# Package

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**Title** PRIME -- Papillomavirus Rapid Interface for Modelling and Economics

**Version** 2.0.12

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**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** 7.1.1

**Suggests** knitr, rmarkdown

**VignetteBuilder** knitr

## R topics documented:

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`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 = "2018",
  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 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.

### Usage

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

### 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) |

### 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")
```

---

## 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_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_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.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.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 12 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)

## 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 rate, 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 rate, cervix uteri, females, by age; annual rate per individual

### Source

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

## 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 2019).

## Usage

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

## Format

A data table with 122850 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 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

## Source

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

## 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 2019.

### 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<br>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

---

# EstimateVaccineImpactVimcCentral

*Generate vaccine impact estimates (VIMC central run)*

---

## Description

Generate vaccine impact estimates for VIMC central runs. The inputs are vaccine 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"
)
```

## 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

## Details

Three disease burden estimates 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)
```

---

# 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 = "2018",
  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: 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