Package ‘cancerradarr’

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Title Cancer RADAR Project Tool

Version 1.3.1

Description
Cancer RADAR is a project which aim is to develop an infrastructure that allows quantifying the risk of cancer by migration background across Europe.
This package contains a set of functions cancer registries partners should use to reshape 5 year-age group cancer incidence data into a set of summary statistics (see Boyle & Parkin (1991, ISBN:978-92-832-1195-2)) in lines with Cancer RADAR data protections rules.

Encoding UTF-8

RoxygenNote 7.3.2

Imports dplyr (>= 1.1.0), epitools, magrittr, openxlsx (>= 4.2.7), purrr, rmarkdown, rlang, stats, stringr, tidyr, utils, plyr

Depends R (>= 4.1.0)

Suggests plotly, shiny, quarto, tidyverse, DT, gtools, testthat (>= 3.0.0), knitr

LazyData true

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Contents

`age_standardized_incidence_rates`

Age-standardized incidence rate (asir)

Description

Age-standardized incidence rate (asir)

Usage

```
age_standardized_incidence_rates(ncan, py, pystd, ncan.min = 5)
```

Arguments

`ncan`	integer, (age-specific) number of cancers in the population of interest
`py`	integer, (age-specific) person-year in the the population of interest
`pystd`	numeric, (age-specific) standard population person-years (e.g. standard world population)

`ncan.min`	integer, minimum number of observation required not to mask the CI's out

Age-standardized incidence rate (asir) and associated 95% confidence interval are computing assuming normal distribution of the asir. asir is a summary statistics that should be computed per group of individuals providing age specific counts.

Value

a 1 line and 3 column data.frame containing the asir (est) and associated 95% CI (lci, uci)

References

Boyle P, Parkin DM. Cancer registration: principles and methods. Statistical methods for registries. IARC Sci Publ. 1991;(95):126-58. PMID: 1894318.

Examples

```
ncan <- 1:10
py <- 101:110
pystd <- 10:1
ncan.min <- 5
age_standardized_incidence_rates(ncan, py, pystd, ncan.min)
age_standardized_incidence_rates(ncan, py, pystd, sum(ncan) + 1)
```

`aggregated_ageg_name` *Compute the aggregated age group names from a vector of more detailed age groups*

Description

Compute the aggregated age group names from a vector of more detailed age groups

Usage

```
aggregated_ageg_name(selected.ageg, ageg.sep = "_")
```

Arguments

`selected.ageg`	character, the fine grain age group vector
`ageg.sep`	character, the ageg group separator character

Value

character, the name of the aggregated age group

Examples

```
ageg.in <- c('15_19', '20_24', '25_29')
aggregated_ageg_name(ageg.in)
```

`chopped.vector.list` *Pre-computed choped combination for vectors size 1 to 18*

Description

This is a list containing all the possible combination of slices to chop vectors of size 1 to 18. It is useful to compute custom age group aggregation to ensure we are not disclosing age group with too few cancer cases.

Usage

```
chopped.vector.list
```

Format

A 18 item list:

> each element is a matrix containing all the possible chop combinations to aggregate a vector of size n. ...

`chop_vector` *Generate all the possible combinations of slices in a chopped vector*

Description

Generate all the possible combinations of slices in a chopped vector

Usage

```
chop_vector(vect.size = 3)
```

Arguments

`vect.size`	int, the size of the vector

Value

a matrix containing all the possible slices to chope a vector per line

Examples

```
chop_vector(3)
```

`create_canradar_summary_file` *Compute summary statistics from 5 years age-group cancer registry data*

Description

Compute summary statistics from 5 years age-group cancer registry data

Usage

```
create_canradar_summary_file(
  filename.in,
  filename.out,
  ncan.min = 5,
  include.by.cob.stat = TRUE,
  verbose = TRUE
)
```

Arguments

`filename.in`	file path, the file containing the 5 years age counts of cancers stratified per cancer type, sex and country of birth
`filename.out`	file path, the file where summary .xlsx file will be save
`ncan.min`	integer, the minimum number of cancer per age group o be displayed
`include.by.cob.stat`	logical, (TRUE by default) should the statistic per country-of-birth be computed and included in the output file.
`verbose`	logical, shall progress message be printed

Value

a .xlsx with all the summary statistics needed for Cancer RADAR project to be transmitted to project PIs.

Examples

```
 ## Update file.in with the path to the input file containing your registry data
 ## (e.g. file.filled <- "cancerRADAR_input.xlsx")
file.in <- system.file("extdata", "ex_cancerRADAR_input_filled.xlsx", package = "cancerradarr")
 file.out <- 'cancerRADAR_input.xlsx'
 ## for cancer radar data submission, we advise to use the parameter ncan.min = 5 and
 ## include.by.cob.stat = TRUE
create_canradar_summary_file(file.in, file.out, ncan.min = 20, include.by.cob.stat = FALSE)
 ## remove the file to pass package computation tests
 unlink(file.out)
```

`create_registry_input_file` *Create a template file to be filled by cancer registry partners*

Description

Create a template file to be filled by cancer registry partners

Usage

```
create_registry_input_file(filename = "cancerRADAR_input.xlsx", verbose = TRUE)
```

Arguments

`filename`	file path, the name of the template file to be created
`verbose`	logical, shall progress message be printed

Value

a template .xlsx file is created on the hard drive.

Examples

```
file.in <- 'input_file_test.xlsx'
create_registry_input_file(file.in)
## remove the file to pass package computation tests
unlink(file.in)
```

`create_static_report` *Create a static report from cancer RADAR output file*

Description

Create a static report from cancer RADAR output file

Usage

```
create_static_report(filename.out = "")
```

Arguments

`filename.out`	file path, the path to a cancer RADAR output file This function will create a html report that could be useful to check the data that will be transmitted to IARC.

Value

nothing is returned, but a html file created with some summary statistics and graphs out of the file that should be transmitted with IARC

`custom_ageg_aggregation`

Smart aggregation of cancer cases per age group

Description

Smart aggregation of cancer cases per age group

Usage

```
custom_ageg_aggregation(
  dat,
  ncan.min = 5,
  add.total = FALSE,
  ncan.lab = "ncan",
  py.lab = "py"
)
```

Arguments

`dat`	tibble, a single cancer/sex/country tibble containing cancer cases from a registry. It sould contains the column ageg and ncan
`ncan.min`	integer, the minimal number of cancer in each category
`add.total`	logical, should the 'total' category added to the output dataset
`ncan.lab`	character, the column label where cancer cases are stored
`py.lab`	character, the column label where (optional) population at risk are stored

Value

aggregated dataset where all the age group contains at least ncan.min cancers cases

Examples

```
dat <-
  dplyr::tribble(
    ~ ageg, ~ ncan,
    '00_04', 0,
    '05_09', 0,
    '10_14', 0,
    '15_19', 0,
    '20_24', 1,
    '25_29', 2,
    '30_34', 4,
```

```
    '35_39', 5,
    '40_44', 1,
    '45_49', 10,
    '50_54', 14,
    '55_59', 1,
    '60_64', 2,
    '65_69', 2,
    '70_74', 5,
    '75_79', 1,
    '80_84', 0,
    '85', 0
  )

custom_ageg_aggregation(dat, 0)
custom_ageg_aggregation(dat, 5)
custom_ageg_aggregation(dat, 10)
custom_ageg_aggregation(dat, 100)
```

`dat.aggr` *Geographical aggregation used for cancerradarr*

Description

In order to prevent loose of data in case of too low effective, several geographical aggregation can be considered. In this table are stored the different level of aggregation and the aggregation correspondence table considered.

Usage

```
dat.aggr
```

Format

A data frame with 250 rows and 5 columns:

cob_iso3	Country ISO3 code
un_region	UN region
un_subregion	UN subregion
hdi_cat	HDI 2023 category
any_migr	any migration background ...

Details

A multi-columns dataset containing all the countries of birth (as ISO3 code) and other geographical aggregation rules

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`dat.asr.cat` *Burden of cancer aggregation category used for cancerradarr*

Description

A multi-columns dataset containing for all the countries of birth (as ISO3 code), sex and cancer type combinations the quariles of cancer burden in country of origin burden. The quariles (`0%-24%`, `25%-49%`, `50%-74%` and `75-100%`) are based on the ASIR from GLOBOCAN 2022.

Usage

```
dat.asr.cat
```

Format

A data frame with 2,220 rows and 5 columns:

cob_iso3 Country ISO3 code

sex targeted sex

can the caqncer type

asr GLOBOCAN 2022 age-standardized cancer incidence rate

asr_rank_cat GLOBOCAN 2022 age-standardized cancer incidence rate quartile category ...

`dat.cob` *Countries label and countries codes*

Description

A 2 column dataset containing all the countries of birth (with associated countries codes) included in Cancer RADAR project

Usage

```
dat.cob
```

Format

A data frame with 251 rows and 3 columns:

cob_label Country name

cob_code Country code

cob_iso3 Country ISO3 code (used as unique id) ...

`globocan.2022.eu` *European countries age-specific cancer burden from GLOBOCAN 2022*

Description

A multi-columns dataset containing for all the European countries (UN definition) (as ISO3 code), sex and cancer type combinations the number of cases and population at risk estimated in GLOBOCAN 2022. This data are used in `cancerradarr` to compute the relative index on a standard reference population that could be more easily compared between registries. In addition to individual European countries, aggregated areas such as E27 (European Union 27 countries) and EUN (all the UN European countries) are stred in the dataset

Usage

```
globocan.2022.eu
```

Format

A data frame with 6,384 rows and 6 columns:

cob_iso3	Country ISO3 code
sex	targeted sex
ageg	targeted age group
can	the caqncer type
ncanref	number of cancer cases estimated in GLOBOCAN 2022
pyref	population at risk estimated in GLOBOCAN 2022 ...

Source

https://gco.iarc.fr/today/en

References

Bray F, Laversanne M, Sung H, Ferlay J, Siegel RL, Soerjomataram I, Jemal A. Global cancer statistics 2022: GLOBOCAN estimates of incidence and mortality worldwide for 36 cancers in 185 countries. CA Cancer J Clin. 2024 May-Jun;74(3):229-263. doi: 10.3322/caac.21834. Epub 2024 Apr 4. PMID: 38572751.

`incidence_rates` *Compute crude incidence rates*

Description

Compute crude incidence rates

Usage

```
incidence_rates(ncan, py, ncan.min = 5)
```

Arguments

`ncan`	integer, number of cancer
`py`	integer, number of person-year
`ncan.min`	integer, minimum number of observation required not to mask the CI's out Crude incidence rates and associated 95% confidence interval are computing assuming a Poisson distribution and the exact method.

Value

a 3 column data.frame containing the crude incidence rate estimate (est) and associated 95% CI (lci, uci)

References

Boyle P, Parkin DM. Cancer registration: principles and methods. Statistical methods for registries. IARC Sci Publ. 1991;(95):126-58. PMID: 1894318.

See Also

`epitools::pois.exact()`

Examples

```
ncan <- c(1, 10, 100)
py <- c(10, 100, 1000)
incidence_rates(ncan, py, 5)
```

`incidence_rates_difference`

Compute incidence rates difference

Description

Compute incidence rates difference

Usage

```
incidence_rates_difference(ncan, py, ncanref, pyref, ncan.min = 5)
```

Arguments

`ncan`	integer, number of cancers in the population of interest
`py`	integer, person-year of the the population of interest
`ncanref`	integer, number of cancers in the reference population
`pyref`	integer, person-year of the the reference population
`ncan.min`	integer, minimum number of observation required not to mask the CI's out Incidence rates differences and associated 95% confidence interval are computing assuming normal distribution of the differences..

Value

a 3 column data.frame containing the incidence rates difference (est) and associated 95% CI (lci, uci)

Examples

```
ncan <- 1:10
py <- 101:110
ncanref <- 41:50
pyref <- 251:260
ncan.min <- 5

incidence_rates_difference(ncan, py, ncanref, pyref, ncan.min)
```

`incidence_rates_ratio` *Compute incidence rates ratio*

Description

Compute incidence rates ratio

Usage

```
incidence_rates_ratio(ncan, py, ncanref, pyref, ncan.min = 5)
```

Arguments

`ncan`	integer, number of cancers in the population of interest
`py`	integer, person-year of the the population of interest
`ncanref`	integer, number of cancers in the reference population
`pyref`	integer, person-year of the the reference population
`ncan.min`	integer, minimum number of observation required not to mask the CI's out Incidence rates ratio and associated 95% confidence interval are computing assuming normal distribution of the ratios on the log scale.

Value

a 3 column data.frame containing the incidence rates ratio (est) and associated 95% CI (lci, uci)

References

Boyle P, Parkin DM. Cancer registration: principles and methods. Statistical methods for registries. IARC Sci Publ. 1991;(95):126-58. PMID: 1894318.

Examples

```
ncan <- 1:10
py <- 101:110
ncanref <- 41:50
pyref <- 251:260
ncan.min <- 5

incidence_rates_ratio(ncan, py, ncanref, pyref, ncan.min)
```

---

indirect_proportional_incidence_ratio

Compute the indirect proportional incidence ratio (pir)

Description

Compute the indirect proportional incidence ratio (pir)

Usage

```
indirect_proportional_incidence_ratio(
  ncan,
  ntot,
  ncanref,
  ntotref,
  ncan.min = 5
)
```

Arguments

`ncan`	integer, (age-specific) number of cancers in the population of interest
`ntot`	integer, (age-specific) total number of cancer the the population of interest
`ncanref`	integer, (age-specific) number of cancers in the reference population
`ntotref`	integer, (age-specific) total number of cancer the the reference of interest
`ncan.min`	integer, minimum number of observation required not to mask the CI's out Indirect proportional incidence ratio and associated 95% confidence interval are computing assuming normal distribution of the pir on the log scale. pir is a summary statistics that should be computed per group of individuals providing age specific counts.

Value

a 1 line and 3 column data.frame containing the pir (est) and associated 95% CI (lci, uci)

References

Boyle P, Parkin DM. Cancer registration: principles and methods. Statistical methods for registries. IARC Sci Publ. 1991;(95):126-58. PMID: 1894318.

Examples

```
ncan <- 1:10
ntot <- 11:20
ncanref <- 41:50
ntotref <- 251:260
ncan.min <- 5
```

```
indirect_proportional_incidence_ratio(ncan, ntot, ncanref, ntotref, ncan.min)
indirect_proportional_incidence_ratio(ncan, ntot, ncanref, ntotref, sum(ncan) + 1)
```

`indirect_standardized_incidence_ratio` *Compute indirect standardized incidence ratio (sir)*

Description

Compute indirect standardized incidence ratio (sir)

Usage

```
indirect_standardized_incidence_ratio(ncan, py, ncanref, pyref, ncan.min = 5)
```

Arguments

`ncan`	integer, (age-specific) number of cancers in the population of interest
`py`	integer, (age-specific) person-year of the the population of interest
`ncanref`	integer, (age-specific) number of cancers in the reference population
`pyref`	integer, (age-specific) person-year of the the reference population
`ncan.min`	integer, minimum number of observation required not to mask the CI's out Standardized incidence ratio (sir) and associated 95% confidence interval are computing assuming normal distribution of the pir on the log scale. sir is a summary statistics that should be computed per group of individuals providing age specific counts.

Value

a 1 line and 3 column data.frame containing the sir (est) and associated 95% CI (lci, uci)

References

Boyle P, Parkin DM. Cancer registration: principles and methods. Statistical methods for registries. IARC Sci Publ. 1991;(95):126-58. PMID: 1894318.

Examples

```
ncan <- 1:10
py <- 101:110
ncanref <- 41:50
pyref <- 251:260
ncan.min <- 5

indirect_standardized_incidence_ratio(ncan, py, ncanref, pyref, ncan.min)
indirect_standardized_incidence_ratio(ncan, py, ncanref, pyref, sum(ncan) + 1)
```

`open_canradar_dictionary` *Open cancer RADAR output file dictionary*

Description

Calling this function will open the dictionary describing sheets and variables stored in the cancer summary file (output file generated by `create_canradar_summary_file` function). It could be useful for the cancer registries to check what kind of data they will be sharing. Note that a temporary copy of the dictionary is created on your hard drive to prevent from unwanted file modification.

Usage

```
open_canradar_dictionary()
```

Value

the path to a temporary file where cancer RADAR dictionary is stored

Examples

```
open_canradar_dictionary()
```

`proportional_rates` *Compute proportional rates*

Description

Compute proportional rates

Usage

```
proportional_rates(ncan, ntot, ncan.min = 5)
```

Arguments

`ncan`	integer, number of cancer of interest
`ntot`	integer, overal number of cancer
`ncan.min`	integer, minimum number of observation required not to mask the CI's out Proportional incidence rates and associated 95% confidence interval are computing assuming a Binomial distribution and the Clopper and Pearson (1934) procedure.

Value

a 3 column data.frame containing the proportional incidence rate estimate (est) and associated 95% CI (lci, uci)

References

C. J. CLOPPER, B.Sc., E. S. PEARSON, D.Sc., THE USE OF CONFIDENCE OR FIDUCIAL LIMITS ILLUSTRATED IN THE CASE OF THE BINOMIAL, Biometrika, Volume 26, Issue 4, December 1934, Pages 404–413, https://doi.org/10.1093/biomet/26.4.404

Boyle P, Parkin DM. Cancer registration: principles and methods. Statistical methods for registries. IARC Sci Publ. 1991;(95):126-58. PMID: 1894318.

See Also

`stats::binom.test()`

Examples

```
ncan <- c(1, 10, 100)
ntot <- c(10, 100, 1000)
proportional_rates(ncan, ntot, 5)
```

`read_cancerradar_output_01`

Read cancer registry summary statistics (non age-specific)

Description

Read cancer registry summary statistics (non age-specific)

Usage

```
read_cancerradar_output_01(filename.out, aggr.level = "cob_iso3")
```

Arguments

`filename.out`	file path, the path to a cancer RADAR output file
`aggr.level`	character, the aggregation level to be considered. Should be one of `cob_iso3` (country of birth; smaller unit), `un_region` (UN region), `un_subergion` (UN sub-region), `hdi_cat` (HDI category), `asr_rank_cat` (cancer burden category in the country of birth), `any_migr` (any migration background)

Value

a tibble with 9 columns

- reg_label: factor, the chosen aggregation level id
- sex: character, male/female
- ageg: character, age group (here `total`)
- can: character, the cancer type
- ref: character, the reference population for relative index
- index: character, the type of index
- est: dbl, the index estimator
- lci: dbl, the index confidence interval lower bound
- uci: dbl, the index confidence interval upper bound

Examples

```
filename.out <- system.file('extdata/ex_cancerRADAR_output.xlsx', package = "cancerradarr")
dat.out <- read_cancerradar_output_01(filename.out, 'un_region')
head(dat.out)
```

`read_cancerradar_output_02` *Read cancer registry summary statistics (age-specific incidence rate and proportional rates)*

Description

Read cancer registry summary statistics (age-specific incidence rate and proportional rates)

Usage

```
read_cancerradar_output_02(filename.out, aggr.level = "cob_iso3")
```

Arguments

`filename.out`	file path, the path to a cancer RADAR output file
`aggr.level`	character, the aggregation level to be considered. Should be one of `cob_iso3` (country of birth; smaller unit), `un_region` (UN region), `un_subergion` (UN sub-region), `hdi_cat` (HDI category), `asr_rank_cat` (cancer burden category in the country of birth), `any_migr` (any migration background)

Value

a tibble with 11 columns

- reg_label: factor, the chosen aggregation level id
- sex: character, male/female
- ageg: character, age group (here `total`)
- can: character, the cancer type
- index: character, the type of index
- est: dbl, the index estimator
- lci: dbl, the index confidence interval lower bound
- uci: dbl, the index confidence interval upper bound
- ageg_sta: dbl, the age group starting age
- ageg_sto: dbl, the age group stopping age
- ageg_mid: dbl, the age group middle age

Examples

```
filename.out <- system.file('extdata/ex_cancerRADAR_output.xlsx', package = "cancerradarr")
dat.out <- read_cancerradar_output_02(filename.out, 'un_region')
head(dat.out)
```

`run_dynamic_report` *Create a dynamic report from cancer RADAR output file*

Description

Create a dynamic report from cancer RADAR output file

Usage

```
run_dynamic_report(filename.out = "")
```

Arguments

`filename.out`	file path, the path to a cancer RADAR output file This function will open a shiny app where cancer registries can visually check the data they will be transmitted to IARC.

Value

nothing is returned

---

standardized_incidence_rate_difference
Age-standardized incidence rates differences (asird)

Description

Age-standardized incidence rates differences (asird)

Usage

```
standardized_incidence_rate_difference(
  ncan,
  py,
  ncanref,
  pyref,
  pystd,
  ncan.min = 5
)
```

Arguments

`ncan`	integer, (age-specific) number of cancers in the population of interest
`py`	integer, (age-specific) person-year in the the population of interest
`ncanref`	integer, (age-specific) number of cancers in the reference population
`pyref`	integer, (age-specific) person-year in the the reference population
`pystd`	numeric, (age-specific) standard population person-years (e.g. standard world population)
`ncan.min`	integer, minimum number of observation required not to mask the CI's out Age-standardized incidence rate difference (asird) is computed without confidence interval estimation for now. asird is a summary statistics that should be computed per group of individuals providing age specific counts.

Value

a 1 line and 3 column data.frame containing the pir (est) and associated 95% CI (lci, uci)

References

https://www.hsph.harvard.edu/thegeocodingproject/analytic-methods/

Examples

```
ncan <- 1:10
py <- 101:110
ncanref <- 41:50
pyref <- 251:260
```

```
pystd <- 10:1
ncan.min <- 5
standardized_incidence_rate_difference(ncan, py, ncanref, pyref, pystd, ncan.min)
standardized_incidence_rate_difference(ncan, py, ncanref, pyref, pystd, sum(ncan) + 1)
```

`standardized_incidence_rate_ratio` *Age-standardized incidence rates ratio (asirr)*

Description

Age-standardized incidence rates ratio (asirr)

Usage

```
standardized_incidence_rate_ratio(
  ncan,
  py,
  ncanref,
  pyref,
  pystd,
  ncan.min = 5
)
```

Arguments

`ncan`	integer, (age-specific) number of cancers in the population of interest
`py`	integer, (age-specific) person-year in the the population of interest
`ncanref`	integer, (age-specific) number of cancers in the reference population
`pyref`	integer, (age-specific) person-year in the the reference population
`pystd`	numeric, (age-specific) standard population person-years (e.g. standard world population)
`ncan.min`	integer, minimum number of observation required not to mask the CI's out Age-standardized incidence rate ratio (asirr) and associated 95% confidence interval are computing Armitage and Berry (1987) formula. asird is a summary statistics that should be computed per group of individuals providing age specific counts.

Value

a 1 line and 3 column data.frame containing the pir (est) and associated 95% CI (lci, uci)

References

Boyle P, Parkin DM. Cancer registration: principles and methods. Statistical methods for registries. IARC Sci Publ. 1991;(95):126-58. PMID: 1894318.

Examples

```
ncan <- 1:10
py <- 101:110
ncanref <- 41:50
pyref <- 251:260
pystd <- 10:1
ncan.min <- 5
standardized_incidence_rate_ratio(ncan, py, ncanref, pyref, pystd, ncan.min)
standardized_incidence_rate_ratio(ncan, py, ncanref, pyref, pystd, sum(ncan) + 1)
```

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