

# Package ‘LTASR’

April 13, 2022

**Title** Functions to Replicate the Center for Disease Control and Prevention's 'LTAS' Software in R

**Version** 0.0.1

**Description** A suite of functions for reading in a rate file in XML format, stratify a cohort, and calculate 'SMRs' from the stratified cohort and rate file.

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**Encoding** UTF-8

**RoxygenNote** 7.1.2

**Imports** dplyr, knitr, lubridate, magrittr, purrr, readr, rlang,  
stringr, tidyverse, XML, zoo

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**VignetteBuilder** knitr

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**LazyData** true

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**NeedsCompilation** no

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checkPerson	<i>Check person dataframe</i>
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**Description**

`checkPerson` checks that the person dataframe is formatted correctly

**Usage**

```
checkPerson(person)
```

**Arguments**

person	person dataframe
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**Value**

No return value, called for side effects

**Examples**

```
library(LTASR)
library(dplyr)

#Import example peron file
person <- person_example %>%
  mutate(dob = as.Date(dob, format='%m/%d/%Y'),
        pybegin = as.Date(pybegin, format='%m/%d/%Y'),
        dlo = as.Date(dlo, format='%m/%d/%Y'))

#Returns nothing
checkPerson(person)
```

---

**checkStrata***Checks all strata in py\_table are contained in rate file*

---

**Description**

Checks all strata in py\_table are contained in rate file

**Usage**

```
checkStrata(py_table, rateobj)
```

**Arguments**

py_table	A stratified cohort created by get_table
rateobj	A rate object created by parseRate

**Value**

A list containing:

1. The py\_table with strata removed not found in rateobj
2. The observations from py\_table that were removed

**Examples**

```
library(LTASR)
library(dplyr)

#Import example person file
person <- person_example %>%
  mutate(dob = as.Date(dob, format='%m/%d/%Y'),
        pybegin = as.Date(pybegin, format='%m/%d/%Y'),
        dlo = as.Date(dlo, format='%m/%d/%Y'))

#Import default rate object
rateobj <- us_119ucod_19602020

#Stratify person table
py_table <- get_table(person, rateobj)

#Check Strata are in rate file
checkStrata(py_table, rateobj)
```

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expand_dates	<i>Expand a data.frame to include all dates between a start and end value defined by parameters x and y</i>
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---

**Description**

Expand a data.frame to include all dates between a start and end value defined by parameters x and y

**Usage**

```
expand_dates(df, start, end)
```

**Arguments**

df	Input data.frame
start	start date
end	end date

**Value**

A data.frame/tibble containing all variables of the input data.frame as well as a new variable, date, with repeated rows for each date between start and end.

**Examples**

```
library(LTASR)
data <- data.frame(start = as.Date('3/1/2015', format='%m/%d/%Y'),
                    end = as.Date('3/15/2015', format='%m/%d/%Y'))
expand_dates(data, start, end)
```

---

get_table	<i>Stratify Person Table</i>
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**Description**

get\_table reads in a data.frame/tibble containing basic demographic information for each person of the cohort and stratifies the person-time and deaths into 5-year age, 5-year calendar period, race, and sex strata. See Details for information on how the person file must be formatted.

**Usage**

```
get_table(persondf, rateobj, batch_size = 25, strata = dplyr::vars())
```

## Arguments

<code>persondf</code>	data.frame like object containing one row per person with the required demographic information
<code>rateobj</code>	a rate object created by the <code>parseRate</code> function
<code>batch_size</code>	a number specifying how many persons to stratify at a time. Default is 25.
<code>strata</code>	any additional variables contained in <code>persondf</code> on which to stratify. Must be wrapped in a <code>vars()</code> call from <code>dplyr</code> .

## Details

The person file must contain the variables:

- `id`,
- `gender` (numeric: 'M'/'F'),
- `race` (numeric: 'W'/'N'),
- `dob` (date),
- `pybegin` (date),
- `dlo` (date),
- `rev` (numeric: 5-10),
- `code` (character: ICD code)

## Value

A data.frame with a row for each strata containing the number of observed deaths within each of the defined minors/outcomes (\_o1-\_xxxx) and the number of person days.

## Examples

```
library(LTASR)
library(dplyr)

#Import example person file
person <- person_example %>%
  mutate(dob = as.Date(dob, format='%m/%d/%Y'),
        pybegin = as.Date(pybegin, format='%m/%d/%Y'),
        dlo = as.Date(dlo, format='%m/%d/%Y'))

#Import default rate object
rateobj <- us_119ucod_19602020

#Stratify person table
py_table <- get_table(person, rateobj)
```

---

`get_table_history`      *Stratify Person Table with Time Varying Co-variate*

---

## Description

`get_table_history` reads in a data.frame/tibble containing basic demographic information for each person of the cohort as well as a data.frame/tibble containing time varying exposure information and stratifies the person-time and deaths into 5-year age, 5-year calendar period, race, sex and exposure categories. See Details for information on how the person file and history file must be formatted.

## Usage

```
get_table_history(
  persondf,
  rateobj,
  batch_size = 25,
  strata = dplyr::vars(),
  historydf,
  exp,
  cutpt,
  lag = 0
)
```

## Arguments

<code>persondf</code>	data.frame like object containing one row per person with the required demographic information
<code>rateobj</code>	a rate object created by the <code>parseRate</code> function
<code>batch_size</code>	a number specifying how many persons to stratify at a time. Default is 25.
<code>strata</code>	any additional variables contained in <code>persondf</code> on which to stratify. Must be wrapped in a <code>vars()</code> call from <code>dplyr</code> .
<code>historydf</code>	data.frame like object containing temporal exposure data. Each row represents a period of time during which the values of the temporal stratifiers remain constant. Multiple rows per id are typical.
<code>exp</code>	the name of the exposure variable found within <code>historydf</code>
<code>cutpt</code>	a numeric vector containing the cut-points to use to stratify the calculated cumulative exposure for variable <code>exp</code> . Should include min and max values (typically -Inf and Inf).
<code>lag</code>	An optional numeric variable indicating a lag, in years, to be applied to exposure variables. Specified in years. Default is 0 yrs (un-lagged).

## Details

The person file must contain the variables:

- id,
- gender (numeric: 'M'/'F'),
- race (numeric: 'W'/'N'),
- dob (date),
- pybegin (date),
- dlo (date),
- rev (numeric: 5-10),
- code (character: ICD code)

Additionally, a history file is read in containing daily exposures levels and the begin and end dates of that level. The history file must contain the following variables:

- id,
- begin\_dt (date),
- end\_dt (date),
- <daily exposure levels>

## Value

A data.frame with a row for each strata containing the number of observed deaths within each of the defined minors/outcomes (\_o1-\_xxxx) and the number of person days.

## Examples

```
library(LTASR)
library(dplyr)
library(lubridate)

#Import example person file
person <- person_example %>%
  mutate(dob = as.Date(dob, format='%m/%d/%Y'),
        pybegin = as.Date(pybegin, format='%m/%d/%Y'),
        dlo = as.Date(dlo, format='%m/%d/%Y'))

#Import example history file
history <- history_example %>%
  mutate(begin_dt = as.Date(begin_dt, format='%m/%d/%Y'),
        end_dt = as.Date(end_dt, format='%m/%d/%Y'))

#Import default rate object
rateobj <- us_119ucod_19602020

#Stratify cohort employed variable. The employed variable indicates (0/1) periods of employment
#and will be summed each day of each exposure period. Therefore, this calculates
#duration of employment in days. The cut-points used below will stratify
```

```
#by person-time with less than and greater than a year of employment (365 days of employment).
py_table <- get_table_history(persondf = person,
                             rateobj = rateobj,
                             historydf = history,
                             exp = employed,
                             cutpt = c(-Inf, 365, Inf))

#Investigate cumulative exposure values for the exposure_level variable.
#This aids in determining appropriate cut-points for stratification.
history_example %>%
  mutate(begin_dt = as.Date(begin_dt, format='%m/%d/%Y'),
         end_dt = as.Date(end_dt, format='%m/%d/%Y')) %>%
  mutate(dur = difftime(end_dt, begin_dt, units = 'days')) %>%
  as.numeric() %>%
  `+`(1),
  cum = dur*exposure_level) %>%
  group_by(id) %>%
  summarize(cum = sum(cum))

#Stratify cohort with exposure variable. This will stratify by person-time with
#with less than and greater than 15000 unit-days of cumulative exposure.
py_table <- get_table_history(persondf = person,
                             rateobj = rateobj,
                             historydf = history,
                             exp = exposure_level,
                             cutpt = c(-Inf, 15000, Inf),
                             lag = 10)
```

**history\_example**      *Example History File for Testing*

## Description

A tibble containing example history file data to be used for testing and demonstration of the package

## Usage

`history_example`

## Format

A data frame with 4 rows and 5 variables:

**id** unique identifier; numeric

**begin\_dt** beginning date of an exposure period; character

**end\_dt** beginning date of an exposure period; character

**employed** a hypothetical variable indicating employment during the given exposure period; numeric (0/1)

**exposure\_level** a hypothetical variable identifying daily exposure levels to be summed to calculate a cumulative exposure; numeric  
...

## Source

Internally Generated

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mapDeaths	<i>Map ICD codes to grouped minors</i>
-----------	--

---

## Description

Map ICD codes to grouped minors

## Usage

```
mapDeaths(persondf, rateobj)
```

## Arguments

persondf	Person data.frame
rateobj	A rate object created from parseRate

## Value

A data.frame for each death observed in the person file with the following variables: id, code, rev: from the persondf minor: the minor/outcome from the rate file that the death was mapped to

## Examples

```
library(LTASR)

#Import example person file
person <- person_example

#Import default rate object
rateobj <- us_119ucod_19602020

#Check mapping of deaths to minors/outcomes
mapDeaths(person, rateobj)
```

**parseRate***Parses LTAS rate file in .xml format***Description**

Parses LTAS rate file in .xml format

**Usage**

```
parseRate(xmlpath)
```

**Arguments**

<code>xmlpath</code>	path of LTAS rate file
----------------------	------------------------

**Value**

returns a list containing:

1. `$residual`: the minor number where all unknown deaths will be assigned
2. `$MinorDesc`: a dataframe/tibble giving descriptions of minor numbers as well as how minors are mapped to majors
3. `$mapping`: a dataframe/tibble listing how each icd-code and revision will be mapped to each minor number

**person\_example***Example Person File for Testing***Description**

A tibble containing example person file data to be used for testing and demonstration of the package

**Usage**

```
person_example
```

**Format**

A tibble with 3 observations and 9 variables:

**id** unique identifier; character

**gender** Gender/Sex; character 'M' or 'F'

**race** Race; character 'W' or 'N'

**dob** Date of Birth; character to be converted to date

**pybegin** date to begin follow-up/at-risk accumulation, character to be converted to date

**dlo** Date last observed; character to be converted to date  
**vs** indicator identifying the vital status of the cohort. A value of 'D' indicates an observed death; character  
**rev** ICD revision of the ICD code; numeric  
**code** ICD-code for the cause of death; character ...

## Source

Internally Generated

smr\_custom

*Calculate SMRs for Custom minor groupings*

## Description

smr\_major will collapse minor outcomes into "major" groupings as defined in the rate object, rateobj.

## Usage

```
smr_custom(smr_minor_table, minor_grouping)
```

## Arguments

smr_minor_table	A data.frame/tibble as created by smr_minor containing observed and expected number of deaths for each minor outcome
minor_grouping	A numeric vector defining which minors to group together

## Value

A data.frame/tibble containing the expected and observed number of deaths as well the SMR, lower CI and upper CI for the outcome by the user

## Examples

```
library(LTASR)
library(dplyr)

#Import example person file
person <- person_example %>%
  mutate(dob = as.Date(dob, format='%m/%d/%Y'),
        pybegin = as.Date(pybegin, format='%m/%d/%Y'),
        dlo = as.Date(dlo, format='%m/%d/%Y'))

#Import default rate object
rateobj <- us_119ucod_19602020
```

```
#Stratify person table
py_table <- get_table(person, rateobj)

#Calculate SMRs for all minors
smr_minor_table <- smr_minor(py_table, rateobj)

#Calculate custom minor grouping for all deaths
smr_custom(smr_minor_table, 1:119)

#' #Calculate custom minor grouping for all deaths
smr_custom(smr_minor_table, 4:40)
```

**smr\_major***Calculate SMRs for Major groupings***Description**

`smr_major` will collapse minor outcomes into "major" groupings as defined in the rate object, `rateobj`.

**Usage**

```
smr_major(smr_minor_table, rateobj)
```

**Arguments**

<code>smr_minor_table</code>	A data.frame/tibble as created by <code>smr_minor</code> containing observed and expected number of deaths for each minor outcome
<code>rateobj</code>	A rate object created by <code>parseRate</code>

**Value**

A data.frame/tibble containing the expected and observed number of deaths as well as SMRs, lower CI and upper CI for each major as defined in the rate object `rateobj`

**Examples**

```
library(LTASR)
library(dplyr)

#Import example person file
person <- person_example %>%
  mutate(dob = as.Date(dob, format='%m/%d/%Y'),
        pybegin = as.Date(pybegin, format='%m/%d/%Y'),
        dlo = as.Date(dlo, format='%m/%d/%Y'))

#Import default rate object
```

```

rateobj <- us_119ucod_19602020

#Stratify person table
py_table <- get_table(person, rateobj)

#Calculate SMRs for all minors
smr_minor_table <- smr_minor(py_table, rateobj)

#Calculate SMRs major groupings found within rate file
smr_major(smr_minor_table, rateobj)

```

**smr\_minor***Calculate SMRs for Minors***Description**

`smr_minor` calculates SMRs for all minor groupings found within the rate object, `rateobj`, for the stratified cohort `py_table`

**Usage**

```
smr_minor(py_table, rateobj)
```

**Arguments**

<code>py_table</code>	A stratified cohort created by <code>get_table</code>
<code>rateobj</code>	A rate object created by <code>parseRate</code>

**Value**

A dataframe/tibble containing the expected and observed number of deaths as well as SMRs, lower CI and upper CI for each minor found in the rate object `rateobj`

**Examples**

```

library(LTASR)
library(dplyr)

#Import example person file
person <- person_example %>%
  mutate(dob = as.Date(dob, format='%m/%d/%Y'),
        pybegin = as.Date(pybegin, format='%m/%d/%Y'),
        dlo = as.Date(dlo, format='%m/%d/%Y'))

#Import default rate object
rateobj <- us_119ucod_19602020

#Stratify person table

```

```
py_table <- get_table(person, rateobj)  
  
#Calculate SMRs for all minors  
smr_minor(py_table, rateobj)
```

---

us\_119ucod\_19602020     *119 UCOD U.S. Death Rate, 1960-2020*

---

## Description

A list containing referent underlying cause of death (UCOD) rate information for the US population from 1960-2020 for the 119 minor/outcome LTAS groupings

## Usage

```
us_119ucod_19602020
```

## Format

A list with 4 elements:

**residual** the minor/outcome number to which unknown/uncategorized outcomes will be mapped to  
**MinorDesc** a data.frame containing descriptions for each minor and major grouping  
**mapping** a tibble detailing which minor number each icd-code and revision combination will be mapped to  
**rates** the population referent rate for each minor for each gender/race/calendar period/age strata ...

## Source

Available upon request from nioshltas@cdc.gov

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