

Package ‘poputils’

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Description Perform tasks commonly encountered when preparing and analysing demographic data. Some functions are intended for end users, and others for developers. Includes functions for working with life tables.

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`.intrinsic_growth_rate`

Calculate Intrinsic Growth Rate

Description

Calculate the intrinsic growth rate implied by fertility and mortality schedules. The intrinsic growth rate is the rate at which all age groups in a population would eventually grow if the population was subject to the fertility and mortality schedules indefinitely. The fertility and mortality schedules apply to a single sex, typically females.

Usage

```
.intrinsic_growth_rate(mx, Lx, age_mid)
```

Arguments

mx	Age specific fertility rates, for a single sex (typically daughters). An ordinary numeric vector or an <code>rvec()</code> .
Lx	Life table mortality measure, for a single sex (typically females). An ordinary numeric vector or an <code>rvec()</code> .
age_mid	The midpoint of each age group. Numeric vector.

Details

The fertility schedule `mx` and mortality schedule `Lx` refer only to the reproductive ages. The mortality schedule `Lx` is the number of years that a newborn baby would be expected to spend in each age group under prevailing mortality rates. It is the life table quantity nLx where the radix l_0 has been set to 1.

Value

A numeric vector of length 1.

Examples

```
mx <- c(0.072, 0.148, 0.156, 0.140, 0.108, 0.054, 0.013)
Lx <- c(3.49, 3.37, 3.23, 3.07, 2.91, 2.74, 2.56)
age_mid <- c(17.5, 22.5, 27.5, 32.5, 37.5, 42.5, 47.5)
.intrinsic_growth_rate(mx = mx, Lx = Lx, age_mid = age_mid)
```

age_group_type	<i>Infer Age Label Type</i>
----------------	-----------------------------

Description

Determine whether a set of age labels refer to one-year, five-year, or life-table age groups.

Usage

```
age_group_type(x)
```

Arguments

x	A vector of age labels
---	------------------------

Details

The valid types of age labels are:

- "single". One-year age groups, eg "0" or "55", and possibly an open age group, eg "90+".
- "five". Five-year age groups, eg "0-4" or "55-59", and possibly an open age group, eg "100+".
- "lt". Life table age groups, eg "0", "1-4", "5-9", "55-59", or "80+".

If `x` does not fit any of these descriptions, then `age_group_type()` throws an error.

If `x` could belong to more than one type, then `age_group_type()` prefers "single" to "five" and "lt", and prefers "five" to "lt".

Value

"single", "five", or "lt".

Examples

```
age_group_type(c("5-9", "0-4", "100+"))
age_group_type(c("2", "5", "1"))
age_group_type(c("0", "1-4"))

## could be any "single" or "lt"
age_group_type("0")

## could be "five" or "lt"
age_group_type("80-84")
```

age_labels

Create Age Labels

Description

Create labels for age groups. The labels depend on the type argument:

- "single". One-year age groups, eg "0" or "55", and possibly an open age group, eg "90+".
- "five". Five-year age groups, eg "0-4" or "55-59", and possibly an open age group, eg "100+".
- "lt". Life table age groups, eg "0", "1-4", "5-9", "55-59", or "80+".

Usage

```
age_labels(type, min = 0, max = 100, open = NULL)
```

Arguments

type	Type of age group labels: "single", "five", or "lt".
min	Minimum age. Defaults to 0.
max	Maximum age for closed age groups. Defaults to 100.
open	Whether the last age group is "open", ie has no upper limit.

Details

The first age group starts at the age specified by min. If open is TRUE, then the final age group starts at the age specified by max. Otherwise, the final age group ends at the age specified by max.

open defaults to TRUE when min equals zero, and to FALSE otherwise.

Value

A character vector.

See Also

[reformat_age\(\)](#)

Examples

```
age_labels(type = "single", min = 15, max = 40)
age_labels(type = "five")
age_labels(type = "lt", max = 80)
```

age_lower

Lower Limits, Midpoints, and Upper Limits of Age Groups

Description

Given a vector x of age group labels, return a numeric vector.

- `age_lower()` returns the lower limits of each age group,
- `age_mid()` returns the midpoints, and
- `age_upper()` returns the upper limits.

Vector x must describe 1-year, 5-year or life-table age groups: see [age_labels\(\)](#) for examples. x can format these age groups in any way understood by [reformat_age\(\)](#).

Usage

```
age_lower(x)
```

```
age_mid(x)
```

```
age_upper(x)
```

Arguments

`x` A vector of age group labels.

Details

These functions can make age groups easier to work with. Lower and upper limits can be used for selecting on age. Replacing age group with midpoints can improve graphs.

Value

A numeric vector, the same length as `x`.

See Also

[reformat_age\(\)](#) [age_labels\(\)](#)

Examples

```
x <- c("15-19", "5-9", "50+")
age_lower(x)
age_mid(x)
age_upper(x)

## non-standard formats are OK
age_lower(c("infants", "100 and over"))

df <- data.frame(age = c("1-4", "10-14", "5-9", "0"),
                 rate = c(0.023, 0.015, 0.007, 0.068))
df
subset(df, age_lower(age) >= 5)
```

booth_standard

Booth Standard

Description

A "standard" distribution for age-specific fertility rates proposed in Booth (1984), and widely used for estimating fertility rates in settings with high fertility and limited data.

Usage

```
booth_standard
```

Format

A tibble with 8 rows and the following columns:

- age Five-year age group, from "10-14" to "45-49"
- value Proportion of total fertility occurring within the age group

Details

The key input for `booth_standard` is 'Yx' from table 2 of Booth (1984).

Source

Booth H (1984) Transforming Gompertz's function for fertility analysis: The development of a standard for the relational Gompertz function. *Population Studies* 38(3): 495-506.

check_age	<i>Validity Checks for Age Labels</i>
-----------	---------------------------------------

Description

Check that age labels can be parsed and, optionally, whether the labels are complete, unique, start at zero, and end with an open age group.

Usage

```
check_age(
  x,
  complete = FALSE,
  unique = FALSE,
  zero = FALSE,
  open = FALSE,
  closed = FALSE
)
```

Arguments

<code>x</code>	A vector of age labels.
<code>complete</code>	If TRUE, test whether x has gaps.
<code>unique</code>	If TRUE, test whether x has duplicates.
<code>zero</code>	If TRUE, test whether youngest age group in x starts at 0.
<code>open</code>	If TRUE, test whether oldest age group in x is open.
<code>closed</code>	If TRUE, test whether oldest age group in x is closed.

Details

By default, `check_age()` only tests whether a set of labels can be parsed as single-year, five-year, or life table age groups. (See [age_group_type\(\)](#) for more on the three types of age group.) However, it can also apply the following tests:

- `complete`. Whether x includes all intermediate age groups, with no gaps. For instance, the labels `c("10-14", "15-19", "5-9")` are complete, while the labels `c("15-19", "5-9")` are not (because they are missing "10-14".)
- `unique`. Whether x has duplicated labels.

- zero. Whether the youngest age group in x starts at age 0, ie whether it includes "0" or "0-4".
- open. Whether the oldest age group in x is "open", with no upper limit, eg "100+" or "65+".
- closed. Whether the oldest age group in x is "closed", with an upper limit, eg "100-104+" or "65".

Value

TRUE, invisibly, or raises an error if a test fails.

See Also

- [reformat_age\(\)](#) to convert age labels to the format used by **poputils**.

Examples

```
try(
  check_age(c("10-14", "0-4", "15+"),
            complete = TRUE)
)

try(
  check_age(c("10-14", "5-9", "0-4", "5-9", "15+"),
            unique = TRUE)
)

try(
  check_age(c("10-14", "5-9", "15+"),
            zero = TRUE)
)

try(
  check_age(c("10-14", "0-4", "5-9"),
            open = TRUE)
)

try(
  check_age(c("10+", "0-4", "5-9"),
            closed = TRUE)
)
```

check_equal_length *Check that Arguments have Same Length*

Description

Check that x and y have the same length.

Usage

```
check_equal_length(x, y, nm_x, nm_y)
```

Arguments

x, y	Arguments to compare
nm_x, nm_y	Names to use in error message

Value

'TRUE', invisibly.

Examples

```
x <- 1:3
y <- 3:1
check_equal_length(x = x,
                   y = y,
                   nm_x = "x",
                   nm_y = "y")
```

 check_n

Check Whole Number

Description

Check that n is finite, non-NA scalar that is an integer or integerish (ie is equal to round(n)), and optionally within a specified range and divisible by a specified number.

Usage

```
check_n(n, nm_n, min, max, divisible_by)
```

Arguments

n	A whole number
nm_n	Name for 'n' to be used in error messages
min	Minimum value 'n' can take. Can be NULL.
max	Maximum values 'n' can take. Can be NULL.
divisible_by	'n' must be divisible by this. Can be NULL.

Value

If all tests pass, check_n() returns TRUE invisibly. Otherwise it throws an error.

Examples

```
check_n(10, nm_n = "count", min = 0, max = NULL, divisible_by = 1)
check_n(10, nm_n = "count", min = NULL, max = NULL, divisible_by = NULL)
check_n(10, nm_n = "n", min = 5, max = 10, divisible_by = 2)
```

`check_no_overlap_colnums`*Check that Colnum Vectors do not Overlap*

Description

Given a named list of colnum vectors, like those produced by `tidyselect::eval_select()`, throw an error if there is an overlap.

Usage

```
check_no_overlap_colnums(x)
```

Arguments

`x` A named list of integer vectors.

Value

TRUE, invisibly

See Also

[tidyselect::eval_select\(\)](#)

Examples

```
x <- list(arg1 = c(age = 1L),
          arg2 = c(gender = 4L, region = 5L))
check_no_overlap_colnums(x)
```

`combine_age`*Aggregate Age Group Labels*

Description

Convert age group labels to a less detailed classification. The three classifications recognized by `combine_age()` are "single", "five", and "lt", as defined on [age_labels\(\)](#). The following conversions are permitted:

- "single" → "lt"
- "single" → "five"
- "lt" → "five"

Usage

```
combine_age(x, to = c("five", "lt"))
```

Arguments

x A vector of age labels
to Type of age classification to convert to: "five" or "1t". Defaults to "five".

Value

If x is a factor, then `combine_age()` returns a factor; otherwise it returns a character vector.

See Also

- `age_labels()` to create age group labels
- `reformat_age()` to convert existing age group labels to a standard format
- `set_age_open()` to set the lower limit of the open age group

Examples

```
x <- c("0", "5", "3", "12")
combine_age(x)
combine_age(x, to = "1t")
```

e0_to_lifetab_logit *Derive Life Tables that Match Life Expectancies, using a Brass Logit Model*

Description

Turn life expectancies at birth into full life tables, using the Brass logit model. The method is simple and is designed for simulations or for settings with little or no data on age-specific mortality rates. In settings where data on age-specific mortality is available, other methods might be more appropriate.

Usage

```
e0_to_lifetab_logit(
  target,
  standard,
  infant = c("constant", "linear", "CD", "AK"),
  child = c("constant", "linear", "CD"),
  closed = c("constant", "linear"),
  open = "constant",
  radix = 1e+05,
  suffix = NULL
)
```

Arguments

target	A data frame containing a variable called "e0", and possibly other variables. See Details.
standard	A data frame containing variables called age and lx, and possibly others. See Details.
infant, child, closed, open	Methods used to calculate life expectancy. See lifetab() for details.
radix	Initial population for the lx column in the derived life table(s). Default is 100000.
suffix	Optional suffix added to life table columns.

Value

A [tibble](#).

Method

The method implemented by `e0_to_lifetab_logit()` is based on the observation that, if populations A and B are demographically similar, then, in many cases,

$$\text{logit}(q_x^B) \approx \alpha + \beta \text{logit}(q_x^A)$$

where q_x is the life table probability of dying between birth and age x . By definition, $q_x = 1 - l_x$, where l_x is the standard life table function, with radix (l_0) equal to 1.

Given (i) target life expectancy, (ii) a set of l_x^A , (referred to as a "standard"), and (iii) a value for β , `e0_to_lifetab_logit()` finds a value for α that yields a set of q_x^B with the required life expectancy. If populations A and B are similar, then *beta* is likely to close to 1.

The target argument

target is a data frame specifying life expectancies for each population being modelled, and, optionally, inputs to the calculations, and 'by' variables.

target contains the following variables:

- A variable called "e0" giving life expectancy at birth.
- Optionally, a variable called "beta" with values for β . Can be an ordinary numeric vector or an [rvec](#). If target does not include a "beta" variable, then `e0_to_lifetab_logit()` sets β to 1.
- A variable called "sex". The "sex" variable must be supplied if the infant argument to `e0_to_lifetab_logit()` is "CD" or "AK", or if the child argument is "CD".
- Optionally, 'by' variables. Typical examples are time, region, and model variant.

The standard argument

standard is a data frame specifying the l_x to be used with each life expectancy in target, and, optionally, values for the average age person-years lived by people who die in each group, ${}_na_x$. Values in standard are age-specific.

standard contains the following variables:

- A variable called "age", with labels that can be parsed by `reformat_age()`.
- A variable called "lx". Cannot be an rvec.
- Additional variables used to match rows in standard to rows in target.

References

Brass W, Coale AJ. 1968. "Methods of analysis and estimation," in Brass, W, Coale AJ, Demeny P, Heisel DF, et al. (eds). The Demography of Tropical Africa. Princeton NJ: Princeton University Press, pp. 88–139.

Moultrie TA, Timæus IM. 2013. Introduction to Model Life Tables. In Moultrie T, Dorrington R, Hill A, Hill K, Timæus I, Zaba B. (eds). Tools for Demographic Estimation. Paris: International Union for the Scientific Study of Population. [online version](#).

See Also

- `tfr_to_asfr_scale` Fertility equivalent of `e0_to_lifetab_logit()`
- `logit()`, `invlogit()` Logit function
- `lifeexp()` Calculate life expectancy from detailed inputs

Examples

```
## create new life tables based on level-1
## 'West' model life tables, but with lower
## life expectancy

library(dplyr, warn.conflicts = FALSE)

target <- data.frame(sex = c("Female", "Male"),
                    e0 = c(17.5, 15.6))

standard <- west_lifetab |>
  filter(level == 1) |>
  select(sex, age, lx)

e0_to_lifetab_logit(target = target,
                   standard = standard,
                   infant = "CD",
                   child = "CD")

## target is an rvec
library(rvec, warn.conflicts = FALSE)
target_rvec <- data.frame(sex = c("Female", "Male"),
                        e0 = rnorm_rvec(n = 2,
```

```

                                mean = c(17.5, 15.6),
                                n_draw = 1000)
e0_to_lifetab_logit(target = target_rvec,
                    standard = standard)

```

ex_to_lifetab_brass *Derive Life Tables that Match Life Expectancies, using a Brass Logit Model*

Description

This function contained an error, and is deprecated. Please use function `e0_to_lifetab_logit()` instead.

Usage

```

ex_to_lifetab_brass(
  target,
  standard,
  infant = c("constant", "linear", "CD", "AK"),
  child = c("constant", "linear", "CD"),
  closed = c("constant", "linear"),
  open = "constant",
  radix = 1e+05,
  suffix = NULL
)

```

Arguments

target	A data frame containing a variable called "ex", and possibly other variables. See Details.
standard	A data frame containing variables called age and lx, and possibly others. See Details.
infant, child, closed, open	Methods used to calculate life expectancy. See <code>lifetab()</code> for details.
radix	Initial population for the lx column in the derived life table(s). Default is 100000.
suffix	Optional suffix added to life table columns.

Details

Function `ex_to_lifetab_brass()` used formula

$$\text{logit}(l_x^B) \approx \alpha + \beta \text{logit}(l_x^A)$$

,

instead of the conventional

$$\text{logit}(1 - l_x^B) \approx \alpha + \beta \text{logit}(1 - l_x^A)$$

Value

A [tibble](#).

find_label_female	<i>Identify Sex or Gender Labels Referring to Females</i>
-------------------	---

Description

Given labels for sex or gender, try to infer which (if any) refer to females. If no elements look like a label for females, or if two or more elements do, then return NULL.

Usage

```
find_label_female(nms)
```

Arguments

nms	A character vector
-----	--------------------

Value

An element of nms or NULL.

See Also

[find_label_male\(\)](#), [find_var_sexgender\(\)](#)

Examples

```
find_label_female(c("Female", "Male")) ## one valid
find_label_female(c("0-4", "5-9"))     ## none valid
find_label_female(c("F", "Fem"))      ## two valid
```

find_label_male	<i>Identify Sex or Gender Labels Referring to Males</i>
-----------------	---

Description

Given labels for sex or gender, try to infer which (if any) refer to males. If no elements look like a label for males, or if two or more elements do, then return NULL.

Usage

```
find_label_male(nms)
```

Arguments

nms	A character vector
-----	--------------------

Value

An element of nms or NULL.

See Also

[find_label_female\(\)](#), [find_var_sexgender\(\)](#)

Examples

```
find_label_male(c("Female", "Male")) ## one valid
find_label_male(c("0-4", "5-9"))     ## none valid
find_label_male(c("male", "m"))      ## two valid
```

find_var_age	<i>Identify an Age Variable</i>
--------------	---------------------------------

Description

Find the element of nms that looks like an age variable. If no elements look like an age variable, or if two or more elements do, then return NULL.

Usage

```
find_var_age(nms)
```

Arguments

nms	A character vector
-----	--------------------

Value

An element of nms, or NULL.

See Also

[find_var_time\(\)](#), [find_var_sexgender\(\)](#)

Examples

```
find_var_age(c("Sex", "Year", "AgeGroup", NA)) ## one valid
find_var_age(c("Sex", "Year"))                ## none valid
find_var_age(c("age", "age.years"))           ## two valid
```

find_var_sexgender *Identify a Sex or Gender Variable*

Description

Find the element of nms that looks like a sex or gender variable. If no elements look like a sex or gender variable, or if two or more elements do, then return NULL.

Usage

```
find_var_sexgender(nms)
```

Arguments

nms A character vector

Value

An element of nms, or NULL.

See Also

[find_var_age\(\)](#), [find_var_time\(\)](#), [find_label_female\(\)](#), [find_label_male\(\)](#)

Examples

```
find_var_sexgender(c("Sex", "Year", "AgeGroup", NA)) ## one valid
find_var_sexgender(c("Age", "Region"))                ## none valid
find_var_sexgender(c("sexgender", "sexes"))           ## two valid
```

find_var_time	<i>Identify a Time Variable</i>
---------------	---------------------------------

Description

Find the element of nms that looks like an time variable. If no elements look like a time variable, or if two or more elements do, then return NULL.

Usage

```
find_var_time(nms)
```

Arguments

nms	A character vector
-----	--------------------

Value

An element of nms, or NULL.

See Also

[find_var_age\(\)](#), [find_var_sexgender\(\)](#)

Examples

```
find_var_time(c("Sex", "Year", "AgeGroup", NA)) ## one valid
find_var_time(c("Sex", "Region"))             ## none valid
find_var_time(c("time", "year"))               ## two valid
```

groups_colnums	<i>Get a named vector of column indices for the grouping variables in a grouped data frame</i>
----------------	--

Description

Constructed a named vector of indices equivalent to the vectors produced by tidyselct::eval_select, but for the grouping variables in an object of class "grouped_df".

Usage

```
groups_colnums(data)
```

Arguments

data	A data frame.
------	---------------

Details

If data is not grouped, then `groups_colnums` returns a zero-length vector.

Value

A named integer vector.

Examples

```
library(dplyr)
df <- data.frame(x = 1:4,
                 g = c(1, 1, 2, 2))
groups_colnums(df)
df <- group_by(df, g)
groups_colnums(df)
```

`irn_fert`*Age-Specific Fertility Rates in Iran*

Description

Estimates of age-specific fertility rates, (births per 1000 person-years lived) for rural and urban areas, in Iran, 1986-2000. Calculated by Mohammad Jalal Abbasi-Shavazi and Peter McDonald from data from the 2000 Iran Demographic and Health Survey.

Usage

```
irn_fert
```

Format

A tibble with 2010 rows and the following columns:

- `time` Calendar year
- `age` Five-year age group from "15-19" to "45-49"
- `area` "Rural" or "Urban"
- `rate` Age-specific fertility rate

Source

Tables 4.1 and 4.2 of Abbasi-Shavazi, M J, McDonald, P (2005). *National and provincial level fertility trends in Iran, 1972-2006*. Australian National University. Working Papers in Demography no. 94.

`lifetab`*Calculate Life Tables or Life Expectancies*

Description

Calculate life table quantities. Function `lifetab()` returns an entire life table. Function `lifeexp()` returns life expectancy at birth. The inputs can be mortality rates (m_x) or probabilities of dying (q_x), though not both.

Usage

```
lifetab(  
  data,  
  mx = NULL,  
  qx = NULL,  
  age = age,  
  sex = NULL,  
  ax = NULL,  
  by = NULL,  
  infant = c("constant", "linear", "CD", "AK"),  
  child = c("constant", "linear", "CD"),  
  closed = c("constant", "linear"),  
  open = "constant",  
  radix = 1e+05,  
  suffix = NULL,  
  n_core = 1  
)
```

```
lifeexp(  
  data,  
  mx = NULL,  
  qx = NULL,  
  at = 0,  
  age = age,  
  sex = NULL,  
  ax = NULL,  
  by = NULL,  
  infant = c("constant", "linear", "CD", "AK"),  
  child = c("constant", "linear", "CD"),  
  closed = c("constant", "linear"),  
  open = "constant",  
  suffix = NULL,  
  n_core = 1  
)
```

Arguments

`data` Data frame with mortality data.

mx	<tidyselect> Mortality rates, expressed as deaths per person-year lived. Possibly an <i>rvec</i> .
qx	<tidyselect> Probability of dying within age interval. An alternative to mx. Possibly an <i>rvec</i> .
age	<tidyselect> Age group labels. The labels must be interpretable by functions such as <code>reformat_age()</code> and <code>age_group_type()</code> . The first age group must start at age 0, and the last age group must be "open", with no upper limit.
sex	<tidyselect> Biological sex, with labels that can be interpreted by <code>reformat_sex()</code> . Needed only when infant is "CD" or "AK", or child is "CD".
ax	<tidyselect> Average age at death within age group. Optional. See Details.
by	<tidyselect> Separate life tables, or life expectancies, calculated for each combination the by variables. If a sex variable was specified, then that variable is automatically included among the by variables. If data is a <i>grouped</i> data frame, then the grouping variables take precedence over by.
infant	Method used to calculate life table values in age group "0". Ignored if age does not include age group "0". Default is "constant".
child	Method used to calculate life table values in age group "1-4". Ignored if age does not include age group "0". Default is "constant".
closed	Method used to calculate life table values in closed age intervals other than "0" and "1-4" (ie intervals such as "10-14" or "12"). Default is "constant".
open	Method used to calculate life table values in the final, open age group (eg "80+" or "110+"). Currently the only option is "constant".
radix	Initial population for the lx column. Default is 100000.
suffix	Optional suffix added to new columns in result.
n_core	Number of cores to use for parallel processing. If n_core is 1 (the default), no parallel processing is done.
at	Age at which life expectancy is calculated (<code>lifeexp()</code> only). Default is 0. Can be a vector with length > 1.

Value

A *tibble*.

Definitions of life table quantities

- mx Deaths per person-year lived.
- qx Probability of surviving from the start of age group 'x' to the end.
- lx Number of people alive at the start of age group x.
- dx Number of deaths in age group x
- Lx Expected number of person years lived in age group x.
- ex Life expectancy, calculated at the start of age group x.

Mortality rates mx are sometimes expressed as deaths per 1000 person-years lived, or per 100,000 person-years lived. `lifetab()` and `lifeexp()` assumed that they are expressed as deaths per person-year lived.

Calculation methods

`lifetab()` and `lifeexp()` implement several methods for calculating life table quantities from mortality rates. Each method makes different assumptions about the way that mortality rates vary within age intervals:

- "constant" Mortality rates are constant within each interval.
- "linear". Life table quantity l_x is a straight line within each interval. Equivalently, deaths are distributed uniformly within each interval.
- "CD". Used only with age groups "0" and "1-4". Mortality rates decline over the age interval, with the slope depending on the absolute level of infant mortality. The formulas were developed by Coale and Demeny (1983), and used in Preston et al (2001).
- "AK". Used only with age group "0". Mortality rates decline over the age interval, with the slope depending on the absolute level of infant mortality. The formulas were developed by Andreev and Kingkade (2015), and are used in the Human Mortality Database [methods protocol](#).

For a detailed description of the methods, see the vignette for `poputils`.

ax

a_x is the average number of years lived in an age interval by people who die in that interval. Demographers sometimes refer to it as the 'separation factor'. If a non-NA value of a_x is supplied for an age group, then the results for that age group are based on the formula

$$m_x = d_x / (n_x l_x + a_x d_x)$$

,

(where n_x is the width of the age interval), over-riding any methods specified via the `infant`, `child`, `closed` and `open` arguments.

Open age group when inputs are qx

The probability of dying, q_x , is always 1 in the final (open) age group. q_x therefore provides no direct information on mortality conditions within the final age group. `lifetab()` and `lifeexp()` use conditions in the second-to-final age group as a proxy for conditions in the final age group. When `open` is "constant" (which is currently the only option), and no value for a_x in the final age group is provided, `lifetab()` and `lifeexp()` assume that $m_A = m_{A-1}$, and set $L_A = l_A / m_A$.

In practice, mortality is likely to be higher in the final age group than in the second-to-final age group, so the default procedure is likely to lead to inaccuracies. When the size of the final age group is very small, these inaccuracies will be inconsequential. But in other cases, it may be necessary to supply an explicit value for a_x for the final age group, or to use m_x rather than q_x as inputs.

Using rvecs to represent uncertainty

An `rvec` is a 'random vector', holding multiple draws from a distribution. Using an `rvec` for the m_x argument to `lifetab()` or `lifeexp()` is a way of representing uncertainty. This uncertainty is propagated through to the life table values, which will also be `rvecs`.

Parallel processing

Calculations can be slow when working with rvecs and many combinations of 'by' variables. In these cases, setting `n_core` to a number greater than 1, which triggers parallel processing, may help.

References

- Preston SH, Heuveline P, and Guillot M. 2001. *Demography: Measuring and Modeling Population Processes* Oxford: Blackwell.
- Coale AJ, Demeny P, and Vaughn B. 1983. *Regional model life tables and stable populations* New York: Academic Press.
- Andreev, E.M. and Kingkade, W.W., 2015. Average age at death in infancy and infant mortality level: Reconsidering the Coale-Demeny formulas at current levels of low mortality. *Demographic Research*, 33, pp.363-390.
- Human Mortality Database [Methods Protocol](#).
- [Tools for Demographic Estimation](#).

See Also

- [ex_to_lifetab_brass\(\)](#) Calculate life table from minimal inputs
- [q0_to_m0\(\)](#) Convert between infant mortality measures
- [tfr\(\)](#) Calculate total fertility rate

Examples

```
library(dplyr)

## life table for females based on 'level 1'
## mortality rates "West" model life table
west_lifetab |>
  filter(sex == "Female",
         level == 1) |>
  lifetab(mx = mx)

## change method for infant and children from
## default ("constant") to "CD"
west_lifetab |>
  filter(sex == "Female",
         level == 1) |>
  lifetab(mx = mx,
         sex = sex,
         infant = "CD",
         child = "CD")

## calculate life expectancies
## for all levels, using the 'by'
## argument to distinguish levels
west_lifetab |>
  lifeexp(mx = mx,
         sex = sex,
```

```

        infant = "CD",
        child = "CD",
        by = level)

## obtain the same result using
## 'group_by'
west_lifetab |>
  group_by(level) |>
  lifeexp(mx = mx,
          sex = sex,
          infant = "CD",
          child = "CD")

## calculations based on 'qx'
west_lifetab |>
  lifeexp(qx = qx,
          sex = sex,
          by = level)

## life expectancy at age 60
west_lifetab |>
  filter(level == 10) |>
  lifeexp(mx = mx,
          at = 60,
          sex = sex)

## life expectancy at ages 0 and 60
west_lifetab |>
  filter(level == 10) |>
  lifeexp(mx = mx,
          at = c(0, 60),
          sex = sex)

```

logit

Logit and Inverse-Logit Functions

Description

Transform values to and from the logit scale. `logit()` calculates

Usage

```
logit(p)
```

```
invlogit(x)
```

Arguments

`p` Values between 0 and 1. Can be an atomic vector, a matrix, or an [rvec](#).

`x` Values in the interval $(-\infty, \infty)$. Can be an atomic vector, a matrix, or an [rvec](#).

Details

$$x = \log\left(\frac{p}{1-p}\right)$$

and `invlogit()` calculates

$$p = \frac{e^x}{1 + e^x}$$

To avoid overflow, `invlogit()` uses $p = \frac{1}{1+e^{-x}}$ internally for x where $x > 0$.

In some of the demographic literature, the logit function is defined as

$$x = \frac{1}{2} \log\left(\frac{p}{1-p}\right).$$

`logit()` and `invlogit()` follow the conventions in statistics and machine learning, and omit the $\frac{1}{2}$.

Value

- A vector of doubles, if `p` or `x` is a vector.
- A matrix of doubles, if `p` or `x` is a matrix.
- An object of class `rvec_dbl`, if `p` or `x` is an `rvec`.

Examples

```
p <- c(0.5, 1, 0.2)
logit(p)
invlogit(logit(p))
```

matrix_to_list_of_cols

Turn a Matrix Into a List of Columns or Rows

Description

Given a matrix, create a list, each element of which contains a column or row from the matrix.

Usage

```
matrix_to_list_of_cols(m)
```

```
matrix_to_list_of_rows(m)
```

Arguments

`m` A matrix

Details

`matrix_to_list_of_cols()` and `matrix_to_list_of_rows()` are internal functions, for use by developers, and would not normally be called directly by end users.

Value

- `matrix_to_list_of_cols()` A list of vectors, each of which is a column from `x`.
- `matrix_to_list_of_rows()`, A list of vectors, each of which is a row from `x`.

Examples

```
m <- matrix(1:12, nrow = 3)
matrix_to_list_of_cols(m)
matrix_to_list_of_rows(m)
```

nzl_mort

Mortality Data for New Zealand

Description

Counts of deaths and population, by age, sex, and calendar year, plus mortality rates, for New Zealand, 2021-2022.

Usage

```
nzl_mort
```

Format

A data frame with 84 rows and the following variables:

- year Calendar year.
- gender "Female", and "Male".
- age Age, in life table age groups, with an open age group of 95+.
- deaths Counts of deaths, randomly rounded to base 3.
- popn Estimates of average annual population.
- mx Mortality rates (deaths / popn).

Source

Modified from data in tables "Deaths by age and sex (Annual-Dec)" and "Estimated Resident Population by Age and Sex (1991+) (Annual-Dec)" from Stats NZ online database *Infoshare*, downloaded on 24 September 2023.

nzl_mort_rvec

Mortality Data and Probabilistic Rates for New Zealand

Description

A modified version of `link{nzl_mort}` where `mx` columns is an [rvec](#), rather than an ordinary R vector. The `rvec` holds the random draws from the posterior distribution obtained from by a Bayesian statistical model.

Usage

```
nzl_mort_rvec
```

Format

An object of class `tbl_df` (inherits from `tbl`, `data.frame`) with 84 rows and 4 columns.

q0_to_m0

Convert q0 to m0

Description

Convert the probability of dying during infancy (q_0) to the mortality rate for infancy (m_0).

Usage

```
q0_to_m0(
  q0,
  sex = NULL,
  a0 = NULL,
  infant = c("constant", "linear", "CD", "AK")
)
```

Arguments

<code>q0</code>	Probability of dying in first year of life. A numeric vector or an rvec .
<code>sex</code>	Biological sex. A vector the same length as <code>q0</code> , with labels that can be interpreted by reformat_sex() . Needed only when <code>infant</code> is "CD" or "AK".
<code>a0</code>	Average age at death for infants who die. Optional. See help for lifetab() .
<code>infant</code>	Calculation method. See help for lifetab() . Default is "constant".

Value

A numeric vector or [rvec](#).

Warning

The term "infant mortality rate" is ambiguous. Demographers sometimes use it to refer to m_0 (which is an actual rate) and sometimes use it to refer to q_0 (which is a probability.)

See Also

- [lifetab\(\)](#) Calculate a full life table.

Examples

```
library(dplyr, warn.conflicts = FALSE)
west_lifetab |>
  filter(age == 0, level <= 5) |>
  select(level, sex, age, mx, qx) |>
  mutate(m0 = q0_to_m0(q0 = qx, sex = sex, infant = "CD"))
```

reformat_age	<i>Reformat Age Group Labels</i>
--------------	----------------------------------

Description

Convert age group labels to one of three formats:

- Single-year age groups, eg "0", "1", ..., "99", "100+".
- Life table age groups, eg "0", "1-4", "5-9", . . . , "95-99", "100+".
- Five-year age groups, eg "0-4", "5-9", ..., "95-99", "100+".

By default `reformat_age()` returns a factor that includes all intermediate age groups. See below for examples.

Usage

```
reformat_age(x, factor = TRUE)
```

Arguments

<code>x</code>	A vector.
<code>factor</code>	Whether the return value should be a factor.

Details

`reformat_age()` applies the following algorithm:

1. Tidy and translate text, eg convert "20 to 24 years" to "20-24", convert "infant" to "0", or convert "100 or more" to "100+".
2. Check whether the resulting labels could have been produced by [age_labels\(\)](#). If not, throw an error.

- If `factor` is `TRUE` (the default), then return a factor. The levels of this factor include all intermediate age groups. Otherwise return a character vector.

When `x` consists entirely of numbers, `reformat_age()` also checks for two special cases:

- If every element of `x` is a multiple of 5, and if $\max(x) \geq 50$, then `x` is assumed to describe 5-year age groups
- If every element of `x` is 0, 1, or a multiple of 5, with $\max(x) \geq 50$, then `x` is assumed to describe life table age groups.

Value

If `factor` is `TRUE`, then `reformat_age()` returns a factor; otherwise it returns a character vector.

See Also

[age_labels\(\)](#), [reformat_sex\(\)](#)

Examples

```
reformat_age(c("80 to 84", "90 or more", "85 to 89"))

## factor contains intermediate level missing from 'x'
reformat_age(c("80 to 84", "90 or more"))

## non-factor
reformat_age(c("80 to 84", "90 or more"),
             factor = FALSE)

## single
reformat_age(c("80", "90plus"))

## life table
reformat_age(c("0",
              "30-34",
              "10--14",
              "1-4 years"))
```

reformat_sex

Reformat a Binary Sex Variable

Description

Reformat a binary sex variable so that it consists entirely of values "Female", "Male", and possibly NA and any values included in `except`.

Usage

```
reformat_sex(x, except = NULL, factor = TRUE)
```

Arguments

x	A vector.
except	Values to exclude when reformatting.
factor	Whether the return value should be a factor.

Details

When parsing labels, `reformat_sex()` ignores case: "FEMALE" and "fEmAlE" are equivalent.

White space is removed from the beginning and end of labels.

`reformat_sex()` does not try to interpreting numeric codes (eg 1, 2).

Value

If `factor` is TRUE, then `reformat_age()` returns a factor; otherwise it returns a character vector.

See Also

[age_labels\(\)](#), [reformat_age\(\)](#)

Examples

```
reformat_sex(c("F", "female", NA, "MALES"))

## values supplied for 'except'
reformat_sex(c("Fem", "Other", "Male", "M"),
             except = c("Other", "Diverse"))

## return an ordinary character vector
reformat_sex(c("F", "female", NA, "MALES"),
             factor = FALSE)
```

rr3

Randomly Round A Vector of Integers to Base 3

Description

Apply the 'Random Round to Base 3' (RR3) algorithm to a vector of integers (or doubles where `round(x) == x`.)

Usage

```
rr3(x)
```

Arguments

x	A vector of integers (in the sense that <code>round(x) == x</code> .) Can be an rvec .
---	--

Details

The RR3 algorithm is used by statistical agencies to confidentialize data. Under the RR3 algorithm, an integer n is randomly rounded as follows:

- If n is divisible by 3, leave it unchanged
- If dividing n by 3 leaves a remainder of 1, then round down (subtract 1) with probability $2/3$, and round up (add 2) with probability $1/3$.
- If dividing n by 3 leaves a remainder of 2, then round down (subtract 2) with probability $1/3$, and round up (add 1) with probability $2/3$.

RR3 has some nice properties:

- The randomly-rounded version of n has expected value n .
- If n non-negative, then the randomly rounded version of n is non-negative.
- If n is non-positive, then the randomly rounded version of n is non-positive.

Value

A randomly-rounded version of x .

Examples

```
x <- c(1, 5, 2, 0, -1, 3, NA)
rr3(x)
```

set_age_open	<i>Specify Open Age Group</i>
--------------	-------------------------------

Description

Set the lower limit of the open age group. Given a vector of age group labels, recode all age groups with a lower limit greater than or equal to $\langle \text{lower} \rangle$ to $\langle \text{lower} \rangle +$.

Usage

```
set_age_open(x, lower)
```

Arguments

x	A vector of age labels.
$lower$	An integer. The lower limit for the open age group.

Details

set_age_open() requires that x and the return value have a a five-year, single-year, or life table format, as described in [age_labels\(\)](#).

Value

A modified version of `x`.

See Also

- `set_age_open()` uses `age_lower()` to identify lower limits
- `age_labels()` for creating age labels from scratch

Examples

```
x <- c("100+", "80-84", "95-99", "20-24")
set_age_open(x, 90)
set_age_open(x, 25)
```

tfr

Calculate Total Fertility Rates

Description

Calculate the total fertility rate (TFR) from age-specific fertility rates.

Usage

```
tfr(
  data,
  asfr = asfr,
  age = age,
  sex = NULL,
  by = NULL,
  denominator = 1,
  suffix = NULL
)
```

Arguments

<code>data</code>	Data frame with age-specific fertility rates and age
<code>asfr</code>	<tidyselect> Age-specific fertility rates. Possibly an <code>rvec</code> . Default is <code>asfr</code> .
<code>age</code>	<tidyselect> Age group labels. The labels must be interpretable by functions such as <code>reformat_age()</code> and <code>age_group_type()</code> . The age groups must not have gaps, and the highest age group must be "closed" (ie have an upper limit.) Default is <code>age</code> .
<code>sex</code>	<tidyselect> Sex/gender of the child (not the parent).
<code>by</code>	<tidyselect> Separate total fertility rates are calculated for each combination the by variables. If data is a <code>grouped</code> data frame, then the grouping variables take precedence over by.
<code>denominator</code>	The denominator used to calculate <code>asfr</code> . Default is 1.
<code>suffix</code>	Optional suffix added to "tfr" column in result.

Details

The total fertility rate is a summary measure for current fertility levels that removes the effect of age structure. It is obtained by summing up age-specific fertility rates, multiplying each rate by the width of the corresponding age group. For instance, the rate for age group "15-19" is multiplied by 5, and the rate for age group "15" is multiplied by 1.

The total fertility rate can be interpreted as the number of average children that a person would have, under prevailing fertility rates, if the person survived to the maximum age of reproduction. The hypothetical person is normally a woman, since age-specific fertility rates normally use person-years lived by women as the denominator. But it can apply to men, if the age-specific fertility rates are "paternity rates", i.e. rates that use person-years lived by men as the denominator.

Value

A [tibble](#).

Sex-specific fertility rates

Age-specific fertility rates do not normally specify the sex of the children who are born. In cases where they do, however, rates have to be summed across sexes to give the total fertility rates. If `tfr()` is supplied with a `sex` argument, it assumes that `sex` applies to the births, and sums over the sexes.

Denominator

Published tables of age-specific fertility rates often express the rates as births per 1000 person-years lived, rather than per person-year lived. (Sometimes this is expressed as "births per 1000 women".) In these cases

Using rvecs to represent uncertainty

An [rvec](#) is a 'random vector', holding multiple draws from a distribution. Using an `rvec` for the `asfr` argument to `tfr()` is a way of representing uncertainty. This uncertainty is propagated through to the TFR, which will also be `rvecs`.

See Also

- [lifeexp\(\)](#) Calculate life expectancy from age-specific mortality rates.

Examples

```
irn_fert |>
  tfr(asfr = rate,
      by = c(area, time),
      denominator = 1000)
```

tfr_to_asfr_scale	<i>Derive Age-Specific Fertility Rates that Match Total Fertility Rates by Scaling</i>
-------------------	--

Description

Turn total fertility rates (TFRs) into sets of age-specific fertility rates, by scaling a set of standard rates upwards or downwards.

Usage

```
tfr_to_asfr_scale(target, standard, suffix = NULL)
```

Arguments

target	A data frame containing a variable called "tfr", and possibly others. See Details.
standard	A data frame containing variables called age and asfr, and possibly others. See Details.
suffix	Optional suffix added to asfr column in results.

Value

A [tibble](#).

Method

Let ${}_n f_x$ be the age-specific fertility rate for people aged between x and $x + n$. Values for ${}_n f_x$ are obtained by scaling the standard rates ${}_n f_x^{\text{std}}$ so that they agree with the target total fertility rate F . That is, `tfr_to_asfr_scale()` sets

$${}_n f_x = \alpha \times {}_n f_x^{\text{std}}$$

where

$$\alpha = \frac{F}{\sum_x n \times {}_n f_x^{\text{std}}}$$

The target argument

target is a data frame specifying total fertility rates for each population being modelled.

target contains the following variables:

- A variable called "tfr". An ordinary numeric vector or an [rvec\(\)](#).
- Optionally, 'by' variables. Typical examples are time, region, and model variant.

The standard argument

standard is a data frame specifying standard fertility schedules to be used with each life expectancy in target. Values in standard are age-specific.

standard contains the following variables:

- A variable called "age", with labels that can be parsed by `reformat_age()`.
- A variable called "value", containing non-negative values. Cannot be an rvec.
- Additional variables used to match rows in standard to rows in target.

See Also

- `ex_to_lifetab_brass()` Life table equivalent of `tfr_to_asfr_scale()`.
- `booth_standard` The 'Booth standard' fertility schedule
- `tfr` Calculate total fertility rate from age-specific fertility rates

Examples

```
## create age-specific fertility rates
## based on the [Booth standard][booth_standard]
library(dplyr, warn.conflicts = FALSE)
target <- data.frame(region = c("A", "B"),
                    tfr = c(5.5, 4.7))

asfr <- tfr_to_asfr_scale(target = target,
                        standard = booth_standard)

asfr

## check consistency with original TFRs
asfr |>
  tfr(asfr = asfr, by = region)

## target is an rvec
library(rvec, warn.conflicts = FALSE)
target_rvec <- data.frame(region = c("A", "B"),
                        tfr = rnorm_rvec(n = 2,
                                       mean = c(5.5, 4.7),
                                       n_draw = 1000))

tfr_to_asfr_scale(target = target_rvec,
                  standard = booth_standard)
```

Description

Build a matrix where the elements are values of a measure variable, and the rows and columns are formed by observed combinations of ID variables. The ID variables picked out by rows and cols must uniquely identify cells. `to_matrix()`, unlike `stats::xtabs()`, does not sum across multiple combinations of ID variables.

Usage

```
to_matrix(x, rows, cols, measure)
```

Arguments

x	A data frame.
rows	The ID variable(s) used to distinguish rows in the matrix.
cols	The ID variable(s) used to distinguish columns in the matrix.
measure	The measure variable, eg rates or counts.

Value

A matrix

Examples

```
x <- expand.grid(age = c(0, 1, 2),
                sex = c("F", "M"),
                region = c("A", "B"),
                year = 2000:2001)
x$count <- 1:24

to_matrix(x,
          rows = c(age, sex),
          cols = c(region, year),
          measure = count)

to_matrix(x,
          rows = c(age, sex, region),
          cols = year,
          measure = count)

## cells not uniquely identified
try(
  to_matrix(x,
            rows = age,
            cols = sex,
            measure = count)
)
```

Description

Trim a vector so that all values are greater than 0 and less than 1.

Usage

```
trim_01(x)
```

Arguments

x A numeric vector. Can be an [rvec](#).

Details

If

- min is lowest element of x that is higher than 0, and
- max is the highest element of x that is lower than 1, then `trim_01()`
- shifts all elements of x that are lower than min upwards, so that they equal min, and
- shifts all elements of x that are higher than max downwards, so that they equal max.

Value

A trimmed version of x

See Also

- [logit\(\)](#), [invlogit\(\)](#) Logit transformation

Examples

```
x <- c(1, 0.98, -0.001, 0.5, 0.01)
trim_01(x)
```

west_lifetab

Coale-Demeny West Model Life Tables

Description

Life table quantities from the "West" family of Coale-Demeny model life tables.

Usage

```
west_lifetab
```

Format

A data frame with 1,050 rows and the following variables:

- level Index for life table. Lower level implies lower life expectancy.
- sex "Female", and "Male".
- age Age, in life table age groups, with an open age group of 95+.
- mx Mortality rate.
- ax Average years lived in age interval by people who die in that interval.
- qx Probability some alive at start of age interval dies during interval.
- lx Number of people still alive at start of age interval.
- dx Number of people dying during age interval.
- Lx Number of person-years lived during age interval.
- ex Expectation of life at start of age interval.

Source

Coale A, Demeny P, and Vaughn B. 1983. Regional model life tables and stable populations. 2nd ed. New York: Academic Press, accessed via `demogR::cdmltw()`.

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