instead. However, `popEpi::Surv` is designed in such a way that this should not become a problem and you should be able to use the two interchangeably.

**See Also**

Other main functions: [rate\(\)](#), [relpois\\_ag\(\)](#), [relpois\(\)](#), [sirspline\(\)](#), [sir\(\)](#), [survmean\(\)](#), [survtab\\_ag\(\)](#), [survtab\(\)](#)

Other `survtab` functions: [lines.survtab\(\)](#), [plot.survtab\(\)](#), [print.survtab\(\)](#), [summary.survtab\(\)](#), [survtab\\_ag\(\)](#), [survtab\(\)](#)

Other `survmean` functions: [lines.survmean\(\)](#), [plot.survmean\(\)](#), [survmean\(\)](#)

survmean

*Compute Mean Survival Times Using Extrapolation***Description**

Computes mean survival times based on survival estimation up to a point in follow-up time (e.g. 10 years), after which survival is extrapolated using an appropriate hazard data file (pophaz) to yield the "full" survival curve. The area under the full survival curve is the mean survival.

**Usage**

```
survmean(
  formula,
  data,
  adjust = NULL,
  weights = NULL,
  breaks = NULL,
  pophaz = NULL,
  e1.breaks = NULL,
  e1.pophaz = pophaz,
  r = "auto",
  surv.method = "hazard",
  subset = NULL,
  verbose = FALSE
)
```

**Arguments**

formula	a formula, e.g. <code>FUT ~ V1</code> or <code>Surv(FUT, lex.Xst) ~ V1</code> . Supplied in the same way as to <a href="#">survtab</a> , see that help for more info.
data	a Lexis data set; see <a href="#">Lexis</a> .
adjust	variables to adjust estimates by, e.g. <code>adjust = "agegr"</code> . <a href="#">Flexible input</a> .
weights	weights to use to adjust mean survival times. See the <a href="#">dedicated help page</a> for more details on weighting. <code>survmean</code> computes curves separately by all variables to adjust by, computes mean survival times, and computes weighted means of the mean survival times. See Examples.
breaks	a list of breaks defining the time window to compute observed survival in, and the intervals used in estimation. E.g. <code>list(FUT = 0:10)</code> when FUT is the follow-up time scale in your data.
pophaz	a data set of population hazards passed to <a href="#">survtab</a> (see the <a href="#">dedicated help page</a> and the help page of <code>survtab</code> for more information). Defines the population hazard in the time window where observed survival is estimated.
e1.breaks	NULL or a list of breaks defining the time window to compute <b>expected</b> survival in, and the intervals used in estimation. E.g. <code>list(FUT = 0:100)</code> when FUT is the follow-up time scale in your data to extrapolate up to 100 years from where

	the observed survival curve ends. <b>NOTE:</b> the breaks on the survival time scale <b>MUST</b> include the breaks supplied to argument breaks; see Examples. If NULL, uses decent defaults (maximum follow-up time of 50 years).
e1.pophaz	Same as pophaz, except this defines the population hazard in the time window where <b>expected</b> survival is estimated. By default uses the same data as argument pophaz.
r	either a numeric multiplier such as 0.995, "auto", or "autoX" where X is an integer; used to determine the relative survival ratio (RSR) persisting after where the estimated observed survival curve ends. See Details.
surv.method	passed to survtab; see that help for more info.
subset	a logical condition; e.g. subset = sex == 1; subsets the data before computations
verbose	logical; if TRUE, the function is returns some messages and results along the run, which may be useful in debugging

## Details

### Basics

survmean computes mean survival times. For median survival times (i.e. where 50 use [survtab](#)).

The mean survival time is simply the area under the survival curve. However, since full follow-up rarely happens, the observed survival curves are extrapolated using expected survival: E.g. one might compute observed survival till up to 10 years and extrapolate beyond that (till e.g. 50 years) to yield an educated guess on the full observed survival curve.

The area is computed by trapezoidal integration of the area under the curve. This function also computes the "full" expected survival curve from T = 0 till e.g. T = 50 depending on supplied arguments. The expected mean survival time is the area under the mean expected survival curve. This function returns the mean expected survival time to be compared with the mean survival time and for computing years of potential life lost (YPLL).

Results can be formed by strata and adjusted for e.g. age by using the formula argument as in survtab. See also Examples.

### Extrapolation tweaks

Argument r controls the relative survival ratio (RSR) assumed to persist beyond the time window where observed survival is computed (defined by argument breaks; e.g. up to FUT = 10). The RSR is simply  $RSR_i = p_{oi} / p_{ei}$  for a time interval i, i.e. the observed divided by the expected (conditional, not cumulative) probability of surviving from the beginning of a time interval till its end. The cumulative product of RSR\_i over time is the (cumulative) relative survival curve.

If r is numeric, e.g.  $r = 0.995$ , that RSR level is assumed to persist beyond the observed survival curve. Numeric r should be  $> 0$  and expressed at the annual level when using fractional years as the scale of the time variables. E.g. if RSR is known to be 0.95 at the month level, then the annualized RSR is  $0.95^{12}$ . This enables correct usage of the RSR with survival intervals of varying lengths. When using day-level time variables (such as Dates; see [as.Date](#)), numeric r should be expressed at the day level, etc.

If  $r = "auto"$  or  $r = "auto1"$ , this function computes RSR estimates internally and automatically uses the RSR\_i in the last survival interval in each stratum (and adjusting group) and assumes that to persist beyond the observed survival curve. Automatic determination of r is a good starting point,

but in situations where the RSR estimate is uncertain it may produce poor results. Using "autoX" such as "auto6" causes `survmean` to use the mean of the estimated RSRs in the last X survival intervals, which may be more stable. Automatic determination will not use values >1 but set them to 1. Visual inspection of the produced curves is always recommended: see Examples.

One may also tweak the accuracy and length of extrapolation and expected survival curve computation by using `e1.breaks`. By default this is whatever was supplied to `breaks` for the survival time scale, to which

```
c(seq(1/12, 1, 1/12), seq(1.2, 1.8, 0.2), 2:19, seq(20, 50, 5))
```

is added after the maximum value, e.g. with `breaks = list(FUT = 0:10)` we have

```
..., 10+1/12, ..., 11, 11.2, ..., 2, 3, ..., 19, 20, 25, ... 50
```

as the `e1.breaks`. Supplying `e1.breaks` manually requires the breaks over time survival time scale supplied to argument `breaks` to be reiterated in `e1.breaks`; see Examples. **NOTE:** the default extrapolation breaks assume the time scales in the data to be expressed as fractional years, meaning this will work extremely poorly when using e.g. day-level time scales (such as `Date` variables). Set the extrapolation breaks manually in such cases.

## Value

Returns a `data.frame` or `data.table` (depending on `getOption("popEpi.datatable")`; see `?popEpi`) containing the following columns:

- `est`: The estimated mean survival time
- `exp`: The computed expected survival time
- `obs`: Counts of subjects in data
- `YPLL`: Years of Potential Life Lost, computed as  $((\text{exp} - \text{est}) * \text{obs})$  - though your time data may be in e.g. days, this column will have the same name regardless.

The returned data also has columns named according to the variables supplied to the right-hand-side of the formula.

## Author(s)

Joonas Miettinen

## See Also

Other `survmean` functions: `Surv()`, `lines.survmean()`, `plot.survmean()`

Other main functions: `Surv()`, `rate()`, `relpois_ag()`, `relpois()`, `sirspline()`, `sir()`, `survtab_ag()`, `survtab()`

## Examples

```
library(Epi)
## take 500 subjects randomly for demonstration
data(sire)
sire <- sire[sire$dg_date < sire$ex_date, ]
set.seed(1L)
```

```

sire <- sire[sample(x = nrow(sire), size = 500),]

## NOTE: recommended to use factor status variable
x <- Lexis(entry = list(FUT = 0, AGE = dg_age, CAL = get.yrs(dg_date)),
          exit = list(CAL = get.yrs(ex_date)),
          data = sire,
          exit.status = factor(status, levels = 0:2,
                               labels = c("alive", "canD", "othD")),
          merge = TRUE)

## phony variable
set.seed(1L)
x$group <- rbinom(nrow(x), 1, 0.5)
## age group
x$agegr <- cut(x$dg_age, c(0,45,60,Inf), right=FALSE)

## population hazards data set
pm <- data.frame(popEpi::popmort)
names(pm) <- c("sex", "CAL", "AGE", "haz")

## breaks to define observed survival estimation
BL <- list(FUT = seq(0, 10, 1/12))

## crude mean survival
sm1 <- survmean(Surv(FUT, lex.Xst != "alive") ~ 1,
               pophaz = pm, data = x, weights = NULL,
               breaks = BL)

sm1 <- survmean(FUT ~ 1,
               pophaz = pm, data = x, weights = NULL,
               breaks = BL)

## mean survival by group
sm2 <- survmean(FUT ~ group,
               pophaz = pm, data = x, weights = NULL,
               breaks = BL)

## ... and adjusted for age using internal weights (counts of subjects)
## note: need also longer extrapolation here so that all curves
## converge to zero in the end.
eBL <- list(FUT = c(BL$FUT, 11:75))
sm3 <- survmean(FUT ~ group + adjust(agegr),
               pophaz = pm, data = x, weights = "internal",
               breaks = BL, e1.breaks = eBL)

## visual inspection of how realistic extrapolation is for each stratum;
## solid lines are observed + extrapolated survivals;
## dashed lines are expected survivals
plot(sm1)

## plotting object with both stratification and standardization
## plots curves for each strata-std.group combination
plot(sm3)

```



```

## for finer control of plotting these curves, you may extract
## from the survmean object using e.g.
attributes(sm3)$survmean.meta$curves

#### using Dates

x <- Lexis(entry = list(FUT = 0L, AGE = dg_date-bi_date, CAL = dg_date),
          exit = list(CAL = ex_date),
          data = sire[sire$dg_date < sire$ex_date, ],
          exit.status = factor(status, levels = 0:2,
                              labels = c("alive", "canD", "othD")),
          merge = TRUE)
## phony group variable
set.seed(1L)
x$group <- rbinom(nrow(x), 1, 0.5)

## NOTE: population hazard should be reported at the same scale
## as time variables in your Lexis data.
data(popmort, package = "popEpi")
pm <- data.frame(popmort)
names(pm) <- c("sex", "CAL", "AGE", "haz")
## from year to day level
pm$haz <- pm$haz/365.25
pm$CAL <- as.Date(paste0(pm$CAL, "-01-01"))
pm$AGE <- pm$AGE*365.25

BL <- list(FUT = seq(0, 8, 1/12)*365.25)
eBL <- list(FUT = c(BL$FUT, c(8.25,8.5,9:60)*365.25))
smd <- survmean(FUT ~ group, data = x,
               pophaz = pm, verbose = TRUE, r = "auto5",
               breaks = BL, e1.breaks = eBL)

plot(smd)

```

---

survtab

*Estimate Survival Time Functions*


---

### Description

This function estimates survival time functions: survival, relative/net survival, and crude/absolute risk functions (CIF).

### Usage

```
survtab(
```

```

    formula,
    data,
    adjust = NULL,
    breaks = NULL,
    pophaz = NULL,
    weights = NULL,
    surv.type = "surv.rel",
    surv.method = "hazard",
    relsurv.method = "e2",
    subset = NULL,
    conf.level = 0.95,
    conf.type = "log-log",
    verbose = FALSE
)

```

### Arguments

formula	a formula; e.g. <code>fot ~ sex</code> , where <code>fot</code> is the time scale over which you wish to estimate a survival time function; this assumes that <code>lex.Xst</code> in your data is the status variable in the intended format (almost always right). To be explicit, use <a href="#">Surv</a> : e.g. <code>Surv(fot, lex.Xst) ~ sex</code> . Variables on the right-hand side of the formula separated by <code>+</code> are considered stratifying variables, for which estimates are computed separately. May contain usage of <code>adjust()</code> — see <a href="#">Details and Examples</a> .
data	a Lexis object with at least the survival time scale
adjust	can be used as an alternative to passing variables to argument <code>formula</code> within a call to <code>adjust()</code> ; e.g. <code>adjust = "agegr"</code> . <a href="#">Flexible input</a> .
breaks	a named list of breaks, e.g. <code>list(FUT = 0:5)</code> . If data is not split in advance, breaks must at the very least contain a vector of breaks to split the survival time scale (mentioned in argument <code>formula</code> ). If data has already been split (using e.g. <a href="#">splitMulti</a> ) along at least the used survival time scale, this may be <code>NULL</code> . It is generally recommended (and sufficient; see <a href="#">Seppa, Dyban and Hakulinen (2015)</a> ) to use monthly intervals where applicable.
pophaz	a <code>data.frame</code> containing expected hazards for the event of interest to occur. See the <a href="#">dedicated help page</a> . Required when <code>surv.type = "surv.rel"</code> or <code>"cif.rel"</code> . <code>pophaz</code> must contain one column named <code>"haz"</code> , and any number of other columns identifying levels of variables to do a merge with split data within <code>survtab</code> . Some columns may be time scales, which will allow for the expected hazard to vary by e.g. calendar time and age.
weights	typically a list of weights or a character string specifying an age group standardization scheme; see the <a href="#">dedicated help page</a> and examples. NOTE: <code>weights = "internal"</code> is based on the counts of persons in follow-up at the start of follow-up (typically <code>T = 0</code> )
surv.type	one of <code>'surv.obs'</code> , <code>'surv.cause'</code> , <code>'surv.rel'</code> , <code>'cif.obs'</code> or <code>'cif.rel'</code> ; defines what kind of survival time function(s) is/are estimated; see <a href="#">Details</a>
surv.method	either <code>'lifetable'</code> or <code>'hazard'</code> ; determines the method of calculating survival time functions, where the former computes ratios such as $p = d/(n - n.cens)$

and the latter utilizes subject-times (typically person-years) for hazard estimates such as `d/pyrs` which are used to compute survival time function estimates. The former method requires argument `n.cens` and the latter argument `pyrs` to be supplied.

<code>relsurv.method</code>	either 'e2' or 'pp'; defines whether to compute relative survival using the EdererII method or using Pohar-Perme weighting; ignored if <code>surv.type != "surv.rel"</code>
<code>subset</code>	a logical condition; e.g. <code>subset = sex == 1</code> ; subsets the data before computations
<code>conf.level</code>	confidence level used in confidence intervals; e.g. 0.95 for 95 percent confidence intervals
<code>conf.type</code>	character string; must be one of "plain", "log-log" and "log"; defines the transformation used on the survival time function to yield confidence intervals via the delta method
<code>verbose</code>	logical; if TRUE, the function is chatty and returns some messages and timings along the process

### Value

Returns a table of life time function values and other information with survival intervals as rows. Returns some of the following estimates of survival time functions:

- `surv.obs` - observed (raw, overall) survival
- `surv.obs.K` - observed cause-specific survival for cause K
- `CIF.k` - cumulative incidence function for cause k
- `CIF.rel` - cumulative incidence function using excess cases
- `r.e2` - relative survival, EdererII
- `r.pp` - relative survival, Pohar-Perme weighted

The suffix `.as` implies adjusted estimates, and `.lo` and `.hi` imply lower and upper confidence limits, respectively. The prefix `SE.` stands for standard error.

### Basics

This function computes interval-based estimates of survival time functions, where the intervals are set by the user. For product-limit-based estimation see packages **survival** and **relsurv**.

if `surv.type = 'surv.obs'`, only 'raw' observed survival is estimated over the chosen time intervals. With `surv.type = 'surv.rel'`, also relative survival estimates are supplied in addition to observed survival figures.

`surv.type = 'cif.obs'` requests cumulative incidence functions (CIF) to be estimated. CIFs are estimated for each competing risk based on a survival-interval-specific proportional hazards assumption as described by Chiang (1968). With `surv.type = 'cif.rel'`, a CIF is estimated with using excess cases as the "cause-specific" cases. Finally, with `surv.type = 'surv.cause'`, cause-specific survivals are estimated separately for each separate type of event.

In hazard-based estimation (`surv.method = "hazard"`) survival time functions are transformations of the estimated corresponding hazard in the intervals. The hazard itself is estimated using counts of

events (or excess events) and total subject-time in the interval. Life table `surv.method = "lifetable"` estimates are constructed as transformations of probabilities computed using counts of events and counts of subjects at risk.

The vignette [survtab\\_examples](#) has some practical examples.

### Relative survival

When `surv.type = 'surv.rel'`, the user can choose `relsurv.method = 'pp'`, whereupon Pohar-Perme weighting is used. By default `relsurv.method = 'e2'`, i.e. the Ederer II method is used to estimate relative survival.

### Adjusted estimates

Adjusted estimates in this context mean computing estimates separately by the levels of adjusting variables and returning weighted averages of the estimates. For example, computing estimates separately by age groups and returning a weighted average estimate (age-adjusted estimate).

Adjusting requires specification of both the adjusting variables and the weights for all the levels of the adjusting variables. The former can be accomplished by using `adjust()` with the argument `formula`, or by supplying variables directly to argument `adjust`. E.g. the following are all equivalent:

```
formula = fot ~ sex + adjust(agegr) + adjust(area)
```

```
formula = fot ~ sex + adjust(agegr, area)
```

```
formula = fot ~ sex, adjust = c("agegr", "area")
```

```
formula = fot ~ sex, adjust = list(agegr, area)
```

The adjusting variables must match with the variable names in the argument `weights`; see the [dedicated help page](#). Typically weights are supplied as a `list` or a `data.frame`. The former can be done by e.g.

```
weights = list(agegr = VEC1, area = VEC2),
```

where `VEC1` and `VEC2` are vectors of weights (which do not have to add up to one). See [survtab\\_examples](#) for an example of using a `data.frame` to pass weights.

### Period analysis and other data selection schemes

To calculate e.g. period analysis (delayed entry) estimates, limit the data when/before supplying to this function. See [survtab\\_examples](#).

### References

Perme, Maja Pohar, Janez Stare, and Jacques Esteve. "On estimation in relative survival." *Biometrics* 68.1 (2012): 113-120. doi: [10.1111/j.15410420.2011.01640.x](https://doi.org/10.1111/j.15410420.2011.01640.x)

Hakulinen, Timo, Karri Seppa, and Paul C. Lambert. "Choosing the relative survival method for cancer survival estimation." *European Journal of Cancer* 47.14 (2011): 2202-2210. doi: [10.1016/j.ejca.2011.03.011](https://doi.org/10.1016/j.ejca.2011.03.011)

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CHIANG, Chin Long. Introduction to stochastic processes in biostatistics. 1968. ISBN-14: 978-0471155003

Seppa K., Dyba T. and Hakulinen T.: Cancer Survival, Reference Module in Biomedical Sciences. Elsevier. 08-Jan-2015. doi: [10.1016/B9780128012383.027458](https://doi.org/10.1016/B9780128012383.027458)

### See Also

[splitMulti](#), [lexpand](#), [ICSS](#), [sire](#) [The survtab\\_examples vignette](#)

Other main functions: [Surv\(\)](#), [rate\(\)](#), [relpois\\_ag\(\)](#), [relpois\(\)](#), [sirspline\(\)](#), [sir\(\)](#), [survmean\(\)](#), [survtab\\_ag\(\)](#)

Other survtab functions: [Surv\(\)](#), [lines.survtab\(\)](#), [plot.survtab\(\)](#), [print.survtab\(\)](#), [summary.survtab\(\)](#), [survtab\\_ag\(\)](#)

### Examples

```
data("sire", package = "popEpi")
library(Epi)

## NOTE: recommended to use factor status variable
x <- Lexis(entry = list(FUT = 0, AGE = dg_age, CAL = get.yrs(dg_date)),
          exit = list(CAL = get.yrs(ex_date)),
          data = sire[sire$dg_date < sire$ex_date, ],
          exit.status = factor(status, levels = 0:2,
                              labels = c("alive", "canD", "othD")),
          merge = TRUE)

## phony group variable
set.seed(1L)
x$group <- rbinom(nrow(x), 1, 0.5)

## observed survival. explicit supplying of status:
st <- survtab(Surv(time = FUT, event = lex.Xst) ~ group, data = x,
             surv.type = "surv.obs",
             breaks = list(FUT = seq(0, 5, 1/12)))
## this assumes the status is lex.Xst (right 99.9 % of the time)
st <- survtab(FUT ~ group, data = x,
             surv.type = "surv.obs",
             breaks = list(FUT = seq(0, 5, 1/12)))

## relative survival (ederer II)
data("popmort", package = "popEpi")
pm <- data.frame(popmort)
names(pm) <- c("sex", "CAL", "AGE", "haz")
st <- survtab(FUT ~ group, data = x,
             surv.type = "surv.rel",
             pophaz = pm,
             breaks = list(FUT = seq(0, 5, 1/12)))

## ICSS weights usage
data("ICSS", package = "popEpi")
```

```

cut <- c(0, 30, 50, 70, Inf)
agegr <- cut(ICSS$age, cut, right = FALSE)
w <- aggregate(ICSS1~agegr, data = ICSS, FUN = sum)
x$agegr <- cut(x$dg_age, cut, right = FALSE)
st <- survtab(FUT ~ group + adjust(agegr), data = x,
              surv.type = "surv.rel",
              pophaz = pm, weights = w$ICSS1,
              breaks = list(FUT = seq(0, 5, 1/12)))

#### using dates with survtab
x <- Lexis(entry = list(FUT = 0L, AGE = dg_date-bi_date, CAL = dg_date),
          exit = list(CAL = ex_date),
          data = sire[sire$dg_date < sire$ex_date, ],
          exit.status = factor(status, levels = 0:2,
                              labels = c("alive", "canD", "othD")),
          merge = TRUE)
## phony group variable
set.seed(1L)
x$group <- rbinom(nrow(x), 1, 0.5)

st <- survtab(Surv(time = FUT, event = lex.Xst) ~ group, data = x,
              surv.type = "surv.obs",
              breaks = list(FUT = seq(0, 5, 1/12)*365.25))

## NOTE: population hazard should be reported at the same scale
## as time variables in your Lexis data.
data(popmort, package = "popEpi")
pm <- data.frame(popmort)
names(pm) <- c("sex", "CAL", "AGE", "haz")
## from year to day level
pm$haz <- pm$haz/365.25
pm$CAL <- as.Date(paste0(pm$CAL, "-01-01"))
pm$AGE <- pm$AGE*365.25

st <- survtab(Surv(time = FUT, event = lex.Xst) ~ group, data = x,
              surv.type = "surv.rel", relsurv.method = "e2",
              pophaz = pm,
              breaks = list(FUT = seq(0, 5, 1/12)*365.25))

```

---

survtab\_ag

*Estimate Survival Time Functions*


---

### Description

This function estimates survival time functions: survival, relative/net survival, and crude/absolute risk functions (CIF).

**Usage**

```

survtab_ag(
  formula = NULL,
  data,
  adjust = NULL,
  weights = NULL,
  surv.breaks = NULL,
  n = "at.risk",
  d = "from0to1",
  n.cens = "from0to0",
  pyrs = "pyrs",
  d.exp = "d.exp",
  n.pp = NULL,
  d.pp = "d.pp",
  d.pp.2 = "d.pp.2",
  n.cens.pp = "n.cens.pp",
  pyrs.pp = "pyrs.pp",
  d.exp.pp = "d.exp.pp",
  surv.type = "surv.rel",
  surv.method = "hazard",
  relsurv.method = "e2",
  subset = NULL,
  conf.level = 0.95,
  conf.type = "log-log",
  verbose = FALSE
)

```

**Arguments**

formula	a formula; the response must be the time scale to compute survival time function estimates over, e.g. <code>tot ~ sex</code> . Variables on the right-hand side of the formula separated by <code>+</code> are considered stratifying variables, for which estimates are computed separately. May contain usage of <code>adjust()</code> — see <a href="#">Details and Examples</a> .
data	since <code>popEpi 0.4.0</code> , a <code>data.frame</code> containing variables used in <code>formula</code> and other arguments. <code>aggre</code> objects are recommended as they contain information on any time scales and are therefore safer; for creating <code>aggre</code> objects see <a href="#">as.aggre</a> when your data is already aggregated and <code>aggre</code> for aggregating split <code>Lexis</code> objects.
adjust	can be used as an alternative to passing variables to argument <code>formula</code> within a call to <code>adjust()</code> ; e.g. <code>adjust = "agegr"</code> . <a href="#">Flexible input</a> .
weights	typically a list of weights or a character string specifying an age group standardization scheme; see the <a href="#">dedicated help page</a> and examples. NOTE: <code>weights = "internal"</code> is based on the counts of persons in follow-up at the start of follow-up (typically <code>T = 0</code> )
surv.breaks	a vector of breaks on the survival time scale. Optional if <code>data</code> is an <code>aggre</code> object and mandatory otherwise. Must define each intended interval; e.g. <code>surv.breaks</code>

= 0:5 when data has intervals defined by breaks `seq(0, 5, 1/12)` will aggregate to wider intervals first. It is generally recommended (and sufficient; see Seppa, Dyban and Hakulinen (2015)) to use monthly intervals where applicable.

n	variable containing counts of subjects at-risk at the start of a time interval; e.g. <code>n = "at.risk"</code> . Required when <code>surv.method = "lifetable"</code> . <a href="#">Flexible input</a> .
d	variable(s) containing counts of subjects experiencing an event. With only one type of event, e.g. <code>d = "deaths"</code> . With multiple types of events (for CIF or cause-specific survival estimation), supply e.g. <code>d = c("canD", "othD")</code> . If the survival time function to be estimated does not use multiple types of events, supplying more than one variable to <code>d</code> simply causes the variables to be added together. Always required. <a href="#">Flexible input</a> .
n.cens	variable containing counts of subjects censored during a survival time interval; E.g. <code>n.cens = "alive"</code> . Required when <code>surv.method = "lifetable"</code> . <a href="#">Flexible input</a> .
pyrs	variable containing total subject-time accumulated within a survival time interval; E.g. <code>pyrs = "pyrs"</code> . Required when <code>surv.method = "hazard"</code> . Flexible input.
d.exp	variable denoting total "expected numbers of events" (typically computed <code>pyrs * pop.haz</code> , where <code>pop.haz</code> is the expected hazard level) accumulated within a survival time interval; E.g. <code>pyrs = "pyrs"</code> . Required when computing EdererII relative survivals or CIFs based on excess counts of events. Flexible input.
n.pp	variable containing total Pohar-Perme weighted counts of subjects at risk in an interval, supplied as argument <code>n</code> is supplied. Computed originally on the subject level as analogous to <code>pp * as.integer(status == "at-risk")</code> . Required when <code>relsurv.method = "pp"</code> . Flexible input.
d.pp	variable(s) containing Pohar-Perme weighted counts of events, supplied as argument <code>d</code> is supplied. Computed originally on the subject level as analogous to <code>pp * as.integer(status == some_event)</code> . Required when <code>relsurv.method = "pp"</code> . Flexible input.
d.pp.2	variable(s) containing total Pohar-Perme "double-weighted" counts of events, supplied as argument <code>d</code> is supplied. Computed originally on the subject level as analogous to <code>pp * pp * as.integer(status == some_event)</code> . Required when <code>relsurv.method = "pp"</code> . Flexible input.
n.cens.pp	variable containing total Pohar-Perme weighted counts censorings, supplied as argument <code>n.cens</code> is supplied. Computed originally on the subject level as analogous to <code>pp * as.integer(status == "censored")</code> . Required when <code>relsurv.method = "pp"</code> . Flexible input.
pyrs.pp	variable containing total Pohar-Perme weighted subject-times, supplied as argument <code>pyrs</code> is supplied. Computed originally on the subject level as analogous to <code>pp * pyrs</code> . Required when <code>relsurv.method = "pp"</code> . Flexible input.
d.exp.pp	variable containing total Pohar-Perme weighted counts of excess events, supplied as argument <code>pyrs</code> is supplied. Computed originally on the subject level as analogous to <code>pp * d.exp</code> . Required when <code>relsurv.method = "pp"</code> . Flexible input.
surv.type	one of 'surv.obs', 'surv.cause', 'surv.rel', 'cif.obs' or 'cif.rel'; defines what kind of survival time function(s) is/are estimated; see Details



surv.method	either 'lifetable' or 'hazard'; determines the method of calculating survival time functions, where the former computes ratios such as $p = d / (n - n.cens)$ and the latter utilizes subject-times (typically person-years) for hazard estimates such as $d / pyrs$ which are used to compute survival time function estimates. The former method requires argument <code>n.cens</code> and the latter argument <code>pyrs</code> to be supplied.
relsurv.method	either 'e2' or 'pp'; defines whether to compute relative survival using the EdererII method or using Pohar-Perme weighting; ignored if <code>surv.type != "surv.rel"</code>
subset	a logical condition; e.g. <code>subset = sex == 1</code> ; subsets the data before computations
conf.level	confidence level used in confidence intervals; e.g. 0.95 for 95 percent confidence intervals
conf.type	character string; must be one of "plain", "log-log" and "log"; defines the transformation used on the survival time function to yield confidence intervals via the delta method
verbose	logical; if TRUE, the function is chatty and returns some messages and timings along the process

### Value

Returns a table of life time function values and other information with survival intervals as rows. Returns some of the following estimates of survival time functions:

- `surv.obs` - observed (raw, overall) survival
- `surv.obs.K` - observed cause-specific survival for cause K
- `CIF_k` - cumulative incidence function for cause k
- `CIF.rel` - cumulative incidence function using excess cases
- `r.e2` - relative survival, EdererII
- `r.pp` - relative survival, Pohar-Perme weighted

The suffix `.as` implies adjusted estimates, and `.lo` and `.hi` imply lower and upper confidence limits, respectively. The prefix `SE.` stands for standard error.

### Basics

This function computes interval-based estimates of survival time functions, where the intervals are set by the user. For product-limit-based estimation see packages **survival** and **relsurv**.

if `surv.type = 'surv.obs'`, only 'raw' observed survival is estimated over the chosen time intervals. With `surv.type = 'surv.rel'`, also relative survival estimates are supplied in addition to observed survival figures.

`surv.type = 'cif.obs'` requests cumulative incidence functions (CIF) to be estimated. CIFs are estimated for each competing risk based on a survival-interval-specific proportional hazards assumption as described by Chiang (1968). With `surv.type = 'cif.rel'`, a CIF is estimated with using excess cases as the "cause-specific" cases. Finally, with `surv.type = 'surv.cause'`, cause-specific survivals are estimated separately for each separate type of event.

In hazard-based estimation (`surv.method = "hazard"`) survival time functions are transformations of the estimated corresponding hazard in the intervals. The hazard itself is estimated using counts of events (or excess events) and total subject-time in the interval. Life table `surv.method = "lifetable"` estimates are constructed as transformations of probabilities computed using counts of events and counts of subjects at risk.

The vignette [survtab\\_examples](#) has some practical examples.

### Relative survival

When `surv.type = 'surv.rel'`, the user can choose `relsurv.method = 'pp'`, whereupon Pohar-Perme weighting is used. By default `relsurv.method = 'e2'`, i.e. the Ederer II method is used to estimate relative survival.

### Adjusted estimates

Adjusted estimates in this context mean computing estimates separately by the levels of adjusting variables and returning weighted averages of the estimates. For example, computing estimates separately by age groups and returning a weighted average estimate (age-adjusted estimate).

Adjusting requires specification of both the adjusting variables and the weights for all the levels of the adjusting variables. The former can be accomplished by using `adjust()` with the argument `formula`, or by supplying variables directly to argument `adjust`. E.g. the following are all equivalent:

```
formula = fot ~ sex + adjust(agegr) + adjust(area)
```

```
formula = fot ~ sex + adjust(agegr, area)
```

```
formula = fot ~ sex, adjust = c("agegr", "area")
```

```
formula = fot ~ sex, adjust = list(agegr, area)
```

The adjusting variables must match with the variable names in the argument `weights`; see the [dedicated help page](#). Typically weights are supplied as a `list` or a `data.frame`. The former can be done by e.g.

```
weights = list(agegr = VEC1, area = VEC2),
```

where `VEC1` and `VEC2` are vectors of weights (which do not have to add up to one). See [survtab\\_examples](#) for an example of using a `data.frame` to pass weights.

### Period analysis and other data selection schemes

To calculate e.g. period analysis (delayed entry) estimates, limit the data when/before supplying to this function. See [survtab\\_examples](#).

### Data requirements

`survtab_ag` computes estimates of survival time functions using pre-aggregated data. For using subject-level data directly, use [survtab](#). For aggregating data, see [lexpand](#) and [aggre](#).

By default, and if data is an `aggre` object (not mandatory), `survtab_ag` makes use of the exact same breaks that were used in splitting the original data (with e.g. `lexpand`), so it is not necessary to specify any `surv.breaks`. If specified, the `surv.breaks` must be a subset of the pertinent pre-existing breaks. When data is not an `aggre` object, breaks must always be specified. Interval lengths

(delta in output) are also calculated based on whichever breaks are used, so the upper limit of the breaks should therefore be meaningful and never e.g. Inf.

## References

Perme, Maja Pohar, Janez Stare, and Jacques Esteve. "On estimation in relative survival." *Biometrics* 68.1 (2012): 113-120. doi: [10.1111/j.15410420.2011.01640.x](https://doi.org/10.1111/j.15410420.2011.01640.x)

Hakulinen, Timo, Karri Seppa, and Paul C. Lambert. "Choosing the relative survival method for cancer survival estimation." *European Journal of Cancer* 47.14 (2011): 2202-2210. doi: [10.1016/j.ejca.2011.03.011](https://doi.org/10.1016/j.ejca.2011.03.011)

Seppa, Karri, Timo Hakulinen, and Arun Pokhrel. "Choosing the net survival method for cancer survival estimation." *European Journal of Cancer* (2013). doi: [10.1016/j.ejca.2013.09.019](https://doi.org/10.1016/j.ejca.2013.09.019)

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Seppa K., Dyba T. and Hakulinen T.: *Cancer Survival, Reference Module in Biomedical Sciences*. Elsevier. 08-Jan-2015. doi: [10.1016/B9780128012383.027458](https://doi.org/10.1016/B9780128012383.027458)

## See Also

[splitMulti](#), [lexpand](#), [ICSS](#), [sire](#) [The survtab\\_examples vignette](#)

Other main functions: [Surv\(\)](#), [rate\(\)](#), [relpois\\_ag\(\)](#), [relpois\(\)](#), [sirspline\(\)](#), [sir\(\)](#), [survmean\(\)](#), [survtab\(\)](#)

Other survtab functions: [Surv\(\)](#), [lines.survtab\(\)](#), [plot.survtab\(\)](#), [print.survtab\(\)](#), [summary.survtab\(\)](#), [survtab\(\)](#)

## Examples

```
## see more examples with explanations in vignette("survtab_examples")

#### survtab_ag usage

data("sire", package = "popEpi")
## prepare data for e.g. 5-year "period analysis" for 2008-2012
## note: sire is a simulated cohort integrated into popEpi.
BL <- list(fot=seq(0, 5, by = 1/12),
           per = c("2008-01-01", "2013-01-01"))
x <- lexpand(sire, birth = bi_date, entry = dg_date, exit = ex_date,
            status = status %in% 1:2,
            breaks = BL,
            pophaz = popmort,
            aggre = list(fot))

## calculate relative EdererII period method
## NOTE: x is an aggre object here, so surv.breaks are deduced
## automatically
st <- survtab_ag(fot ~ 1, data = x)

summary(st, t = 1:5) ## annual estimates
summary(st, q = list(r.e2 = 0.75)) ## 1st interval where r.e2 < 0.75 at end
```

```

plot(st)

## non-aggre data: first call to survtab_ag would fail
df <- data.frame(x)
# st <- survtab_ag(fot ~ 1, data = x)
st <- survtab_ag(fot ~ 1, data = x, surv.breaks = BL$fot)

## calculate age-standardised 5-year relative survival ratio using
## Ederer II method and period approach

sire$agegr <- cut(sire$dg_age,c(0,45,55,65,75,Inf),right=FALSE)
BL <- list(fot=seq(0, 5, by = 1/12),
           per = c("2008-01-01", "2013-01-01"))
x <- leexpand(sire, birth = bi_date, entry = dg_date, exit = ex_date,
             status = status %in% 1:2,
             breaks = BL,
             pophaz = popmort,
             aggre = list(agegr, fot))

## age standardisation using internal weights (age distribution of
## patients diagnosed within the period window)
## (NOTE: what is done here is equivalent to using weights = "internal")
w <- aggregate(at.risk ~ agegr, data = x[x$fot == 0], FUN = sum)
names(w) <- c("agegr", "weights")

st <- survtab_ag(fot ~ adjust(agegr), data = x, weights = w)
plot(st, y = "r.e2.as", col = c("blue"))

## age standardisation using ICSS1 weights
data(ICSS)
cut <- c(0, 45, 55, 65, 75, Inf)
agegr <- cut(ICSS$age, cut, right = FALSE)
w <- aggregate(ICSS1~agegr, data = ICSS, FUN = sum)
names(w) <- c("agegr", "weights")

st <- survtab_ag(fot ~ adjust(agegr), data = x, weights = w)
lines(st, y = "r.e2.as", col = c("red"))

## cause-specific survival
sire$stat <- factor(sire$status, 0:2, c("alive", "canD", "othD"))
x <- leexpand(sire, birth = bi_date, entry = dg_date, exit = ex_date,
             status = stat,
             breaks = BL,
             pophaz = popmort,
             aggre = list(agegr, fot))
st <- survtab_ag(fot ~ adjust(agegr), data = x, weights = w,
               d = c("fromalivetocanD", "fromalivetoothD"),
               surv.type = "surv.cause")
plot(st, y = "surv.obs.fromalivetocanD.as")
lines(st, y = "surv.obs.fromalivetoothD.as", col = "red")

```

---

try2int	<i>Attempt coercion to integer</i>
---------	------------------------------------

---

**Description**

Attempts to convert a numeric object to integer, but won't if loss of information is imminent (if values after decimal are not zero for even one value in obj)

**Usage**

```
try2int(obj, tol = .Machine$double.eps^0.5)
```

**Arguments**

obj	a numeric vector
tol	tolerance; if each numeric value in obj deviate from the corresponding integers at most the value of tol, they are considered to be integers; e.g. by default $1 + \text{.Machine\$double.eps}$ is considered to be an integer but $1 + \text{.Machine\$double.eps}^{0.49}$ is not.

**Value**

An 'integer' vector if no information is lost in coercion; else 'numeric' vector.

**Author(s)**

James Arnold

**Source**

[Stackoverflow thread](#)

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