Package

October 28, 2022

Title PRIME -- Papillomavirus Rapid Interface for Modelling and Economics

Version 2.0.17

Author Modelling and Economic Evaluation of Vaccines group, LSHTM (https://meev.lshtm.ac.uk)

Maintainer MEEV <meev@lshtm.ac.uk>

Description PRIME is a static model of HPV vaccination that uses proportional impact to estimate the health impact and cost-effectiveness of HPV vaccination in low- and middle-income countries.

Depends R (>= 3.5.0)

Imports data.table, foreach, wbstats, lhs, stats, prevalence

License GPL-3

Encoding UTF-8

LazyData true

RoxygenNote 7.2.1

Suggests knitr,
    rmarkdown

VignetteBuilder knitr

R topics documented:

---

ageCoverage   *Get age-specific coverage-rates*

Description

Get age-specific coverage-rates

Usage

```
ageCoverage(
  ages,
  routine_coverage,
  vaccine_efficacy_nosexdebut,
  vaccine_efficacy_sexdebut,
  campaigns,
  lifetab,
  cohort,
  agevac,
```

```
    country_iso3 = NULL
)
```

Arguments

ages   Numeric vector (required): ages in model

routine_coverage
                     Number (required): proportion of population that receives routine vaccination

campaigns   List or number (required): if a list, applies MAC vaccination (needs to change)

lifetab   Data.table (required): lifetable generated with lifeTable()

cohort   Number (required): cohort-size (only used in MAC campaigns)

agevac   Number (required): target age for vaccination

vaccine_efficacy
                     Number (required): proportion indicating vaccine-efficacy

Value

Data.table with coverage and effective coverage by age. Used in RunCohort()

Examples

```
ages <- c(0:100)
routine_coverage <- 0.75
vaccine_efficacy <- 0.8
lifetab <- lifeTable(unlist(data.mortall[iso3=="AFG", as.character(0:100),
  with=FALSE], use.names=FALSE), 9)
agevac <- 9
ageCoverage (ages, routine_coverage, vaccine_efficacy, -1,
  lifetab, cohort, agevac)
```

---

analyseCosts   *Returns cost-effectiveness for a single birthcohort in a single country*

Description

Usually called using RunCountry(..., analyseCosts=TRUE)

Usage

```
analyseCosts(results, vaccine_cost, gdp_per_capita)
```

Arguments

results   Data.table (required): results from RunCohort()

vaccine_cost   Number (required): cost of a single vaccine

gdp_per_capita   Number (required): GDP per capita

Value

Data.table with cost-analysis

Examples

```
analyseCosts(RunCountry("AFG"), 100, 561)
```

BatchRun   *Run multiple cohorts in a batch*

Description

Runs multiple cohorts in one batch, based on the data in .data.batch

Usage

```
BatchRun(
  countries = -1,
  coverage = -1,
  agevac = -1,
  agecohort = -1,
  canc.inc = "2020",
  sens = -1,
  unwpp_mortality = TRUE,
  year_born = -1,
  year_vac = -1,
  runs = 1,
  vaccine_efficacy_beforesexdebut = 1,
  vaccine_efficacy_aftersexdebut = 0,
  log = -1,
  by_calendaryear = FALSE,
  use_proportions = TRUE,
  analyseCosts = FALSE,
  canc.cost = "unadj",
  discounting = FALSE,
  disc.cost = 0.03,
  disc.ben = 0.03,
  psa = 0,
  psa_vals = ".data.batch.psa",
  disability.weights = "gbd_2017",
  wb.indicator = "NY.GDP.PCAP.PP.CD",
  wb.year = 2017,
  vaccine = "4vHPV"
)
```

Arguments

countries	ignore, read from .data.batch
coverage	ignore, read from .data.batch
agevac	ignore, read from .data.batch
agecohort	ignore, read from .data.batch
canc.inc	year from where incidence data is read (2018; old data: 2012) – with updated 2018 Globocan data, DALY weights from GBD, and DALY estimation based on prevalence instead of age of incidence

sens	ignore, does not do anything anymore
unwpp_mortality	
	logical, whether to create lifetables based on UNWPP mortality estimates or WHO data
year_born	ignore
year_vac	ignore
runs	ignore
vaccine_efficacy_beforesexdebut	
	vaccine efficacy before sexual debut
vaccine_efficacy_aftersexdebut	
	vaccine efficacy after sexual debut
log	name of log file
by_calendaryear	
	logical, output values by calendar year or by year of birth cohort
use_proportions	
	logical, output data as rates per capita or in totals
analyseCosts	logical, directly run cost-effectiveness analysis on output or not
canc.cost	Character (optional): Is cost of cancer adjusted ("adj" for International $) or not ("unadj" for US$)
discounting	Logical (optional): If TRUE, run cost-effectiveness analysis undiscounted and discounted. If FALSE, only uses undiscounted
disc.cost	Number (optional): Discounting for health costs (only if discounting=TRUE)
disc.ben	Number (optional): Discounting for health outcomes (only if discounting=TRUE)
psa	integer, number of runs for probabilistic sensitivity analysis (PSA)
psa_vals	data table with values to use in probabilistic sensitivity analysis, usually .data.batch.psa, generated by RegisterBatchData* functions (currently only RegisterBatchDataVimc)
disability.weights	
	character, disability weights for cervical cancer from GBD 2017 or GBD 2001
wb.indicator	character, World Bank indicator for GDP/GNI per capita in I$/US$ and current/constant data
wb.year	numeric, year of the World Bank indicator value
vaccine	character, bivalent/quadrivalent (4vHPV) or nonavalent (9vHPV) vaccine

Value

Returns combined results

Examples

```
#
```

---

checkSize   *Checks whether the size of a variable is larger than 0*

Description

Used to determine that all required variables are passed to a function Checks whether a vector has length > 0 or a data.table/data.frame has nrow > 0

Usage

```
checkSize(v)
```

Arguments

v   Variable (required)

Value

Logical: TRUE if size is not 0, false if size is 0

Examples

```
x <- c()
checkSize(x)

x <- c(2,5)
checkSize(x)

A <- c()
B <- c(1,2,3)
sapply(c("A","B"),function(x){checkSize(get(x))})
```

CreatePsaData   *Generate/read Latin hyper cube sample of parameters for sensitivity analysis*

Description

Generate Latin hyper cube sample of input parameters based on their distributions for probabilistic sensitivity analysis. If file (sample of parameters) already exists, then read Latin hyper cube sample of input parameters.

Usage

```
CreatePsaData(
  country_codes,
  vaccine = "4vHPV",
  psa_runs = 0,
  seed_state = 1,
  psadat_file = "psadat.csv",
  psadat_vimc_file = "psadat_vimc.csv",
  run_lhs = FALSE
)
```

Arguments

country_codes	ISO3 country codes of countries
vaccine	bivalent/quadrivalent or nonavalent HPV vaccine
psa_runs	integer, simulation runs for sensitivity analysis
seed_state	integer, seed value for random number generator
psadat_file	character string, file to save Latin hyper cube sample of input parameters
psadat_vimc_file	
	character string, file to save Latin hyper cube sample of input parameters (VIMC format)
run_lhs	logical, if TRUE create new sample of input parameters, if FALSE, read sample of input parameters from file

Value

Null return value; disease burden estimates are saved to corresponding files

Examples

```
CreatePsaData (
  country_codes    = c("AFG", "ALB"),
  vaccine          = "4vHPV",
  psa_runs         = 200,
  seed_state       = 1,
  psadat_file      = "psadat.csv",
  psadat_vimc_file = "psadat_vimc.csv",
  run_lhs          = TRUE)
```

---

data.cecx_1y_prevalence

1-year prevalence of cervical cancer

Description

A dataset containing the 1-year prevalence (proportion) of cervical cancer in 185 countries, as reported by IARC's Globocan 2018 database.

Usage

```
data.cecx_1y_prevalence
```

Format

A data table containing 185 observations of 103 variables.

Country Country name

iso3 ISO3 country code

Source Data source

Year Data source (year)

0..100 Age 0-100

Details

As per IARC definition – The (1-year) prevalence of a given cancer is the number of individuals within a defined population who have been diagnosed with that cancer (within 1 year) and who are still alive at a given point in time (i.e. the survivors).

Source

https://gco.iarc.fr/today/online-analysis-table

---

data.cecx_1y_prevalence2020

1-year prevalence of cervical cancer

Description

A dataset containing the 1-year prevalence (proportion) of cervical cancer in 185 countries, as reported by IARC's Globocan 2020 database.

Usage

data.cecx_1y_prevalence2020

Format

A data table containing 185 observations of 103 variables.

Country Country name

iso3 ISO3 country code

Source Data source

Year Data source (year)

0..100 Age 0-100

Details

As per IARC definition – The (1-year) prevalence of a given cancer is the number of individuals within a defined population who have been diagnosed with that cancer (within 1 year) and who are still alive at a given point in time (i.e. the survivors).

Source

https://gco.iarc.fr/today/online-analysis-table?v=2020

---

data.cecx_3y_prevalence

3-year prevalence of cervical cancer

Description

A dataset containing the 3-year prevalence (proportion) of cervical cancer in 185 countries, as reported by IARC's Globocan 2018 database.

Usage

data.cecx_3y_prevalence

Format

A data table containing 185 observations of 103 variables.

Country Country name

iso3 ISO3 country code

Source Data source

Year Data source (year)

0..100 Age 0-100

Details

As per IARC definition – The (3-year) prevalence of a given cancer is the number of individuals within a defined population who have been diagnosed with that cancer (within 3 years) and who are still alive at a given point in time (i.e. the survivors).

Source

https://gco.iarc.fr/today/online-analysis-table

---

data.cecx_3y_prevalence2020

3-year prevalence of cervical cancer

Description

A dataset containing the 3-year prevalence (proportion) of cervical cancer in 185 countries, as reported by IARC's Globocan 2020 database.

Usage

data.cecx_3y_prevalence2020

Format

A data table containing 185 observations of 103 variables.

Country Country name

iso3 ISO3 country code

Source Data source

Year Data source (year)

0..100 Age 0-100

Details

As per IARC definition – The (3-year) prevalence of a given cancer is the number of individuals within a defined population who have been diagnosed with that cancer (within 3 years) and who are still alive at a given point in time (i.e. the survivors).

Source

https://gco.iarc.fr/today/online-analysis-table?v=2020

---

data.cecx_5y_prevalence

5-year prevalence of cervical cancer

Description

A dataset containing the 5-year prevalence (proportion) of cervical cancer in 185 countries, as reported by IARC's Globocan 2018 database.

Usage

data.cecx_5y_prevalence

Format

A data table with 185 observations of 103 variables.

Country Country name

iso3 ISO3 country code

Source Data source

Year Data source (year)

0..100 Age 0-100

Details

As per IARC definition – The (5-year) prevalence of a given cancer is the number of individuals within a defined population who have been diagnosed with that cancer (within 5 years) and who are still alive at a given point in time (i.e. the survivors).

Source

https://gco.iarc.fr/today/online-analysis-table

---

data.cecx_5y_prevalence2020

5-year prevalence of cervical cancer

Description

A dataset containing the 5-year prevalence (proportion) of cervical cancer in 185 countries, as reported by IARC's Globocan 2020 database.

Usage

data.cecx_5y_prevalence2020

Format

A data table with 185 observations of 103 variables.

Country Country name

iso3 ISO3 country code

Source Data source

Year Data source (year)

0..100 Age 0-100

Details

As per IARC definition – The (5-year) prevalence of a given cancer is the number of individuals within a defined population who have been diagnosed with that cancer (within 5 years) and who are still alive at a given point in time (i.e. the survivors).

Source

https://gco.iarc.fr/today/online-analysis-table?v=2020

---

data.costcecx *Cost of cervical cancer treatment*

Description

A dataset containing the cost of cervical cancer treatment.

Usage

data.costcecx

Format

A data table with 194 observations of 7 variables.

country Country name

cancer_cost cost per cancer episode, in 2017 US$

cancer_cost_adj cost per cancer episode – adjusted, in 2017 US$ – "adjusted" cancer costs are based on a GDP/capita based adjustment within the region

iso3 ISO3 country code

cancer_cost_2011 cost per cancer episode, in 2011 US$

cancer_cost_adj_2011 cost per cancer episode – adjusted, in 2011 US$ – "adjusted" cancer costs are based on a GDP/capita based adjustment within the region

inflation_factor Inflation factor from 2011 to 2017 estimated from Inflation, GDP deflator (annual %) – https://data.worldbank.org/indicator/NY.GDP.DEFL.KD.ZG

---

data.countryname   *Country names and codes*

Description

A dataset containing the country names and codes (ISO/WHO/WB/UN).

Usage

```
data.countryname
```

Format

A data table with 251 observations of 13 variables.

name1, name2, name3, name4 Country names

iso2, iso3 ISO2 and ISO3 country codes

isonum ISO number

WHOcode WHO country code

who_region WHO region

who_mort WHO mortality stratum - A/B/C/D/E

WBincome WB income classification of countries

UNgroup UN group classification of countries

GDPpc2011id GDP per capita (2011)

data.cross_protection   *Cross-protection effect of bivalent and quadrivalent vaccines*

Description

A dataset containing cross-protection effect of bivalent and quadrivalent vaccines

Usage

```
data.cross_protection
```

Format

A data table with 5 observations of 7 variables.

hpv_type HPV strain type

bivalent Cross-protection of bivalent vaccine against the corresponding HPV strain type (mean)

bivalent_low Cross-protection of bivalent vaccine against the corresponding HPV strain type (lower bound of 95% uncertainty interval)

bivalent_high Cross-protection of bivalent vaccine against the corresponding HPV strain type (upper bound of 95% uncertainty interval)

quadrivalent Cross-protection of quadrivalent vaccine against the corresponding HPV strain type (mean)

quadrivalent_low Cross-protection of quadrivalent vaccine against the corresponding HPV strain type (lower bound of 95% uncertainty interval)

quadrivalent_high Cross-protection of quadrivalent vaccine against the corresponding HPV strain type (upper bound of 95% uncertainty interval)

Source

Malagón T, Drolet M, Boily MC, Franco EL, Jit M, Brisson J, Brisson M. Cross-protective efficacy of two human papillomavirus vaccines: a systematic review and meta-analysis. Lancet Infect Dis. 2012 Oct;12(10):781-9. https://doi.org/10.1016/S1473-3099(12)70187-1

---

data.disability_weights

Disability weights and duration of cervical cancer stages

Description

A dataset containing disability weights and duration of different phases of cervical cancer.

Usage

```
data.disability_weights
```

Format

A data table with 13 observations of 8 variables.

Source Source of disability weights - IHME / WHO

Sequela Sequelae / stage / phase of cervical cancer

Duration Duration of cervical cancer phase

WHO_MortalityStratum WHO moratlity stratum – applicable only for long term sequelae from WHO source

Mid Disability weight (mid)

Low Disability weight (low)

High Disability weight (high)

Description Description of cervical cancer phase

---

data.global   *Global data table*

Description

A dataset containing a global range of variables.

Usage

data.global

Format

A data table with 194 observations of 35 variables.

Country Country name

iso2 ISO2 country code

WHO Region WHO regions

WHO Mortality Stratum WHO mortality stratum

World Bank Income Group (2011) World Bank income group levels

GAVI Eligibility GAVI eligibility status

PAHO Revolving Fund PAHO revolving fund status

Cohort size (2010) [1] Cohort size

Coverage (3 doses at year 10) [2] Vaccination coverage at age 10

Vaccine efficacy vs vaccine type infection [2] Vaccine efficacy

Duration of protection [2] Duration of vaccine protection

Age group [3] Age group

Vaccine price USD [4] Vaccine price for 2 doses US$

Vaccine delivery/ operational/ admin costs (USD) [5] Vaccine delivery, operational and administration costs US$

Cancer treatment costs - primary level hospital i$ (per episode, over lifetime) [6] Cancer treatment costs - primary level hospital i$ (per episode, over lifetime)

Cancer treatment costs - primary level hospital US\$ (per episode, over lifetime) [6] Cancer treatment costs - primary level hospital US\$ (per episode, over lifetime)

Cancer treatment costs - secondary level hospital i\$ (per episode, over lifetime) [6] Cancer treatment costs - secondary level hospital i\$ (per episode, over lifetime)

Cancer treatment costs - secondary level hospital US\$ (per episode, over lifetime) [6] Cancer treatment costs - secondary level hospital US\$ (per episode, over lifetime)

Cancer treatment costs - teaching hospital i\$ (per episode, over lifetime) [6] Cancer treatment costs - teaching hospital i\$ (per episode, over lifetime)

Cancer treatment costs - teaching hospital US\$ (per episode, over lifetime) [6] Cancer treatment costs - teaching hospital US\$ (per episode, over lifetime)

Discount rate [2] Disount rate

Perspective [2] Perspective

Costs [2]

Time horizon [2] Time horizon

"Percent" CeCx due to 16/18 Percentage of cervical cancer due to HPV strains 16 and 18

Vaccine programme Vaccine programme

Vaccine programme Oct2013 Vaccine programme Oct2013

Econ evaluation Economic evaluation

GDP per capita (2011 US\$) [7] GDP per capita (2011 US\$)

GDP per capita (2011 i\$) [7] GDP per capita (2011 i\$)

GNI per capita (2011 i\$) [7] GNI per capita (2011 i\$)

GNI per capita (2011 US\$) [7] GNI per capita (2011 US\$)

V33 International\$

V34 US\$

iso3 ISO3 country code

---

data.hpv_distribution *Relative contribution of HPV 16/18/31/33/45/52/58 in ICC HPV-positive cases*

Description

A dataset containing relative contribution of HPV 16/18/31/33/45/52/58 in cases of ICC HPV-positive, by region and country

Usage

```
data.hpv_distribution
```

Format

A data table with 249 observations of 39 variables.

Global World

Region UN region

Subregion UN subregion

Intermediate_region UN intermediate region

Country Country name

iso3 ISO3 country code

hpv_4v Relative contribution (%) of HPV 16/18 in ICC HPV-positive cases (mean)

hpv_4v_low Relative contribution (%) of HPV 16/18 in ICC HPV-positive cases (lower bound of 95% uncertainty interval)

hpv_4v_high Relative contribution (%) of HPV 16/18 in ICC HPV-positive cases (upper bound of 95% uncertainty interval)

hpv_9v Relative contribution (%) of HPV 16/18/31/33/45/52/58 in ICC HPV-positive cases (mean)

hpv_9v_low Relative contribution (%) of HPV 16/18/31/33/45/52/58 in ICC HPV-positive cases (lower bound of 95% uncertainty interval)

hpv_9v_high Relative contribution (%) of HPV 16/18/31/33/45/52/58 in ICC HPV-positive cases (upper bound of 95% uncertainty interval)

hpv_16 Relative contribution (%) of HPV 16 in ICC HPV-positive cases (mean)

hpv_16_low Relative contribution (%) of HPV 16 in ICC HPV-positive cases (lower bound of 95% uncertainty interval)

hpv_16_high Relative contribution (%) of HPV 16 in ICC HPV-positive cases (upper bound of 95% uncertainty interval)

hpv_18 Relative contribution (%) of HPV 18 in ICC HPV-positive cases (mean)

hpv_18_low Relative contribution (%) of HPV 18 in ICC HPV-positive cases (lower bound of 95% uncertainty interval)

hpv_18_high Relative contribution (%) of HPV 18 in ICC HPV-positive cases (upper bound of 95% uncertainty interval)

hpv_31 Relative contribution (%) of HPV 31 in ICC HPV-positive cases (mean)

hpv_31_low Relative contribution (%) of HPV 31 in ICC HPV-positive cases (lower bound of 95% uncertainty interval)

hpv_31_high Relative contribution (%) of HPV 31 in ICC HPV-positive cases (upper bound of 95% uncertainty interval)

hpv_33 Relative contribution (%) of HPV 33 in ICC HPV-positive cases (mean)

hpv_33_low Relative contribution (%) of HPV 33 in ICC HPV-positive cases (lower bound of 95% uncertainty interval)

hpv_33_high Relative contribution (%) of HPV 33 in ICC HPV-positive cases (upper bound of 95% uncertainty interval)

hpv_45 Relative contribution (%) of HPV 45 in ICC HPV-positive cases (mean)

hpv_45_low Relative contribution (%) of HPV 45 in ICC HPV-positive cases (lower bound of 95% uncertainty interval)

hpv_45_high Relative contribution (%) of HPV 45 in ICC HPV-positive cases (upper bound of 95% uncertainty interval)

hpv_52 Relative contribution (%) of HPV 52 in ICC HPV-positive cases (mean)

hpv_52_low Relative contribution (%) of HPV 52 in ICC HPV-positive cases (lower bound of 95% uncertainty interval)

hpv_52_high Relative contribution (%) of HPV 52 in ICC HPV-positive cases (upper bound of 95% uncertainty interval)

hpv_58 Relative contribution (%) of HPV 58 in ICC HPV-positive cases (mean)

hpv_58_low Relative contribution (%) of HPV 58 in ICC HPV-positive cases (lower bound of 95% uncertainty interval)

hpv_58_high Relative contribution (%) of HPV 58 in ICC HPV-positive cases (upper bound of 95% uncertainty interval)

hpv_6 Relative contribution (%) of HPV 6 in ICC HPV-positive cases (mean)

hpv_6_low Relative contribution (%) of HPV 6 in ICC HPV-positive cases (lower bound of 95% uncertainty interval)

hpv_6_high Relative contribution (%) of HPV 6 in ICC HPV-positive cases (upper bound of 95% uncertainty interval)

hpv_11 Relative contribution (%) of HPV 11 in ICC HPV-positive cases (mean)

hpv_11_low Relative contribution (%) of HPV 11 in ICC HPV-positive cases (lower bound of 95% uncertainty interval)

hpv_11_high Relative contribution (%) of HPV 11 in ICC HPV-positive cases (upper bound of 95% uncertainty interval)

Source

Serrano B, Alemany L, Tous S, Bruni L, Clifford GM, Weiss T, et al. Potential impact of a nine-valent vaccine in human papillomavirus related cervical disease. Infect Agents Cancer. 2012;7: 38. https://doi.org/10.1186/1750-9378-7-38

---

data.incidence	*Incidence of cervical cancer, by age and country*

Description

A dataset containing the incidence of cervical cancer in 185 countries, as reported by IARC's Globocan 2018 database. Crude rates, cervix uteri, females, by age.

Usage

```
data.incidence
```

Format

A data table with 185 observations of 103 variables.

Country Country name

iso3 ISO3 country code

Source Data source

Year Data source (year)

0..100 Age 0-100 – Crude rates, cervix uteri, females, by age; annual rate per individual

Source

<https://gco.iarc.fr/today/online-analysis-table>

---

data.incidence2020   *Incidence of cervical cancer, by age and country*

Description

A dataset containing the incidence of cervical cancer in 185 countries, as reported by IARC's Globocan 2020 database. Crude rates, cervix uteri, females, by age.

Usage

```
data.incidence2020
```

Format

A data table with 185 observations of 103 variables.

Country Country name

iso3 ISO3 country code

Source Data source

Year Data source (year)

0..100 Age 0-100 – Crude rates, cervix uteri, females, by age; annual rate per individual

Source

<https://gco.iarc.fr/today/online-analysis-table?v=2020>

---

data.incidence_ui   *Incidence of cervical cancer with uncertainty intervals, all ages and by country*

Description

A dataset containing the incidence of cervical cancer with uncertainty intervals in 185 countries, as reported by IARC's Globocan 2018 database. Estimated number of new cases in 2018, cervix uteri, females, all ages.

Usage

```
data.incidence_ui
```

Format

A data table with 185 observations of 5 variables.

Country Country name

iso3 ISO3 country code

Mid Estimated number of new cases in 2018, cervix uteri, females, all ages (mean)

Low Estimated number of new cases in 2018, cervix uteri, females, all ages (lower bound of 95% uncertainty interval)

High Estimated number of new cases in 2018, cervix uteri, females, all ages (upper bound of 95% uncertainty interval)

Source Data source

Year Data source (year)

Source

https://gco.iarc.fr/today/online-analysis-table

---

data.mortall *WHO life table*

Description

A dataset containing the WHO life table.

Usage

```
data.mortall
```

Format

A data table with 196 observations of 107 variables.

Country ¦ Age [12] Country name

0..100 Age 0-100

V103..V106 na

iso3 ISO3 country code

Source

https://www.who.int/gho/mortality_burden_disease/life_tables/life_tables/en/

```
data.mortall.unwpp.nqx
```
                                    UNWPP life table

Description

A dataset containing the UNWPP life table (World Population Prospects 2022).

Usage

```
data.mortall.unwpp.nqx
```

Format

A data table with 647790 observations of 8 variables.

country_code_numeric Country code numeric

country_code ISO3 country code

country Country name

age_from age from (start-age)

age_to age to (end-age)

year Year

gender Gender

value nqx - probability of dying between ages x and x+n

Source

<https://population.un.org/wpp/>

```
data.mortcecx
```
                      Mortality from cervical cancer, by age and country

Description

A dataset containing the mortality (crude rates) from cervical cancer in 185 countries, as reported by IARC's Globocan 2018 database.

Usage

```
data.mortcecx
```

Format

A data table with 185 observations of 103 variables.

Country Country name

iso3 ISO3 country code

Source Data source

Year Data source (year)

0..100 Age 0-100 - Crude rates, cervix uteri, females, by age; annual rate per individual

Source

<https://gco.iarc.fr/today/online-analysis-table>

---

data.mortcecx2020 *Mortality from cervical cancer, by age and country*

Description

A dataset containing the mortality (crude rates) from cervical cancer in 185 countries, as reported by IARC's Globocan 2020 database.

Usage

data.mortcecx2020

Format

A data table with 185 observations of 103 variables.

Country Country name

iso3 ISO3 country code

Source Data source

Year Data source (year)

0..100 Age 0-100 - Crude rates, cervix uteri, females, by age; annual rate per individual

Source

<https://gco.iarc.fr/today/online-analysis-table?v=2020>

---

data.mortcecx_ui *Mortality from cervical cancer with uncertainty intervals, all ages and by country*

Description

A dataset containing the number of deaths from cervical cancer with uncertainty intervals in 185 countries, as reported by IARC's Globocan 2018 database. Estimated number of deaths in 2018, cervix uteri, females, all ages.

Usage

data.mortcecx_ui

Format

A data table with 185 observations of 5 variables.

Country Country name

iso3 ISO3 country code

Mid Estimated number of deaths in 2018, cervix uteri, females, all ages (mean)

Low Estimated number of deaths in 2018, cervix uteri, females, all ages (lower bound of 95% uncertainty interval)

High Estimated number of deaths in 2018, cervix uteri, females, all ages (upper bound of 95% uncertainty interval)

Source Data source

Year Data source (year)

Source

https://gco.iarc.fr/today/online-analysis-table

---

data.pop	*UNWPP population estimates*

Description

A dataset containing the UNWPP population estimates – World Population Prospects 2022.

Usage

    data.pop

Format

A data table with 3392220 observations of 8 variables.

country_code_numeric Country code numeric

country_code ISO3 country code

country Country name

age_from age from (start-age)

age_to age to (end-age)

year Year

gender Gender

value Population size

Source

https://population.un.org/wpp/Download/Standard/Population/

VIMC

---

data.popproj *Population projections of 5-year old girls*

Description

A dataset containing population projections of 5-year old girls. (not used – to be removed)

Usage

```
data.popproj
```

Format

A data table with 98 observations of 91 variables.

iso3 ISO3 country code

2011..2100 Year – 2011..2100

---

data.quality *Data quality of incidence and mortality*

Description

A dataset indicating data quality of cervical cancer incidence and mortality.

Usage

```
data.quality
```

Format

A data table with 186 observations of 4 variables.

Country Country name

Incidence Quality of cervical cancer incidence data

Mortality Quality of cervical cancer mortality data

iso3 ISO3 country code

---

data.sexual_debut   *Sexual debut data*

Description

A dataset containing sexual debut data and (2) parameters for the sexual debut curve (logistic model).

Usage

data.sexual_debut

Format

A data table with 94 observations of 14 variables.

V1 Row number

iso2 ISO2 country code

country Country name

iso3 ISO3 country code

who WHO region

X15 Proportion of people who have sexually debuted at age 15

X18 Proportion of people who have sexually debuted at age 18

X20 Proportion of people who have sexually debuted at age 20

X22 Proportion of people who have sexually debuted at age 22

X25 Proportion of people who have sexually debuted at age 25

Never Proportion of people who had not sexually debuted

cluster.id Clustering countries with similar characteristics

a Parameter for sexual debut curve (logistic model)

b Parameter for sexual debut curve (logistic model)

---

data.valid   *Model validation*

Description

A dataset containing data for validation.

Usage

data.valid

Format

A data table with 26 observations of 49 variables.

Country Country name

iso2 ISO2 country code

WHO Region WHO region

World Bank Income Group (2011) World Bank income group classification (2011)

Author Author

Year Year of publication

Title Title of publication

Currency Currency

Currency year Currency year

Conversion to I$2011 International dollar (I$2011)

ICER vs no prevention Incremental cost-effectiveness ratio of vaccination versus no prevention (CHECK)

ICER vs screen Incremental cost-effectiveness ratio of vaccination versus no prevention (CHECK)

Denominator Denominator for health impact

Vaccine total costs Vaccine total costs

Vaccine coverage Vaccine coverage

Vaccine efficacy vs vaccine type infection Vaccine efficacy versus vaccine type infection

Duration of protection Duration of protective immunity from vaccination

Cohort size Cohort size

Age at vaccination Age at vaccination, years

Cancer treatment cost per episode Cancer treatment cost per episode, dollars

Discount rate: costs Discount rate for costs

Discount rate: benefits Discount rate for benefits

Perspective Perspective of economic evaluation

Comparator is no screening Comparator refers to no scereening, logical (Y/N)

Time horizon Time horizon of analysis

GDP per capita GDP per capita

Cervical cancer due to 16/18 Proportion of cervical cancer due to HPV types 16 and 18

CeCx cost low original Cervical cancer cost / low / original

CeCx cost high original Cervical cancer cost / high / original

CeCx cost low Cervical cancer cost / low

CeCx cost high Cervical cancer cost / high

CeCx data available Cervical cancer data available, logical (Y/N)

0-4 0-4 years

5-9 5-9 years

9-14 9-14 years

15-19 15-19 years

20-24 20-24 years

25-29 25-29 years
30-34 30-34 years
35-39 35-39 years
40-44 40-44 years
45-49 45-49 years
50-54 50-54 years
55-59 55-59 years
60-64 60-64 years
65-69 65-69 years
70-74 70-74 years
75-79 75-79 years
80+ 80+ years

---

dtAggregate   *Collapse data-tables*

Description

Collapse data-tables

Usage

```
dtAggregate(
  DT,
  aggr_on,
  measure.vars = c(),
  id.vars = c(),
  func = "sum",
  na.rm = TRUE
)
```

Arguments

DT	Data-table (required)
aggr_on	Character string (required): column-name that will be used to collapse on (i.e. combine all age-strata)
measure.vars	Character string (optional): column-names that will be collapsed (function will be applied to all these columns)
id.vars	Character string (optional): column-names that will remain stratified
	N.b. if measure.vars is not provided, all columns that are not in id.vars and aggr_on will be assumed to be assumed
func	Character string (optional): function that will be applied to data (if optional, values will be summed)
na.rm	Logical (optional): if TRUE, removes NA from measure.vars columns before applying function (or passes na.rm=TRUE to function)

Value

Returns collapsed data.table

---

dtColMatch   *Match two data-tables on multiple columns*

Description

Returns vector with column-of-interest where columns match

Usage

```
dtColMatch(
  input,
  input_match_on,
  reference,
  reference_match_on,
  reference_return
)
```

Arguments

input	Data.table (required): input-table to match
input_match_on	Character vector (required): column-names in input-table to match
reference	Data.table (required): reference-table to match
reference_match_on	
	Character vector (required): column-names in reference-table to match
reference_return	
	Character string (required): column-name in reference-table that is returned (where values match)

Details

If at least one value in any of the input_match_on columns matches with a value in any of the reference_match_on columns, the two rows will match

Value

Character vector with values from reference_return column in reference_match_on data.table where values match

Examples

```
dtColMatch (data.global, c("Country"), data.countryname,
  c("name1", "name2", "name3", "name4"), "iso3")
```

EmulateVaccineImpactVimcStochastic
                    Emulate vaccine impact estimates (VIMC stochastic runs)

Description

Emulate vaccine impact estimates for VIMC stochastic runs/sensitivity analysis. The inputs are central disease burden estimates, input parameter distributions (latin hyper sampling), runs for sensitivity analysis, and filename for stochastic burden estimates. The outputs are stochastic disease burden estimates (full results file plus a file per country).

Usage

```
EmulateVaccineImpactVimcStochastic(
  disease_burden_template_file,
  centralBurdenResultsFile,
  psaData,
  diseaseBurdenStochasticFolder,
  diseaseBurdenStochasticFile,
  psa_runs,
  countryCodes = -1,
  vaccination_scenario
)
```

Arguments

disease_burden_template_file
                    csv file (required), central disease burden template (vimc format); add column with run_id to get stochastic disease burden template

centralBurdenResultsFile
                    csv file (required), central disease burden estimates pre and post vaccination

psaData   data table (required), latin hyper cube sample of input parameters

diseaseBurdenStochasticFolder
                    character string (required), stochastic disease burden estimates folder (output)

diseaseBurdenStochasticFile
                    character string (required), stochastic disease burden estimates file(s) (output)

psa_runs   integer (required), simulation runs for sensitivity analysis

countryCodes   list (optional), If country codes are provided, stochastic burden estimates are generated for these countries. If set to -1, then stochastic burden estimates are generated for the countries included in the central burden estimates.

vaccination_scenario
                    logical (required), generate stochastic burden estimates for (vaccination) or (no vaccination) scenario

Details

Stochastic disease burden estimates are generated. (i) full results files 1 full results file for pre-vaccination (optional) 1 full results file for post-vaccination (ii) 1 file per country for all runs 1 file per country for all runs – pre-vaccination (optional) 1 file per country for all runs – post-vaccination

Value

Null return value; disease burden estimates are saved to corresponding files

---

EmulateVaccineImpactVimcStochastic_all_cecx_burden

Emulate vaccine impact estimates (VIMC stochastic runs) - all cervical cancer burden

---

Description

Emulate vaccine impact estimates for VIMC stochastic runs/sensitivity analysis. The inputs are central disease burden estimates, input parameter distributions (latin hyper sampling), runs for sensitivity analysis, and filename for stochastic burden estimates. The outputs are stochastic disease burden estimates – all cervical cancer burden. (full results file plus a file per country).

Usage

```
EmulateVaccineImpactVimcStochastic_all_cecx_burden(
  disease_burden_template_file,
  centralBurdenResultsFile,
  centralBurdenResultsFile_all_cecx_burden,
  central_disease_burden_file_all,
  psaData,
  diseaseBurdenStochasticFile_all_cecx_burden,
  diseaseBurden_central_StochasticFile_all_cecx_burden,
  psa_runs,
  countryCodes = -1,
  vaccination_scenario
)
```

Arguments

disease_burden_template_file
:   csv file (required), central disease burden template (vimc format); add column with run_id to get stochastic disease burden template

centralBurdenResultsFile
:   csv file (required), central disease burden estimates pre and post vaccination (HPV 16/18 types)

centralBurdenResultsFile_all_cecx_burden
:   csv file (required), central disease burden estimates pre and post vaccination (all HPV types)

central_disease_burden_file_all
:   csv file (required), central disease burden estimates (vimc format)

psaData   data table (required), latin hyper cube sample of input parameters

diseaseBurdenStochasticFile_all_cecx_burden
:   character string (required), stochastic disease burden estimates file(s) (output) - all cervical cancer burden

diseaseBurden_central_StochasticFile_all_cecx_burden
:   character string (required), (central + 95 (output) - all cervical cancer burden

psa_runs   integer (required), simulation runs for sensitivity analysis

countryCodes   list (optional), If country codes are provided, stochastic burden estimates are
                  generated for these countries. If set to -1, then stochastic burden estimates are
                  generated for the countries included in the central burden estimates.

vaccination_scenario

                  logical (required), generate stochastic burden estimates for (vaccination) or (no
                  vaccination) scenario

Details

Stochastic disease burden estimates are generated. (i) full results files 1 full results file for pre-
vaccination (optional) 1 full results file for post-vaccination (ii) 1 file per country for all runs 1 file
per country for all runs – pre-vaccination (optional) 1 file per country for all runs – post-vaccination

Value

Null return value; disease burden estimates are saved to corresponding files

---

EstimateVaccineImpactVimcCentral

                            Generate vaccine impact estimates - HPV 16/18 types (VIMC central
                            run)

Description

Generate vaccine impact estimates (HPV 16/18 types) for VIMC central runs. The inputs are vac-
cine coverage and disease burden template files and outputs are disease burden estimates (pre-
vaccination and post-vaccination).

Usage

```
EstimateVaccineImpactVimcCentral(
  vaccine_coverage_file,
  disease_burden_template_file,
  disease_burden_no_vaccination_file,
  disease_burden_vaccination_file,
  disease_burden_results_file,
  campaign_vaccination,
  routine_vaccination,
  vaccine = "4vHPV",
  canc.inc = "2020",
  country_set = "all"
)
```

Arguments

vaccine_coverage_file

                  csv file (input), vaccine coverage data (vimc format)

disease_burden_template_file

                  csv file (input), disease burden template (vimc format)

disease_burden_no_vaccination_file

                csv file (output), disease burden estimates for no vaccination (vimc format)

disease_burden_vaccination_file

                csv file (output), disease burden estimates for vaccination (vimc format)

disease_burden_results_file

                csv file (output), disease burden estimates pre-vaccination and post-vaccination

campaign_vaccination

                logical, indicates campaign vaccination

routine_vaccination

                logical, indicates routine vaccination

vaccine   character, bivalent/quadrivalent/nonovalent HPV vaccine

canc.inc   character, year of GLOBOCAN estimates

country_set   character, run for all countries specified in disease burden template file (or) run for a set of countries

Details

Three disease burden estimates (HPV 16/18 types) are generated. (i) disease burden estimates for no vaccination (vimc format) (ii) disease burden estimates for vaccination (vimc format) (iii) disease burden estimates for vaccination (pre- and post-vaccination) and includes YLDs and YLLs

Value

Null return value; disease burden estimates are saved to corresponding files

Examples

```
EstimateVaccineImpactVimcCentral (
  vaccine_coverage_file             = "coverage_hpv-routine-default.csv",
  disease_burden_template_file      = "central-burden-template.csv",
  disease_burden_no_vaccination_file = "central_burden_no_vaccination.csv",
  disease_burden_vaccination_file   = "central_burden_vaccination.csv",
  disease_burden_results_file       = "central_burden_results.csv",
  routine_vaccination               = TRUE,
  campaign_vaccination              = TRUE)
```

Estimate_all_cecx_burden_central

Generate vaccine impact estimates - HPV all types (VIMC central run)

Description

Generate vaccine impact estimates (HPV all types) for VIMC central runs. The inputs are cecx burden estimates pre- and post-vaccination with 4vHPV / 9vHPV at different ages. The outputs are cecx burden estimates pre- and post-vaccination with HPV all types at different ages.

Usage

```
Estimate_all_cecx_burden_central(
  cecx_burden_file,
  cecx_burden_file_all,
  vaccine,
  disease_burden_template_file = "",
  disease_burden_no_vaccination_file_all = "",
  disease_burden_vaccination_file_all = "",
  vimc_output = TRUE
)
```

Arguments

cecx_burden_file

> csv file (input), disease burden estimates (cecx burden attributable to HPV 16/18)

cecx_burden_file_all

> csv file (output), disease burden estimates (cecx burden attributable to HPV all types)

vaccine   character, bivalent/quadrivalent/nonovalent HPV vaccine

disease_burden_template_file

> csv file (input), disease burden template (vimc format)

disease_burden_no_vaccination_file_all

> csv file (output), disease burden estimates for no vaccination (cecx burden attributable to HPV all types - vimc format)

disease_burden_vaccination_file_all

> csv file (output), disease burden estimates for vaccination (cecx burden attributable to HPV all types - vimc format)

Details

Three disease burden estimates (HPV all types) are generated. (i) disease burden estimates for no vaccination (vimc format) (ii) disease burden estimates for vaccination (vimc format) (iii) disease burden estimates for vaccination (pre- and post-vaccination) and includes YLDs and YLLs

Value

Null return value; disease burden estimates are saved to corresponding files

Examples

```
    Estimate_all_cecx_burden_central (
      cecx_burden_file                   = "central_burden_results_file.csv",
      cecx_burden_file_all               = "central_burden_results_file_all.csv",
      vaccine                            = "4vHPV",
      disease_burden_template_file       = "central_burden_template_file.csv",
    disease_burden_no_vaccination_file_all = "central_burden_no_vaccination_file_all_vimc_format.csv",
    disease_burden_vaccination_file_all  = "central_burden_vaccination_file_all_vimc_format.csv",
      vimc_output                        = TRUE)
```

Generate_diagnostic_plots

Generate diagnostic plots of vaccine coverage and burden estimates

---

Description

Generate diagnostic plots of vaccine coverage and burden estimates (cases, deaths, dalys)

Usage

```
Generate_diagnostic_plots(
  vaccine_coverage_folder,
  coverage_prefix,
  touchstone,
  scenarios,
  no_vaccine_scenario,
  plot_no_vaccine_scenario = TRUE,
  burden_estimate_folder,
  plot_folder,
  plot_file,
  plot_type,
  countries,
  start_year = -1,
  end_year = -1,
  compare_plots = FALSE,
  vaccine_prefix,
  no_vaccine_prefix
)
```

Arguments

vaccine_coverage_folder
: character, folder to read vaccine coverage of different scenarios

coverage_prefix
: character, prefix of coverage file

touchstone
: character, touchstone (VIMC)

scenarios
: character, names of vaccination scenarios

no_vaccine_scenario
: character, name of no vaccination scenario

plot_no_vaccine_scenario,
: logical, if TRUE then also generate plots for no vaccine scenario

burden_estimate_folder
: character, folder to read burden estimates of different scenarios

plot_folder
: character, diagnostic plot folder

plot_file
: character, diagnostic plot file

plot_type
: character, diagnostic plot type (central or stochastic)

countries,
: character, "all" countries or specific countries (iso3 codes)

start_year
: numeric, start year of plot

```
end_year          numeric, end year of plot

compare_plots     logical, if TRUE then generate comparative plots

vaccine_prefix    character, prefix of burden estimates file (vaccination scenarios)

no_vaccine_prefix
                  character, prefix of burden estimates file (no vaccination scenario)
```

Details

Diagnostic plots of vaccine coverage and burden estimates (cases, deaths, dalys) are generated for each country and scenario. Optionally, comparative plots across all scenarios can be generated.

Value

Null return value; diagnostic plots are saved to file

Examples

```
Generate_diagnostic_plots (
    vaccine_coverage_folder    = "vaccine_coverage",
    coverage_prefix            = "coverage_",
    touchstone                 = "touchstone",
    scenarios                  = c ("hpv-routine-default", "hpv-routine-best"),
    no_vaccine_scenario        = "hpv-no-vaccination",
    plot_no_vaccine_scenario   = TRUE,
    burden_estimate_folder     = "output_all",
    plot_folder                = "plots"
    plot_file                  = "plot_file.pdf",
    plot_type                  = "central"
    countries                  = "all",
    start_year                 = 2000,
    end_year                   = 2100,
    compare_plots              = TRUE,
    vaccine_prefix             = "central-burden-vaccination_all_",
    no_vaccine_prefix          = "central-burden-novaccination_all_" )
```

---

getISO3   *Retrieve ISO3-code of country*

Description

Retrieve ISO3-code of country

Usage

```
getISO3(countryname, name = FALSE)
```

Arguments

```
countryname       Character string (required): Full name of the country

name              Logical (optional): If TRUE, returns full name and alternative names of returned
                  country (may be useful to double-check that it is the correct country)
```

Value

Character string with ISO3 code. Will also return full name if name=TRUE.

Examples

```
getISO3("Afghanistan")
getISO3("Congo",name=TRUE)
```

---

lifeTable   *Construct lifetable based on qx-column*

Description

qx = age-specific probability of dying

Usage

```
lifeTable(qx = NULL, mx = NULL, agecohort = 0)
```

Arguments

qx	Numeric vector (required): Age-specific probabilities of dying
agecohort	Number (optional): Age at which cohort is started

Value

Data.table with lifetable

Examples

```
qx <- unlist(data.mortall[iso3=="AFG", as.character(0:100), with=FALSE], use.names=FALSE)
lifeTable(qx, 9)
```

---

monetary_to_number   *Convert monetary character-strings to numeric values*

Description

Convert monetary character-strings to numeric values

Usage

```
monetary_to_number(x)
```

Arguments

x	Character string to convert

Value

Returns number with value, stripped from any currency symbols and thousand-seperators (i.e. "B#2,010.50" becomes 2010.5)

Examples

```
monetary_to_number ("$2,200.20")

# Note that values using German or Dutch notation (i.e. using a comma to
  separate decimals and a dot to seperate thousands) are converted as well.
  monetary_to_number ("$2.200,20")
```

OutputVimc   *Formatting output for VIMC Montagu*

Description

`OutputVimc` takes result of BatchRun and outputs it in format to be uploaded to VIMC Montagu.

Usage

```
OutputVimc(
  DT,
  age_stratified = TRUE,
  calendar_year = FALSE,
  vimc_template = -1
)
```

Arguments

DT   data table with results

age_stratified   logical, whether output should be stratified by age

calendar_year   logical, whether output should be given by calendar year of event OR by year of birth of cohort

vimc_template   data table with template file downloaded from montagu

Value

#

Examples

#

| prime | *prime: Papillomavirus Rapid Interface for Modelling and Economics (PRIME).* |

Description

PRIME stands for "Papillomavirus Rapid Interface for Modelling and Economics". The R package is based of the spreadsheet-based tool (see http://primetool.org).

PRIME provides estimates of

The magnitude of the burden of cervical cancer.

The impact of introducing HPV vaccination for girls prior to sexual debut.

Healthcare costs incurred as a result of cervical cancer treatment.

Costs associated with vaccination.

Long-term savings which may result from a vaccination program.

| propSexDebut | *Proportion of girls sexually debuted* |

Description

propSexDebut returns proportion of girls sexually debuted in country `country_iso3` at age age.

Usage

```
propSexDebut(age, country_iso3)
```

Arguments

age	age of girls
country_iso3	ISO3 country code

Value

Returns proportion of girls in a given country that has sexually debuted at a given age.

Examples

```
propSexDebut (20, "IND")
propSexDebut (30, "ETH")
```

RegisterBatchData   *Creates .data.batch for running multiple birth cohorts*

Description

Creates .data.batch which is used when running/looping over multiple birth cohorts (runCohort()) at once.

Usage

```
RegisterBatchData(coverage_data, reporting_years = -1, force = FALSE)
```

Arguments

coverage_data   Data table with columns country_code, year (of vaccination), age_first, age_last, coverage.

reporting_years
                 Numeric_vector, years that should be reported (parameter: not required)

force   Logical, whether .data.batch should be overwritten if it already exists (parameter: not required)

Details

.data.batch is based on the data.table (DT) coverage_data, which is a DT with columns country_code (ISO3), year (of vaccination), age_first (age at vaccination), age_last (age at vaccination), coverage (in proportion, for all the agegroups specified).

If you only want to run 1 age in this country/coverage combination, age_first==age_last

Value

batch data of cohorts with vaccination coverage

Examples

```
#
```

RegisterBatchDataVimc   *Creates .data.batch for running multiple birth cohorts (VIMC runs)*

Description

Creates .data.batch which is used when running/looping over multiple birth cohorts (runCohort()) at once. Similar to RegisterBatchData, but for when we make runs for VIMC.

Usage

```
RegisterBatchDataVimc(
  vimc_coverage,
  vimc_template,
  use_campaigns,
  use_routine,
  restrict_to_coverage_data = FALSE,
  force = FALSE,
  psa = 0
)
```

Arguments

`vimc_coverage`	data table with coverage estimates as downloaded from VIMC montagu
`vimc_template`	data table with reporting template as downloaded from VIMC montagu
`use_campaigns`	logical, whether campaigns as stated in coverage files should be modelled
`use_routine`	logical, whether routine vaccination as stated in coverage file should be modelled
`restrict_to_coverage_data`	
	logical, whether the first birth-cohort should be the first cohort that is mentioned in the coverage data. If TRUE, restrict to coverage data. If FALSE, restrict to cohorts provided in vimc_template.
`force`	logical, whether .data.batch should be overwritten if it already exists
`psa`	integer, indicating how many runs for probabilistic sensitivity analysis (PSA). 0 to run no PSA.

Details

.data.batch is based on the data.table (DT) coverage_data, which is a DT with columns country_code (ISO3), year (of vaccination), age_first (age at vaccination), age_last (age at vaccination), coverage (in proportion, for all the age groups specified).

Value

batch data of cohorts with vaccination coverage

Examples

```
#
```

RunCohort	*Run PRIME for a single birth-cohort*

Description

Runs PRIME for one birth-cohort. Usually called by another function such as RunCountry().

Usage

```
RunCohort(
  lifetab,
  cohort,
  incidence,
  mortality_cecx,
  prevalence,
  agevac,
  coverage,
  campaigns,
  vaccine_efficacy_nosexdebut,
  vaccine_efficacy_sexdebut,
  cost_cancer,
  discounting = FALSE,
  disc.cost = 0.03,
  disc.ben = 0.03,
  country_iso3 = NULL,
  run_country = FALSE,
  disability.weights = "gbd_2017"
)
```

Arguments

lifetab	Data.table: The life-table for this cohort. Can be created using the lifeTable() function.
cohort	Number: The cohort-size of this birth-cohort at the time where the lifetable starts.
incidence	Numeric vector: Age-specific CeCx(16/18) incidence-rates.
mortality_cecx	Numeric vector: Age-specific CeCx(16/18) mortality-rates.
prevalence	Numeric vector: Age-specific CeCx(16/18) prevalence rates (5-year prevalence) – referring to people who are alive within 5 years of diagnosis.
agevac	Number: Age at which the cohort is vaccinated.
coverage	Number: Proportion of the cohort that will receive a vaccination.
campaigns	List or number: MAC cohort-vaccinations (needs to be changed).
vaccine_efficacy_nosexdebut	
	Number: proportion indicating vaccine-efficacy before sexual debut.
vaccine_efficacy_sexdebut	
	Number: proportion indicating vaccine-efficacy after sexual debut.
cost_cancer	Number: total per capita cost of cancer.
discounting	Logical (optional): If TRUE, run cost-effectiveness analysis undiscounted and discounted. If FALSE, only uses undiscounted
disc.cost	Number (optional): Discounting for health costs (only if discounting=TRUE)
disc.ben	Number (optional): Discounting for health outcomes (only if discounting=TRUE)

Value

Returns a data.table with size of the birth-cohort and age-specific incidence-rates, mortality-rates, years-of-life-lost, years-of-healthy-life-lost, and cancer-costs before and after vaccination. Also displays whether discounting has been used ("type" column).

Examples

```
lifetab <- lifeTable(unlist(data.mortall[iso3=="AFG",
  as.character(0:100), with=FALSE], use.names=FALSE), 9)
cohort <- -1
incidence <- unlist(data.incidence[iso3=="AFG", as.character(0:100), with=FALSE],
  use.names=FALSE)
mortality_cecx <- unlist(data.mortall[iso3=="AFG", as.character(0:100), with=FALSE],
  use.names=FALSE)
prevalence <- unlist(data.cecx_5y_prevalence[iso3=="AFG",
  as.character(0:100), with=FALSE], use.names=FALSE)
agevac <- 9
coverage <- 0.8
campaigns <- -1
vaccine_efficacy_nosexdebut <- 0.95
vaccine_efficacy_sexdebut <- 0
cost_cancer <- 100

RunCohort(lifetab, cohort, incidence, mortality_cecx, prevalence, agevac,
  coverage, campaigns, vaccine_efficacy_nosexdebut, vaccine_efficacy_sexdebut,
  cost_cancer, disc.cost=0.03, disc.ben=0.03,
  discounting=FALSE, country_iso3="AFG", run_country=FALSE)
```

RunCountry	*Run PRIME for a specific country*

Description

Runs RunCohort() using country-specific estimates. If year_born and year_vac are not provided, assumes vaccination occurs in the current year.

Usage

```
RunCountry(
  country_iso3,
  vaceff_beforesexdebut = 1,
  vaceff_aftersexdebut = 0,
  cov = 1,
  agevac = 10,
  agecohort = 10,
  cohort = -1,
  canc.inc = "2020",
  sens = -1,
  unwpp_mortality = TRUE,
  year_born = -1,
  year_vac = -1,
  campaigns = -1,
  analyseCosts = FALSE,
  canc.cost = "unadj",
  discounting = FALSE,
  disc.cost = 0.03,
  disc.ben = 0.03,
```

```
    run_batch = FALSE,
    psadat = -1,
    disability.weights = "gbd_2017",
    wb.indicator = "NY.GDP.PCAP.PP.CD",
    wb.year = 2017,
    vaccine = "4vHPV"
)
```

Arguments

country_iso3	Character string (required): ISO3 code of the country
cov	Number (optional): Proportion with routine coverage
agevac	Integer (optional): Target age for HPV vaccination
agecohort	Integer (optional): Reference age for cohort-size (only used when 'cohort' is not provided)
cohort	Integer (optional): Cohort-size. -1 if unknown
canc.inc	Integer (optional): Reference year for cancer incidence rates (Globocan: 2020 or 2018 or 2012)
sens	Numeric-vector (optional): Specific values to be used in a PSA. -1 if PSA's are not used
unwpp_mortality	
	Logical (optional): If TRUE, uses year-specific UNWPP mortality estimates to construct life-tables. If FALSE, use WHO based mortality estimates.
year_born	Integer (optional): Year in which cohort is born
year_vac	Integer (optional): Year in which cohort is vaccinated
campaigns	List (optional): Multi-Age-Cohort campaigns (needs to be changed)
analyseCosts	Logical (optional): If FALSE, returns result from RunCohort() function. If TRUE, runs analyseCosts() with country-specific results.
canc.cost	Character (optional): Is cost of cancer adjusted ("adj" for International $) or not ("unadj" for US$)
discounting	Logical (optional): If TRUE, run cost-effectiveness analysis undiscounted and discounted. If FALSE, only uses undiscounted
disc.cost	Number (optional): Discounting for health costs (only if discounting=TRUE)
disc.ben	Number (optional): Discounting for health outcomes (only if discounting=TRUE)
disability.weights	
	character, disability weights for cervical cancer from GBD 2017 or GBD 2001
wb.indicator	character, World Bank indicator for GDP/GNI per capita in I$/US$ and current/constant data
wb.year	numeric, year of the World Bank indicator value
vaccine	character, bivalent/quadrivalent (4vHPV) or nonavalent (9vHPV) vaccine
vaceff	Number (optional): Proportion indicating vaccine-efficacy

Value

data.table with country-specific results of HPV vaccination. Returns cost-analysis if analyseCosts=TRUE

Examples

```
RunCountry("AFG")
RunCountry("AFG", year_vac=2020, agevac=10, cov=0.75, vaceff_beforesexdebut =0.88)
RunCountry("AFG", year_vac=2020, agevac=10, cov=0.75, vaceff_beforesexdebut =0.88,
          analyseCosts=TRUE)
```

---

writelog	*Simulation log reporting*

Description

Appends message of simulation run (x) to log file (logname).

Usage

```
writelog(logname, x)
```

Arguments

logname	log filename
x	message of simulation run

Value

None

Examples

```
#
```

Index