

Package ‘lillies’

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Title Estimation of Life Years Lost

Version 0.2.12

Description Estimation of life expectancy and Life Years Lost (LYL, or lillies for short) for a given population, for example those with a given disease or condition. In addition, the package can be used to compare estimates from different populations, or to estimate confidence intervals. Technical details of the method are available in Plana-Ripoll et al. (2020) <[doi:10.1371/journal.pone.0228073](https://doi.org/10.1371/journal.pone.0228073)> and Andersen (2017) <[doi:10.1002/sim.7357](https://doi.org/10.1002/sim.7357)>.

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Contents

aggreg_data	2
lyl	3
lyl_2plot	5
lyl_aggregated	6
lyl_aggregated_range	8

lyl_checkplot	11
lyl_ci	12
lyl_compare_plot	13
lyl_diff	15
lyl_diff_ref	17
lyl_range	19
plot.lyl	22
plot.lyl_aggregated	23
plot.lyl_ci	24
plot.lyl_range	25
pop_ref	26
simu_data	27
summary.lyl	28
summary.lyl_aggregated	29
summary.lyl_ci	30
summary.lyl_range	31

Index 33

aggreg_data	<i>Simulated aggregated data for Life Years Lost estimation.</i>
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Description

A dataset containing age-specific number of new cases, number of deaths and mortality rates for a simulated disease with onset after age 40 years. Data is available for ages 40-90 years.

Usage

```
aggreg_data
```

Format

A data frame with 50 rows and 4 variables:

age age

new_cases number of new cases diagnosed at that specific age

deaths number of deaths among the diagnosed at that specific age

rate age-specific mortality rates among the diagnosed

Source

Simulated data

lyl *Life Years Lost at one specific age.*

Description

lyl estimates remaining life expectancy and Life Years Lost for a given population after a specific age `age_specific` and restricted to a maximum theoretical age τ .

Usage

```
lyl(
  data,
  t0 = NULL,
  t,
  status,
  age_specific,
  censoring_label = "Alive",
  death_labels = "Dead",
  tau = 100
)
```

Arguments

<code>data</code>	A dataframe, where each row represents a person. The dataframe will have a time-to-event format with at least two variables: age at end of follow-up (<code>t</code>) and status indicator with death/censoring (<code>status</code>). Note that this package is not developed to be used with tibbles.
<code>t0</code>	Age at start of the follow-up time. Default is NULL, which means all subjects are followed from birth. For delayed entry, <code>t0</code> indicates age at beginning of follow-up.
<code>t</code>	Age at the end of the follow-up time (death or censoring).
<code>status</code>	Status indicator, normally 0=alive, 1=dead. Other choices are TRUE/FALSE (TRUE = death) or 1/2 (2=death). For multiple causes of death (competing risks analysis), the status variable will be a factor, whose first level is treated as censoring; or a numeric variable, whose lowest level is treated as censoring. In the latter case, the label for censoring is <code>censoring_label</code> ("Alive" by default).
<code>age_specific</code>	Specific age at which the Life Years Lost have to be estimated.
<code>censoring_label</code>	Label for censoring status. If <code>status</code> is not a factor, "Alive" by default. If <code>status</code> is a factor, the first level will be treated as censoring label.
<code>death_labels</code>	Label for event status. For only one cause of death, "Dead" is the default. For multiple causes, the default are the values given in variable <code>status</code> .
<code>tau</code>	Remaining life expectancy and Life Years Lost are estimated restricted to a maximum theoretical age τ ($\tau=100$ years by default).

Value

A list with class "lyl" containing the following components:

- `data`: Data frame with 3 variables and as many observations as the original data provided to estimate Life Years Lost: t_0 , t , and `status`
- `LYL`: Data frame with 1 observation and at least 3 variables: `age` which corresponds to `age_specific`; `life_exp` which is the estimated remaining life expectancy at age `age_specific` years and before age `tau` years; and one variable corresponding to the estimated Life Years Lost for each specific cause of death. If only one cause of death is considered (no competing risks), this variable is `Dead` and includes the total overall Life Years Lost
- `tau`: Maximum theoretical age τ
- `age_specific`: Specific age at which the Life Years Lost have been estimated
- `data_plot`: A data frame in long format with 3 variables `time`, `cause`, and `cip` used to create a Figure of Life Years Lost with function `plot`.
- `censoring_label`: Label for censoring status
- `death_labels`: Label(s) for death status
- `competing_risks`: Logical value (TRUE = more than one cause of death (competing risks))
- `type`: Whether the estimation is at "age_specific" or "age_range".

References

- Andersen PK. Life years lost among patients with a given disease. *Statistics in Medicine*. 2017;36(22):3573- 3582.
- Andersen PK. Decomposition of number of life years lost according to causes of death. *Statistics in Medicine*. 2013;32(30):5278-5285.
- Plana-Ripoll et al. lillies – An R package for the estimation of excess Life Years Lost among patients with a given disease or condition. *PLoS ONE*. 2020;15(3):e0228073.

See Also

- `lyl_range` for estimation of Life Years Lost for a range of different ages.
- `lyl_ci` to estimate bootstrapped confidence intervals.
- `lyl_diff` to compare Life Years Lost for two populations.
- `summary.lyl` to summarize objects obtained with function `lyl`.
- `plot.lyl` to plot objects obtained with function `lyl`.

Examples

```
# Load simulated data as example
data(simu_data)

# Estimate remaining life expectancy and Life Years
# Lost after age 45 years and before age 95 years
lyl_estimation <- lyl(data = simu_data, t = age_death, status = death,
                    age_specific = 45, tau = 95)
```

```

# Summarize and plot the data
summary(lyl_estimation)
plot(lyl_estimation)

# Estimate remaining life expectancy and Life Years
# Lost due to specific causes of death after age 45
# years and before age 95 years

lyl_estimation2 <- lyl(data = simu_data, t = age_death, status = cause_death,
                      age_specific = 45, tau = 95)

# Summarize and plot the data
summary(lyl_estimation2)
plot(lyl_estimation2)

```

lyl_2plot

Plot Life Years Lost at one specific age for two different populations

Description

lyl_2plot was used to create a figure of Life Years Lost at one specific age for two different populations. Please use lyl_compare_plot instead.

Usage

```

lyl_2plot(
  x,
  y,
  color_alive = NA,
  colors = NA,
  labels = c("Population of interest", "Reference population"),
  ...
)

```

Arguments

x	An object of class lyl (obtained with function lyl).
y	An object of class lyl (obtained with function lyl).
color_alive	Color to be used for the censoring category. Default is NA, and default color is "white".
colors	Vector with one color for each cause of death. Default is NA, and default colors are used.
labels	Vector with labels for the two populations (default are "Population of interest" for x, and "Reference population" for y)
...	Additional arguments affecting the plot produced.

Value

A plot with survival function and stacked cause-specific cumulative incidences for two populations side by side.

References

- Plana-Ripoll et al. lillies – An R package for the estimation of excess Life Years Lost among patients with a given disease or condition. *PLoS ONE*. 2020;15(3):e0228073.

See Also

- [lyl](#) for estimation of Life Years Lost at one specific age.
- [lyl_diff](#) to compare Life Years Lost for two populations.

Examples

```
# Load simulated data as example
data(simu_data)

# Estimate remaining life expectancy and Life Years
# Lost after age 45 years and before age 95 years
lyl_estimation <- lyl(data = simu_data, t = age_death, status = cause_death,
                    age_specific = 45, tau = 95)

# Same estimate for those with a specific disease
diseased <- simu_data[!is.na(simu_data$age_disease), ]

lyl_estimation1 <- lyl(data = diseased, t0 = age_disease,
                    t = age_death, status = cause_death,
                    age_specific = 45, tau = 95)

# Plot the data
lyl_compare_plot(list(lyl_estimation1, lyl_estimation))
```

lyl_aggregated

Life Years Lost at one specific age using aggregated data.

Description

lyl estimates differences in remaining life expectancy and Life Years Lost for two given life tables data and data0 after a specific age age_speficic and restricted to a maximum theoretical age τ .

Usage

```
lyl_aggregated(
  data,
  age,
  rates,
```

```

    surv,
    data0,
    age0,
    rates0,
    surv0,
    age_specific,
    censoring_label = "Alive",
    death_labels = "Dead",
    tau = 100
  )

```

Arguments

<code>data</code>	A dataframe, where each row represents an age, for the population of interest. The dataframe will contain information on age-specific mortality rates or survival probability (if both parameters are provided, rates will be used).
<code>age</code>	Variable in <code>data</code> containing information on age.
<code>rates</code>	Variable in <code>data</code> containing information on age-specific mortality rates.
<code>surv</code>	Variable in <code>data</code> containing information on age-specific survival probability.
<code>data0</code>	A dataframe, where each row represents an age, for the population of reference. The dataframe will contain information on age-specific mortality rates or survival probability (if both parameters are provided, rates will be used).
<code>age0</code>	Variable in <code>data0</code> containing information on age.
<code>rates0</code>	Variable in <code>data0</code> containing information on age-specific mortality rates.
<code>surv0</code>	Variable in <code>data0</code> containing information on age-specific survival probability.
<code>age_specific</code>	Specific age at which the Life Years Lost have to be estimated.
<code>censoring_label</code>	Label for censoring status ("Alive" by default).
<code>death_labels</code>	Label for event status ("Dead" by default).
<code>tau</code>	Remaining life expectancy and Life Years Lost are estimated restricted to a maximum theoretical age τ ($\tau=100$ years by default).

Value

A list with class "lyl_aggregated" containing the following components:

- `data`: Name of the dataset provided in parameter `data`
- `data0`: Name of the dataset provided in parameter `data0`
- `LYL`: Data frame with 1 observation and 3 variables: `age` which corresponds to `age_specific`; and `life_exp` and `life_exp0` which are the estimated remaining life expectancies at age `age_specific` years and before age `tau` years for the population provided in `data` and `data0`, respectively
- `tau`: Maximum theoretical age τ
- `age_specific`: Specific age at which the Life Years Lost have been estimated

- `data_plot`: A data frame in long format with 3 variables `time`, `cause`, and `cip` used to create a Figure of Life Years Lost with function `plot`.
- `censoring_label`: Label for censoring status
- `death_labels`: Label(s) for death status
- `type`: Whether the estimation is at "age_specific" or "age_range"

References

- Andersen PK. Life years lost among patients with a given disease. *Statistics in Medicine*. 2017;36(22):3573- 3582.
- Andersen PK. Decomposition of number of life years lost according to causes of death. *Statistics in Medicine*. 2013;32(30):5278-5285.
- Plana-Ripoll et al. lillies – An R package for the estimation of excess Life Years Lost among patients with a given disease or condition. *PLoS ONE*. 2020;15(3):e0228073.#

See Also

- [lyl_aggregated_range](#) for estimation of Life Years Lost for a range of different ages.
- [summary.lyl_aggregated](#) to summarize objects obtained with function `lyl_aggregated`.
- [plot.lyl_aggregated](#) to plot objects obtained with function `lyl_aggregated`.

Examples

```
# Load simulated data as example
data(aggreg_data)
data(pop_ref)

# Estimate remaining life expectancy and Life Years
# Lost after age 70 years and before age 90 years
lyl_summary_data70 <- lyl_aggregated(data = aggre_data, age = age, rates = rate,
                                   data0 = pop_ref, age0 = age, surv0 = survival,
                                   age_specific = 70, tau = 90)

# Summarize and plot the data
summary(lyl_summary_data70)
plot(lyl_summary_data70)
```

`lyl_aggregated_range` *Life Years Lost at a range of different ages using aggregated data.*

Description

`lyl` estimates differences in remaining life expectancy and Life Years Lost for two given life tables `data` and `data0` after a range of specific ages (`age_begin` to `age_end`) and restricted to a maximum theoretical age τ .

Usage

```

lyl_aggregated_range(
  data,
  age,
  rates,
  surv,
  weights,
  data0,
  age0,
  rates0,
  surv0,
  age_begin,
  age_end,
  censoring_label = "Alive",
  death_labels = "Dead",
  tau = 100
)

```

Arguments

<code>data</code>	A dataframe, where each row represents an age, for the population of interest. The dataframe will contain information on age-specific mortality rates or survival probability (if both parameters are provided, rates will be used).
<code>age</code>	Variable in <code>data</code> containing information on age.
<code>rates</code>	Variable in <code>data</code> containing information on age-specific mortality rates.
<code>surv</code>	Variable in <code>data</code> containing information on age-specific survival probability.
<code>weights</code>	Variable in <code>data</code> containing information on number of new cases per age. A weighted average is provided using these weights.
<code>data0</code>	A dataframe, where each row represents an age, for the population of reference. The dataframe will contain information on age-specific mortality rates or survival probability (if both parameters are provided, rates will be used).
<code>age0</code>	Variable in <code>data0</code> containing information on age.
<code>rates0</code>	Variable in <code>data0</code> containing information on age-specific mortality rates.
<code>surv0</code>	Variable in <code>data0</code> containing information on age-specific survival probability.
<code>age_begin</code>	Specific starting age at which the Life Years Lost have to be estimated.
<code>age_end</code>	Specific ending age at which the Life Years Lost have to be estimated.
<code>censoring_label</code>	Label for censoring status ("Alive" by default).
<code>death_labels</code>	Label for event status ("Dead" by default).
<code>tau</code>	Remaining life expectancy and Life Years Lost are estimated restricted to a maximum theoretical age τ ($\tau=100$ years by default).

Value

A list with class "lyl_aggregated" containing the following components:

- data: Name of the dataset provided in parameter data
- data0: Name of the dataset provided in parameter data0
- LYL: Data frame with 1 observation and 2 variables: life_exp and life_exp0 which are the estimated remaining life expectancies averaged over the age range and before age tau years for the population provided in data and data0, respectively
- tau: Maximum theoretical age τ
- age_begin: Specific starting age at which the Life Years Lost have been estimated
- age_end: Specific ending age at which the Life Years Lost have been estimated
- data_plot: A data frame in long format with 3 variables time, cause, and cip used to create a Figure of Life Years Lost with function [plot](#).
- censoring_label: Label for censoring status
- death_labels: Label(s) for death status
- type: Whether the estimation is at "age_specific" or "age_range".

References

- Andersen PK. Life years lost among patients with a given disease. *Statistics in Medicine*. 2017;36(22):3573- 3582.
- Andersen PK. Decomposition of number of life years lost according to causes of death. *Statistics in Medicine*. 2013;32(30):5278-5285.
- Plana-Ripoll et al. lillies – An R package for the estimation of excess Life Years Lost among patients with a given disease or condition. *PLoS ONE*. 2020;15(3):e0228073.#

See Also

- [lyl_aggregated](#) for estimation of Life Years Lost at one specific age.
- [summary.lyl_aggregated](#) to summarize objects obtained with function `lyl_aggregated_range`.

Examples

```
# Load simulated data as example
data(aggreg_data)
data(pop_ref)

# Estimate remaining life expectancy and Life Years
# Lost after each age from 40 to 89 years and before age 90 years
lyl_summary_data <- lyl_aggregated_range(data = aggreg_data, age = age,
                                       rates = rate, weights = new_cases,
                                       data0 = pop_ref, age0 = age, surv0 = survival,
                                       age_begin = 40, age_end = 89, tau = 90)

# Summarize the data
summary(lyl_summary_data)
```

lyl_checkplot	<i>Plot number of persons at risk at each specific age.</i>
---------------	---

Description

Given a `lyl_range`-class object, `lyl_checkplot` draws numbers of persons at risk of dying at each specific age from `age_begin` until age τ .

Usage

```
lyl_checkplot(x)
```

Arguments

`x` An object of class `lyl_range` obtained with the `lyl_range` function.

Value

A plot with the number of persons at risk at each specific age.

References

- Plana-Ripoll et al. lillies – An R package for the estimation of excess Life Years Lost among patients with a given disease or condition. *PLoS ONE*. 2020;15(3):e0228073.

See Also

[lyl_range](#) for estimation of Life Years Lost for a range of different ages.

Examples

```
# Load simulated data as example
data(simu_data)

# Estimate remaining life expectancy and Life Years
# Lost after each age from 0 to 94 years and before age 95 years
lyl_estimation <- lyl_range(data = simu_data, t = age_death, status = death,
                           age_begin = 45, age_end = 50, tau = 95)

# Check whether small numbers could compromise the results
lyl_checkplot(lyl_estimation)

# The plot can be modified with a usual ggplot2 format
lyl_checkplot(lyl_estimation) +
  ggplot2::geom_hline(yintercept = 10, linetype = "dashed", color = "red") +
  ggplot2::xlab("Age [in years]") +
  ggplot2::ggtitle("Persons at risk of dying at each age 0-94 years")
```

lyl_ci *Confidence intervals for Life Years Lost.*

Description

lyl_ci estimates confidence intervals for Life Years Lost using non-parametric bootstrap. The confidence level can be specified when summarizing the results with the function `summary.lyl_ci`.

Usage

```
lyl_ci(lyl_estimation, niter = 1000)
```

Arguments

`lyl_estimation` An object of class `lyl` or `lyl_range`.
`niter` Number of iterations for the bootstrap (default is 1,000).

Value

A list with class "lyl_ci" containing the following components:

- `LYL`: Data frame with one observation per age and at least 3 variables: `age`; `life_exp` which is the estimated remaining life expectancy at age `age_specific` years and before age `tau` years; and one variable corresponding to the estimated Life Years Lost for each specific cause of death. If only one cause of death is considered (no competing risks), this variable is `Dead` and includes the total overall Life Years Lost
- `LYL_ci`: Data frame with one observation per age-iteration and at least 4 variables: `age`; `iteration`, which correspond to each specific iteration; `life_exp` which is the estimated remaining life expectancy at age `age_specific` years and before age `tau` years; and one variable corresponding to the estimated Life Years Lost for each specific cause of death. If only one cause of death is considered (no competing risks), this variable is `Dead` and includes the total overall Life Years Lost
- `tau`: Maximum theoretical age τ
- `age_specific`: Specific age at which the Life Years Lost have been estimated
- `age_begin`: Specific starting age at which the Life Years Lost have been estimated
- `age_end`: Specific ending age at which the Life Years Lost have been estimated
- `death_labels`: Label(s) for death status
- `competing_risks`: Logical value (TRUE = more than one cause of death (competing risks))
- `type`: Whether the estimation is at "age_specific" or "age_range".
- `niter`: Number of iterations used to estimate the confidence intervals

References

- Plana-Ripoll et al. lillies – An R package for the estimation of excess Life Years Lost among patients with a given disease or condition. *PLoS ONE*. 2020;15(3):e0228073.

See Also

- [lyl](#) for estimation of Life Years Lost at one specific age.
- [lyl_range](#) for estimation of Life Years Lost for a range of different ages.
- [lyl_diff](#) to compare Life Years Lost for two populations.
- [summary.lyl_ci](#) to summarize objects obtained with function `lyl_ci`.
- [plot.lyl_ci](#) to plot objects obtained with function `lyl_ci`.

[lyl_range](#) for estimation of Life Years Lost for a range of different ages.

Examples

```
# Load simulated data as example
data(simu_data)

# Estimate remaining life expectancy and Life Years
# Lost after age 45 years and before age 95 years
lyl_estimation <- lyl(data = simu_data, t = age_death, status = death,
                    age_specific = 45, tau = 95)

# Calculate bootstrapped confidence interval (3 iterations to test; more are necessary)
lyl_estimation_ci <- lyl_ci(lyl_estimation, niter = 3)
summary(lyl_estimation_ci)
plot(lyl_estimation_ci)

# Estimate remaining life expectancy and Life Years
# Lost after each age from 0 to 94 years and before age 95 years
lyl_estimation2 <- lyl_range(data = simu_data, t = age_death, status = death,
                          age_begin = 0, age_end = 94, tau = 95)

# Calculate bootstrapped confidence interval (3 iterations to test; more are necessary)
lyl_estimation_ci2 <- lyl_ci(lyl_estimation2, niter = 3)
summary(lyl_estimation_ci2, weights = simu_data$age_disease)
plot(lyl_estimation_ci2, weights = simu_data$age_disease)
```

lyl_compare_plot

Plot Life Years Lost at one specific age for two or more different populations

Description

`lyl_compare_plot` creates a figure of Life Years Lost at one specific age for two or more different populations.

Usage

```
lyl_compare_plot(
  x,
  color_alive = NA,
  colors = NA,
  nrow = NULL,
  ncol = NULL,
  dir = "h",
  reverse_legend = FALSE,
  labels = NA,
  ...
)
```

Arguments

<code>x</code>	A list of objects of class <code>lyl</code> (obtained with function <code>lyl</code>).
<code>color_alive</code>	Color to be used for the censoring category. Default is <code>NA</code> , and default color is "white".
<code>colors</code>	Vector with one color for each cause of death. Default is <code>NA</code> , and default colors are used.
<code>nrow</code>	Number of rows to be passed to <code>facet_wrap</code> .
<code>ncol</code>	Number of columns to be passed to <code>facet_wrap</code> .
<code>dir</code>	Direction to be passed to <code>facet_wrap</code> : either "h" for horizontal, the default, or "v", for vertical.
<code>reverse_legend</code>	Reverse the order of elements in the legend. Default is <code>FALSE</code> , indicating that first is the censoring label and then all causes of death.
<code>labels</code>	Vector with labels for the two populations (default are "Population of interest" for <code>x</code> , and "Reference population" for <code>y</code>)
<code>...</code>	Additional arguments affecting the plot produced.

Value

A plot with survival function and stacked cause-specific cumulative incidences for two populations side by side.

References

- Plana-Ripoll et al. *lillies* – An R package for the estimation of excess Life Years Lost among patients with a given disease or condition. *PLoS ONE*. 2020;15(3):e0228073.

See Also

- [lyl](#) for estimation of Life Years Lost at one specific age.
- [lyl_diff](#) to compare Life Years Lost for two populations.

Examples

```

# Load simulated data as example
data(simu_data)

# Estimate remaining life expectancy and Life Years
# Lost after age 45 years and before age 95 years
lyl_estimation <- lyl(data = simu_data, t = age_death, status = cause_death,
                    age_specific = 45, tau = 95)

# Same estimate for those with a specific disease
diseased <- simu_data[!is.na(simu_data$age_disease), ]

lyl_estimation1 <- lyl(data = diseased, t0 = age_disease,
                    t = age_death, status = cause_death,
                    age_specific = 45, tau = 95)

# Plot the data
lyl_compare_plot(list(lyl_estimation1, lyl_estimation))
lyl_compare_plot(list(lyl_estimation1, lyl_estimation),
                labels = c("Population with a disease", "General population"))

# The plot can be modified with a usual ggplot2 format
lyl_compare_plot(list(lyl_estimation1, lyl_estimation)) +
  ggplot2::xlab("Age [in years]") +
  ggplot2::ggtitle("Differences in Life Years Lost at age 45 years")

```

lyl_diff

Summarize differences in Life Years Lost.

Description

lyl_diff summarizes differences in estimated Life Years Lost in two different populations: lyl_estimation compared to lyl_estimation0.

Usage

```

lyl_diff(
  lyl_population1,
  lyl_population0,
  decimals = 2,
  level = 0.95,
  weights = NA
)

```

Arguments

lyl_population1	Population of interest: An object of class <code>lyl</code> or <code>lyl_range</code> (obtained with functions <code>lyl</code> or <code>lyl_range</code>). Alternatively, an object of class <code>lyl_ci</code> can be provided for bootstrapped confidence intervals.
lyl_population0	Reference population: An object of class <code>lyl</code> or <code>lyl_range</code> (obtained with functions <code>lyl</code> or <code>lyl_range</code>). Alternatively, an object of class <code>lyl_ci</code> can be provided for bootstrapped confidence intervals.
decimals	Number of decimals to be reported (default is 2).
level	Confidence level if <code>lyl_population1</code> or <code>lyl_population0</code> is obtained with the <code>lyl_ci</code> function (default is 0.95 for 95% confidence intervals)
weights	Vector with age distribution of disease/condition onset to be used when Life Years Lost are estimated over a range of ages (with <code>lyl_range</code> function). If weights are not provided (default is <code>weights = NA</code>), then the differences in Life Years Lost at each age is provided. If weights are provided, then a weighted average is provided.

Value

A table with the summary of the differences between two populations.

References

- Plana-Ripoll et al. lillies – An R package for the estimation of excess Life Years Lost among patients with a given disease or condition. *PLoS ONE*. 2020;15(3):e0228073.

See Also

- [lyl](#) for estimation of Life Years Lost at one specific age.
- [lyl_range](#) for estimation of Life Years Lost for a range of different ages.

Examples

```
# Load simulated data as example
data(simu_data)

### For the overall population and for those with a disease
diseased <- simu_data[!is.na(simu_data$age_disease), ]

# Estimate remaining life expectancy and Life Years
# Lost due to specific causes of death after age 45
# years and before age 95 years
lyl_estimation0 <- lyl(data = simu_data, t = age_death, status = cause_death,
  age_specific = 45, tau = 95)
lyl_estimation1 <- lyl(data = diseased, t0 = age_disease,
  t = age_death, status = cause_death,
  age_specific = 45, tau = 95)
lyl_diff(lyl_estimation1, lyl_estimation0)
```

```

lyl_compare_plot(list(lyl_estimation1, lyl_estimation0))

# Calculate bootstrapped confidence interval (3 iterations to test; more are necessary)
lyl_estimation1_ci <- lyl_ci(lyl_estimation1, niter = 3)

lyl_estimation0_ci <- lyl_ci(lyl_estimation0, niter = 3)
lyl_diff(lyl_estimation1_ci, lyl_estimation0_ci)

# It is also possible to assume no uncertainty for one of the estimates
lyl_diff(lyl_estimation1_ci, lyl_estimation0)

# Estimate remaining life expectancy and Life Years
# Lost due to specific causes of death after each age
# from 0 to 94 years and before age 95 years
lyl_estimation2 <- lyl_range(data = simu_data, t = age_death, status = cause_death,
                           age_begin = 0, age_end = 94, tau = 95)
lyl_estimation3 <- lyl_range(data = diseased, t0 = age_disease,
                           t = age_death, status = cause_death,
                           age_begin = 0, age_end = 94, tau = 95)
lyl_diff(lyl_estimation3, lyl_estimation2)
lyl_diff(lyl_estimation3, lyl_estimation2, weights = diseased$age_disease)

# Calculate bootstrapped confidence interval (3 iterations to test; more are necessary)
lyl_estimation3_ci <- lyl_ci(lyl_estimation3, niter = 3)
lyl_diff(lyl_estimation3_ci, lyl_estimation2, weights = diseased$age_disease)

```

lyl_diff_ref

Summarize differences in Life Years Lost.

Description

lyl_diff summarizes differences in estimated Life Years Lost in two different populations: lyl_estimation1 compared to a life table provided in data_ref.

Usage

```

lyl_diff_ref(
  lyl_population1,
  data_ref,
  age,
  surv,
  rates,
  decimals = 2,
  level = 0.95,
  weights = NA,
  lyl_population0
)

```

Arguments

lyl_population1	Population of interest: An object of class lyl or lyl_range (obtained with functions lyl or lyl_range). Alternatively, an object of class lyl_ci can be provided for bootstrapped confidence intervals.
data_ref	A dataframe, where each row represents an age, for the population of reference. The dataframe will contain information on age-specific mortality rates or survival probability (if both parameters are provided, rates will be used).
age	Variable in data_ref containing information on age.
surv	Variable in data_ref containing information on age-specific survival probability.
rates	Variable in data_ref containing information on age-specific mortality rates.
decimals	Number of decimals to be reported (default is 2).
level	Confidence level if lyl_population1 or lyl_population0 is obtained with the lyl_ci function (default is 0.95 for 95% confidence intervals)
weights	Vector with age distribution of disease/condition onset to be used when Life Years Lost are estimated over a range of ages (with lyl_range function). If weights are not provided (default is weights = NA), then the differences in Life Years Lost at each age is provided. If weights are provided, then a weighted average is provided.
lyl_population0	Parameter automatically created.

Value

A table with the summary of the differences between two populations.

References

- Plana-Ripoll et al. lillies – An R package for the estimation of excess Life Years Lost among patients with a given disease or condition. *PLoS ONE*. 2020;15(3):e0228073.

See Also

- [lyl](#) for estimation of Life Years Lost at one specific age.
- [lyl_range](#) for estimation of Life Years Lost for a range of different ages.

Examples

```
# Load simulated data as example
data(simu_data)
data(pop_ref)

# Estimate remaining life expectancy and Life Years
# Lost due to specific causes of death after age 45
# years and before age 95 years for those with a disease
diseased <- simu_data[!is.na(simu_data$age_disease), ]
```

```

lyl_estimation1 <- lyl(data = diseased, t0 = age_disease,
                      t = age_death, status = cause_death,
                      age_specific = 45, tau = 95)
lyl_diff_ref(lyl_estimation1, pop_ref, age = age, surv = survival)
lyl_diff_ref(lyl_estimation1, pop_ref, age = age, rates = mortality_rates)

# Calculate bootstrapped confidence interval (3 iterations to test; more are necessary)
lyl_estimation1_ci <- lyl_ci(lyl_estimation1, niter = 3)
lyl_diff_ref(lyl_estimation1_ci, pop_ref, age = age, surv = survival)

# Estimate remaining life expectancy and Life Years
# Lost due to specific causes of death after each age
# from 0 to 94 years and before age 95 years
lyl_estimation2 <- lyl_range(data = diseased, t0 = age_disease,
                            t = age_death, status = cause_death,
                            age_begin = 0, age_end = 94, tau = 95)
lyl_diff_ref(lyl_estimation2, pop_ref, age = age, surv = survival)
lyl_diff_ref(lyl_estimation2, pop_ref, age = age, surv = survival, weights = diseased$age_disease)

```

lyl_range

Life Years Lost at a range of different ages.

Description

lyl estimates remaining life expectancy and Life Years Lost for a given population after a range of specific ages (age_begin to age_end) and restricted to a maximum theoretical age τ .

Usage

```

lyl_range(
  data,
  t0 = NULL,
  t,
  status,
  age_begin,
  age_end,
  censoring_label = "Alive",
  death_labels = "Dead",
  tau = 100
)

```

Arguments

data A dataframe, where each row represents a person. The dataframe will have a time-to-event format with at least two variables: age at end of follow-up (t) and status indicator with death/censoring (status). Note that this package is not developed to be used with tibbles.

t0	Age at start of the follow-up time. Default is NULL, which means all subjects are followed from birth. For delayed entry, t0 indicates beginning of follow-up.
t	Age at the end of the follow-up time (death or censoring).
status	Status indicator, normally 0=alive, 1=dead. Other choices are TRUE/FALSE (TRUE = death) or 1/2 (2=death). For multiple causes of death (competing risks analysis), the status variable will be a factor, whose first level is treated as censoring; or a numeric variable, whose lowest level is treated as censoring. In the latter case, the label for censoring is censoring_label ("Alive" by default).
age_begin	Specific starting age at which the Life Years Lost have to be estimated.
age_end	Specific ending age at which the Life Years Lost have to be estimated.
censoring_label	Label for censoring status. If status is not a factor, "Alive" by default. If status is a factor, the first level will be treated as censoring label.
death_labels	Label for event status. For only one cause of death, "Dead" is the default. For multiple causes, the default are the values given in variable status.
tau	Remaining life expectancy and Life Years Lost are estimated restricted to a maximum theoretical age τ ($\tau=100$ years by default).

Value

A list with class "lyl_range" containing the following components:

- data: Data frame with 3 variables and as many observations as the original data provided to estimate Life Years Lost: t0, t, and status
- LYL: Data frame with (age_end - age_begin + 1) observations and at least 3 variables: age which corresponds to each specific age from age_begin to age_end; life_exp which is the estimated remaining life expectancy at age specific age and before age tau years; and one variable corresponding to the estimated Life Years Lost for each specific cause of death. If only one cause of death is considered (no competing risks), this variable is Dead and includes the total overall Life Years Lost
- tau: Maximum theoretical age τ
- age_begin: Specific starting age at which the Life Years Lost have been estimated
- age_end: Specific ending age at which the Life Years Lost have been estimated
- censoring_label: Label for censoring status
- death_labels: Label(s) for death status
- competing_risks: Logical value (TRUE = more than one cause of death (competing risks))
- numbers_at_risk: Data frame with (tau - age_begin + 1) observations and 2 variables: age which corresponds to each specific age from age_begin to tau; and number which is the number of persons at risk of dying at each specific age
- type: Whether the estimation is at "age_specific" or "age_range".

References

- Andersen PK. Life years lost among patients with a given disease. *Statistics in Medicine*. 2017;36(22):3573- 3582.
- Andersen PK. Decomposition of number of life years lost according to causes of death. *Statistics in Medicine*. 2013;32(30):5278-5285.
- Plana-Ripoll et al. lillies – An R package for the estimation of excess Life Years Lost among patients with a given disease or condition. *PLoS ONE*. 2020;15(3):e0228073.

See Also

- [lyl](#) for estimation of Life Years Lost at one specific age.
- [lyl_diff](#) to compare average Life Years Lost for two populations.
- [lyl_checkplot](#) to check whether small numbers could compromise the estimation.
- [lyl_ci](#) to estimate bootstrapped confidence intervals.
- [summary.lyl_range](#) to summarize objects obtained with function `lyl_range`.
- [plot.lyl_range](#) to plot objects obtained with function `lyl_range`.

Examples

```
# Load simulated data as example
data(simu_data)

# Estimate remaining life expectancy and Life Years
# Lost after each age from 0 to 94 years and before age 95 years
lyl_estimation <- lyl_range(data = simu_data, t = age_death, status = death,
                           age_begin = 0, age_end = 94, tau = 95)

# Visualize data at each different specific age
summary(lyl_estimation)
plot(lyl_estimation)

# Summarize data over an age distribution
summary(lyl_estimation, weights = simu_data$age_disease)

# Estimate remaining life expectancy and Life Years
# Lost due to specific causes of death after each age
# from 0 to 94 years and before age 95 years
lyl_estimation2 <- lyl_range(data = simu_data, t = age_death, status = cause_death,
                            age_begin = 0, age_end = 94, tau = 95)

# Visualize data at each different specific age
summary(lyl_estimation2)
plot(lyl_estimation2)

# Summarize data over an age distribution
summary(lyl_estimation2, weights = simu_data$age_disease)
```

`plot.lyl`*Plot Life Years Lost at one specific age*

Description

plot for objects of class `lyl` creates a figure of Life Years Lost at one specific age.

Usage

```
## S3 method for class 'lyl'  
plot(x, color_alive = NA, colors = NA, reverse_legend = FALSE, ...)
```

Arguments

<code>x</code>	An object of class <code>lyl</code> (obtained with function <code>lyl</code>).
<code>color_alive</code>	Color to be used for the censoring category. Default is <code>NA</code> , and default color is "white".
<code>colors</code>	Vector with one color for each cause of death. Default is <code>NA</code> , and default colors are used.
<code>reverse_legend</code>	Reverse the order of elements in the legend. Ddefault is <code>FALSE</code> , indicating that first is the censoring label and then all causes of death.
<code>...</code>	Additional arguments affecting the plot produced.

Value

A plot with survival function and stacked cause-specific cumulative incidences.

References

- Plana-Ripoll et al. lillies – An R package for the estimation of excess Life Years Lost among patients with a given disease or condition. *PLoS ONE*. 2020;15(3):e0228073.

See Also

- [lyl](#) for estimation of Life Years Lost at one specific age.

Examples

```
# Load simulated data as example  
data(simu_data)  
  
# Estimate remaining life expectancy and Life Years  
# Lost after age 45 years and before age 95 years  
lyl_estimation <- lyl(data = simu_data, t = age_death, status = cause_death,  
                    age_specific = 45, tau = 95)  
  
# Summarize and plot the data
```

```

plot(lyl_estimation)
plot(lyl_estimation, colors = c("chocolate", "cornflowerblue"))

# The plot can be modified with a usual ggplot2 format
plot(lyl_estimation) +
  ggplot2::xlab("Age [in years]") +
  ggplot2::ggtitle("Life Years Lost at age 45 years")

```

plot.lyl_aggregated *Plot Life Years Lost at one specific age for two different populations obtained from aggregated data*

Description

plot for objects of class `lyl_aggregated` creates a figure of Life Years Lost at one specific age for two different populations.

Usage

```

## S3 method for class 'lyl_aggregated'
plot(
  x,
  color_alive = NA,
  colors = NA,
  labels = c("Population of interest", "Reference population"),
  ...
)

```

Arguments

<code>x</code>	An object of class <code>lyl_aggregated</code> (obtained with function <code>lyl_aggregated</code>).
<code>color_alive</code>	Color to be used for the censoring category. Default is <code>NA</code> , and default color is "white".
<code>colors</code>	Vector with one color for each cause of death. Default is <code>NA</code> , and default colors are used.
<code>labels</code>	Vector with labels for the two populations (default are "Population of interest" for <code>data</code> , and "Reference population" for <code>data0</code> ; which are provided to function <code>lyl_aggregated</code> .)
<code>...</code>	Additional arguments affecting the plot produced.

Value

A plot with survival function and stacked cause-specific cumulative incidences for two populations side by side.

References

- Plana-Ripoll et al. lillies – An R package for the estimation of excess Life Years Lost among patients with a given disease or condition. *PLoS ONE*. 2020;15(3):e0228073.

See Also

- [lyl_aggregated](#) for estimation of Life Years Lost at one specific age.

Examples

```
# Load simulated data as example
data(aggreg_data)
data(pop_ref)

# Estimate remaining life expectancy and Life Years
# Lost after age 70 years and before age 90 years
lyl_summary_data70 <- lyl_aggregated(data = aggre_data, age = age, rates = rate,
                                   data0 = pop_ref, age0 = age, surv0 = survival,
                                   age_specific = 70, tau = 90)

# Plot the data
plot(lyl_summary_data70)
```

plot.lyl_ci

Plot evolution of bootstrapped parameters for Life Years Lost

Description

plot for objects of class `lyl_ci` creates a figure of the bootstrapped Life Years Lost to examine if the number of iterations is enough.

Usage

```
## S3 method for class 'lyl_ci'
plot(x, level = 0.95, weights, ...)
```

Arguments

<code>x</code>	An object of class <code>lyl_ci</code> (obtained with function <code>lyl_ci</code>).
<code>level</code>	Confidence level (default is 0.95 for 95% confidence intervals)
<code>weights</code>	Vector with age distribution of disease/condition onset to be used when Life Years Lost are estimated over a range of ages (with <code>lyl_range</code> function).
<code>...</code>	Additional arguments affecting the plot produced.

Value

A plot with the evolution of bootstrapped parameters.

References

- Plana-Ripoll et al. lillies – An R package for the estimation of excess Life Years Lost among patients with a given disease or condition. *PLoS ONE*. 2020;15(3):e0228073.

See Also

- [lyl_range](#) for estimation of Life Years Lost for a range of different ages.
- [lyl](#) for estimation of Life Years Lost at one specific age.
- [lyl_ci](#) to estimate bootstrapped confidence intervals.

Examples

```
# Load simulated data as example
data(simu_data)

# Estimate remaining life expectancy and Life Years
# Lost after age 45 years and before age 95 years
lyl_estimation <- lyl(data = simu_data, t = age_death, status = death,
                    age_specific = 45, tau = 95)

# Calculate bootstrapped confidence interval (10 iterations to test)
lyl_estimation_ci <- lyl_ci(lyl_estimation, niter = 10)
plot(lyl_estimation_ci)

# Estimate remaining life expectancy and Life Years
# Lost after each age from 0 to 94 years and before age 95 years
lyl_estimation2 <- lyl_range(data = simu_data, t = age_death, status = death,
                          age_begin = 0, age_end = 94, tau = 95)

# Calculate bootstrapped confidence interval
lyl_estimation_ci2 <- lyl_ci(lyl_estimation2)
plot(lyl_estimation_ci2, weights = simu_data$age_disease)
```

plot.lyl_range

Plot Life Years Lost at a range of different ages

Description

plot for objects of class `lyl_range` creates a figure of Life Years Lost at a range of different ages.

Usage

```
## S3 method for class 'lyl_range'
plot(x, colors = NA, ...)
```

Arguments

x	An object of class <code>lyl_range</code> (obtained with function <code>lyl_range</code>).
colors	Vector with one color for each cause of death. Default is NA, and default colors are used.
...	Additional arguments affecting the plot produced.

Value

A plot with age-specific life expectancy and life years lost.

References

- Plana-Ripoll et al. lillies – An R package for the estimation of excess Life Years Lost among patients with a given disease or condition. *PLoS ONE*. 2020;15(3):e0228073.

See Also

- [lyl_range](#) for estimation of Life Years Lost for a range of different ages.

Examples

```
# Load simulated data as example
data(simu_data)

# Estimate remaining life expectancy and Life Years
# Lost due to specific causes of death after each age
# from 30 to 40 years and before age 95 years
lyl_estimation <- lyl_range(data = simu_data, t = age_death, status = cause_death,
                           age_begin = 30, age_end = 40, tau = 95)

# Summarize and plot the data
plot(lyl_estimation)
plot(lyl_estimation, colors = c("chocolate", "cornflowerblue"))

# The plot can be modified with a usual ggplot2 format
plot(lyl_estimation) +
  ggplot2::xlab("Age [in years]") +
  ggplot2::ggtitle("Life Years Lost at ages 30-40 years")
```

pop_ref

Aggregated data for Life Years Lost estimation.

Description

A dataset containing age-specific survival probability and mortality rates for Danish women in years 2017-2018.

Usage

pop_ref

Format

A data frame with 100 rows and 3 variables:

age age

survival survival probability at that specific age

mortality_rates age-specific mortality rates

Source

Statistics Denmark (<https://www.dst.dk/en/Statistik/emner/befolkning-og-valg/>)

simu_data

Simulated population for Life Years Lost estimation.

Description

A dataset containing age and cause of death, as well as age at disease diagnosis (or start of a condition) for 100,000 simulated persons.

Usage

simu_data

Format

A data frame with 100000 rows and 6 variables:

id unique identifier of each person

age_start age at start of follow-up (0 for all individuals)

age_death age at end of follow-up (death or censoring)

death logical variable (TRUE = death / FALSE = censoring)

cause_death factor variable with 3 levels: "Alive" (for those censored) and "Natural" and "Unnatural" (for those dying of natural and unnatural causes of death, respectively)

age_disease age at developing a specific disease or condition for those 32,391 individuals that develop the disease (missing for the remaining 67,609)

Source

Simulated data

`summary.lyl`*Summarize Life Years Lost at one specific age*

Description

`summary` for objects of class `lyl` summarizes Life Years Lost at one specific age.

Usage

```
## S3 method for class 'lyl'  
summary(object, decimals = 2, difference = FALSE, ...)
```

Arguments

<code>object</code>	An object of class <code>lyl</code> (obtained with function <code>lyl</code>).
<code>decimals</code>	Number of decimals to be reported (default is 2).
<code>difference</code>	Parameter automatically created by the package.
<code>...</code>	Additional arguments affecting the summary produced.

Value

A table with the summary of the results.

References

- Plana-Ripoll et al. lillies – An R package for the estimation of excess Life Years Lost among patients with a given disease or condition. *PLoS ONE*. 2020;15(3):e0228073.

See Also

- [lyl](#) for estimation of Life Years Lost at one specific age.

Examples

```
# Load simulated data as example  
data(simu_data)  
  
# Estimate remaining life expectancy and Life Years  
# Lost after age 45 years and before age 95 years  
lyl_estimation <- lyl(data = simu_data, t = age_death, status = death,  
                    age_specific = 45, tau = 95)  
  
# Summarize and plot the data  
summary(lyl_estimation)
```

`summary.lyl_aggregated`*Summarize Life Years Lost at one specific age*

Description

summary for objects of class `lyl_aggregated` summarizes Life Years Lost.

Usage

```
## S3 method for class 'lyl_aggregated'  
summary(object, decimals = 2, ...)
```

Arguments

<code>object</code>	An object of class <code>lyl_aggregated</code> (obtained with function <code>lyl_aggregated</code> or <code>lyl_aggregated_range</code>).
<code>decimals</code>	Number of decimals to be reported (default is 2).
<code>...</code>	Additional arguments affecting the summary produced.

Value

A table with the summary of the results.

References

- Plana-Ripoll et al. lillies – An R package for the estimation of excess Life Years Lost among patients with a given disease or condition. *PLoS ONE*. 2020;15(3):e0228073.

See Also

- [lyl_aggregated](#) for estimation of Life Years Lost at one specific age.
- [lyl_aggregated_range](#) for estimation of Life Years Lost for a range of different ages.

Examples

```
# Load simulated data as example  
data(aggreg_data)  
data(pop_ref)  
  
# Estimate remaining life expectancy and Life Years  
# Lost after age 70 years and before age 90 years  
lyl_summary_data70 <- lyl_aggregated(data = aggreg_data, age = age, rates = rate,  
                                   data0 = pop_ref, age0 = age, surv0 = survival,  
                                   age_specific = 70, tau = 90)  
  
# Summarize and plot the data  
summary(lyl_summary_data70)
```

summary.lyl_ci *Summarize Life Years Lost with confidence intervals*

Description

summary for objects of class `lyl_ci` summarizes Life Years Lost at one specific age or over a range of different ages, including bootstrapped confidence intervals

Usage

```
## S3 method for class 'lyl_ci'
summary(
  object,
  decimals = 2,
  level = 0.95,
  weights = NA,
  difference = FALSE,
  ...
)
```

Arguments

<code>object</code>	An object of class <code>lyl_ci</code> (obtained with function <code>lyl_ci</code>).
<code>decimals</code>	Number of decimals to be reported (default is 2).
<code>level</code>	Confidence level (default is 0.95 for 95% confidence intervals)
<code>weights</code>	Vector with age distribution of disease/condition onset to be used when Life Years Lost are estimated over a range of ages (with <code>lyl_range</code> function). If weights are not provided (default is <code>weights = NA</code>), then the differences in Life Years Lost at each age is provided. If weights are provided, then a weighted average is provided.
<code>difference</code>	Parameter automatically created by the package.
<code>...</code>	Additional arguments affecting the summary produced.

Value

A table with the summary of the results.

References

- Plana-Ripoll et al. lillies – An R package for the estimation of excess Life Years Lost among patients with a given disease or condition. *PLoS ONE*. 2020;15(3):e0228073.

See Also

- [lyl](#) for estimation of Life Years Lost at one specific age.
- [lyl_range](#) for estimation of Life Years Lost for a range of different ages.
- [lyl_ci](#) to estimate bootstrapped confidence intervals.

Examples

```
# Load simulated data as example
data(simu_data)

# Estimate remaining life expectancy and Life Years
# Lost after age 45 years and before age 95 years
lyl_estimation <- lyl(data = simu_data, t = age_death, status = death,
                    age_specific = 45, tau = 95)

# Calculate bootstrapped confidence interval (3 iterations to test; more are necessary)
lyl_estimation_ci <- lyl_ci(lyl_estimation, niter = 3)
summary(lyl_estimation_ci)

# Estimate remaining life expectancy and Life Years
# Lost after each age from 0 to 94 years and before age 95 years
lyl_estimation2 <- lyl_range(data = simu_data, t = age_death, status = death,
                           age_begin = 0, age_end = 94, tau = 95)

# Calculate bootstrapped confidence interval (3 iterations to test; more are necessary)
lyl_estimation_ci2 <- lyl_ci(lyl_estimation2, niter = 3)
summary(lyl_estimation_ci2, weights = simu_data$age_disease)
```

summary.lyl_range	<i>Summarize Life Years Lost over a range of differents ages</i>
-------------------	--

Description

summary for objects of class lyl_range summarizes Life Years Lost over a range of different ages.

Usage

```
## S3 method for class 'lyl_range'
summary(object, decimals = 2, weights = NA, difference = FALSE, ...)
```

Arguments

object	An object of class lyl_range (obtained with function lyl_range).
decimals	Number of decimals to be reported (default is 2).
weights	Vector with age distribution of disease/condition onset. If weights are not provided (dafault is weights = NA), then the differences in Life Years Lost at each age are summarized. If weights are provided, then a weighted average is provided.
difference	Parameter automatically created by the package.
...	Additional arguments affecting the summary produced.

Value

A table with the summary of the results.

References

- Plana-Ripoll et al. lillies – An R package for the estimation of excess Life Years Lost among patients with a given disease or condition. *PLoS ONE*. 2020;15(3):e0228073.

See Also

- [lyl_range](#) for estimation of Life Years Lost for a range of different ages.

Examples

```
# Load simulated data as example
data(simu_data)

# Estimate remaining life expectancy and Life Years
# Lost after each age from 0 to 94 years and before age 95 years
lyl_estimation <- lyl_range(data = simu_data, t = age_death, status = death,
                           age_begin = 0, age_end = 94, tau = 95)

# Visualize data at each different specific age
summary(lyl_estimation)

# Summarize data over an age distribution
summary(lyl_estimation, weights = simu_data$age_disease)
```

Index

* datasets

- aggreg_data, 2
- pop_ref, 26
- simu_data, 27

aggreg_data, 2

lyl, 3, 6, 13, 14, 16, 18, 21, 22, 25, 28, 30

lyl_2plot, 5

lyl_aggregated, 6, 10, 24, 29

lyl_aggregated_range, 8, 8, 29

lyl_checkplot, 11, 21

lyl_ci, 4, 12, 21, 25, 30

lyl_compare_plot, 13

lyl_diff, 4, 6, 13, 14, 15, 21

lyl_diff_ref, 17

lyl_range, 4, 11, 13, 16, 18, 19, 25, 26, 30, 32

plot, 4, 8, 10

plot.lyl, 4, 22

plot.lyl_aggregated, 8, 23

plot.lyl_ci, 13, 24

plot.lyl_range, 21, 25

pop_ref, 26

simu_data, 27

summary.lyl, 4, 28

summary.lyl_aggregated, 8, 10, 29

summary.lyl_ci, 12, 13, 30

summary.lyl_range, 21, 31