

# Package ‘prime’

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

**Version** 2.0.1

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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 (>= 3.4.3)

**Imports** data.table, foreach

**License** GPL-3

**Encoding** UTF-8

**LazyData** true

**RoxygenNote** 6.1.1

**Suggests** knitr,  
rmarkdown

**VignetteBuilder** knitr

## R topics documented:

ageCoverage . . . . .	2
analyseCosts . . . . .	3
BatchRun . . . . .	3
checkSize . . . . .	5
data.cecx_1y_prevalence . . . . .	5
data.cecx_3y_prevalence . . . . .	6
data.cecx_5y_prevalence . . . . .	7
data.costcecx . . . . .	7
data.countryname . . . . .	8
data.global . . . . .	8
data.incidence . . . . .	10
data.mortall . . . . .	10
data.mortall.unwpp.mx . . . . .	11
data.mortcecx . . . . .	11
data.pop . . . . .	12
data.popproj . . . . .	12
data.quality . . . . .	13

data.sexual_debut . . . . .	13
data.valid . . . . .	14
dtAggregate . . . . .	15
dtColMatch . . . . .	16
getISO3 . . . . .	17
lifeTable . . . . .	17
monetary_to_number . . . . .	18
OutputGavi . . . . .	18
prime . . . . .	19
propSexDebut . . . . .	19
RegisterBatchData . . . . .	20
RegisterBatchDataGavi . . . . .	21
RunCohort . . . . .	22
RunCountry . . . . .	23
writelog . . . . .	25

<b>Index</b>	<b>26</b>
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ageCoverage	<i>Get age-specific coverage-rates</i>
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---

## 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=F], use.names=F), 9)
cohort <- unlist(data.popproj[iso3=="AFG", "2020"], use.names=F)
agevac <- 9
ageCoverage(ages, routine_coverage, vaccine_efficacy, -1, lifetab, cohort, agevac)

```

---

analyseCosts	<i>Returns cost-effectiveness for a single birthcohort in a single country</i>
--------------	--

---

**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	<i>Run multiple cohorts in a batch</i>
----------	--

---

**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", daly.canc.diag = 0.288,
daly.canc.control = 0.049, daly.canc.metastatic = 0.451,
daly.canc.terminal = 0.54, sens = -1, unwpp_mortality = FALSE,
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, psa = 0, psa_vals = ".data.batch.psa")

```

**Arguments**

<code>countries</code>	ignore, read from <code>.data.batch</code>
<code>coverage</code>	ignore, read from <code>.data.batch</code>
<code>agevac</code>	ignore, read from <code>.data.batch</code>
<code>agecohort</code>	ignore, read from <code>.data.batch</code>
<code>canc.inc</code>	year from where incidence data is read (2018; old data: 2008/2012) – with updated 2018 Globocan data, DALY weights from GBD, and DALY estimation based on prevalence instead of age of incidence, only 2018 is valid and 2008/2012 is not sensible
<code>daly.canc.diag</code>	disability weight of diagnosis and primary therapy phase of cervical cancer
<code>daly.canc.control</code>	Number: daly-weight for controlled phase of cervical cancer
<code>daly.canc.metastatic</code>	Number: daly-weight for metastatic phase of cervical cancer
<code>daly.canc.terminal</code>	disability weight of terminal phase of cervical cancer
<code>sens</code>	ignore, doesn't do anything anymore
<code>unwpp_mortality</code>	logical, whether to create lifetables based on UNWPP mx estimates or WHO data
<code>year_born</code>	ignore
<code>year_vac</code>	ignore
<code>runs</code>	ignore
<code>vaccine_efficacy_beforesexdebut</code>	vaccine efficacy before sexual debut
<code>vaccine_efficacy_aftersexdebut</code>	vaccine efficacy after sexual debut
<code>log</code>	name of log file
<code>by_calendaryear</code>	logical, output values by calendar year or by year of birth cohort
<code>use_proportions</code>	logical, output data as rates per capita or in totals
<code>analyseCosts</code>	logical, directly run cost-effectiveness analysis on output or not
<code>psa</code>	integer, number of runs for probabilistic sensitivity analysis (PSA)
<code>psa_vals</code>	data table with values to use in probabilistic sensitivity analysis, usually <code>.data.batch.psa</code> , generated by <code>RegisterBatchData*</code> functions (currently only <code>RegisterBatchdata-Gavi</code> )

**Value**

Returns combined results

**Examples**

```
#
```

---

checkSize	<i>Checks whether the size of a variable is larger than 0</i>
-----------	---

---

**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))})
```

---

data.cecex_1y_prevalence	<i>1-year prevalence of cervical cancer</i>
--------------------------	---

---

**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.cecex_1y_prevalence
```

**Format**

A data table containing 185 observations of 103 variables.

**Country** Country name

**0..100** Age 0-100

**iso3** ISO3 country code

**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

**0..100** Age 0-100

**iso3** ISO3 country code

**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	<i>5-year prevalence of cervical cancer</i>
-------------------------	---

---

### 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

**0..100** Age 0-100

**iso3** ISO3 country code

### 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	<i>Cost of cervical cancer treatment</i>
---------------	--

---

### Description

A dataset containing the cost of cervical cancer treatment.

### Usage

```
data.costcecx
```

### Format

A data table with 194 observations of 4 variables.

**country** Country name

**cancer\_cost** cost per cancer episode, in \$US

**cancer\_cost\_adj** cost per cancer episode – adjusted, in international/PPP \$

**iso3** ISO3 country code

---

data.countryname	<i>Country names and codes</i>
------------------	--------------------------------

---

### 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.global	<i>Global data table</i>
-------------	--------------------------

---

### 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** [4 ] Vaccine price

**Vaccine delivery/ operational/ admin costs** [5 ] Vaccine delivery, operational and administration costs

**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 ] Discount 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.incidence	<i>Incidence of cervical cancer</i>
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---

### Description

A dataset containing the incidence of cervical cancer in 185 countries, as reported by IARC's Globocan 2018 database.

### Usage

```
data.incidence
```

### Format

A data table with 185 observations of 103 variables.

**Country** Country name

**0..100** Age 0-100

**iso3** ISO3 country code

### Source

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

---

data.mortall	<i>WHO life table</i>
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---

### 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/](https://www.who.int/gho/mortality_burden_disease/life_tables/life_tables/en/)

---

data.mortall.unwpp.mx *UNWPP life table*


---

**Description**

A dataset containing the UNWPP life table (World Population Prospects 2017).

**Usage**

```
data.mortall.unwpp.mx
```

**Format**

A data table with 115710 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** mx mortality rate in year = proportion of individuals of age x dying by age x+1

**Source**

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

---

data.mortcecx *Mortality from cervical cancer*


---

**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

**0..100** Age 0-100

**iso3** ISO3 country code

**Source**

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

---

data.pop	<i>UNWPP population estimates</i>
----------	-----------------------------------

---

**Description**

A dataset containing the UNWPP population estimates – World Population Prospects 2017.

**Usage**

data.pop

**Format**

A data table with 3306163 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	<i>Population projections of 5-year old girls</i>
--------------	---

---

**Description**

A dataset containing population projections of 5-year old girls.

**Usage**

data.popproj

**Format**

A data table with 98 observations of 91 variables.

**iso3** ISO3 country code

**2011..2100** Year – 2011..2100

---

data.quality	<i>Data quality of incidence and mortality</i>
--------------	--

---

**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	<i>Sexual debut data</i>
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---

**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 screening, 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

**Examples**

```
dtAggregate(data.popproj, "iso3", id.vars="")
```

---

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")
```

---

getISO3	<i>Retrieve ISO3-code of country</i>
---------	--------------------------------------

---

**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	<i>Construct lifetable based on qx-column</i>
-----------	---

---

**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=F], use.names=F)
lifeTable(qx, 9)
```

---

monetary_to_number	<i>Convert monetary character-strings to numeric values</i>
--------------------	---

---

**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 separate t
monetary_to_number("$2.200,20")
```

---

OutputGavi	<i>Formatting output for VIMC Montagu</i>
------------	---

---

**Description**

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

**Usage**

```
OutputGavi(DT, age_stratified = TRUE, calendar_year = FALSE,
  gavi_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
gavi_template	data table with template file downloaded from montagu

**Value**

#

**Examples**

#

---

prime	<i>prime: Papillomavirus Rapid Interface for Modelling and Economics (PRIME).</i>
-------	---

---

**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	<i>Proportion of girls sexually debuted</i>
--------------	---

---

**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	<i>Creates .data.batch for running multiple birth cohorts</i>
-------------------	---

---

**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**

None

**Examples**

```
#
```

---

RegisterBatchDataGavi *Creates .data.batch for running multiple birth cohorts (Gavi 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 Gavi.

## Usage

```
RegisterBatchDataGavi(gavi_coverage, gavi_template, use_campaigns,
  use_routine, restrict_to_coverage_data = FALSE, force = FALSE,
  psa = 0)
```

## Arguments

gavi_coverage	data table with coverage estimates as downloaded from VIMC montagu
gavi_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 gavi_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

None

## 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_efficiency_nosexdebut,
  vaccine_efficiency_sexdebut, daly.canc.diag, daly.canc.seq,
  daly.canc.control, daly.canc.metastatic, daly.canc.terminal, cost_cancer,
  disc.cost = 0.03, disc.ben = 0.03, discounting = TRUE,
  country_iso3 = NULL, run_country = FALSE)
```

**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_efficiency_nosexdebut	Number: proportion indicating vaccine-efficacy before sexual debut.
vaccine_efficiency_sexdebut	Number: proportion indicating vaccine-efficacy after sexual debut.
daly.canc.diag	Number: daly-weight for cancer diagnosis.
daly.canc.seq	Number: daly-weight for cancer treatment.
daly.canc.control	Number: daly-weight for controlled phase of cervical cancer
daly.canc.metastatic	Number: daly-weight for metastatic phase of cervical cancer
daly.canc.terminal	Number: daly-weight for death from cancer.
cost_cancer	Number: total per capita cost of cancer.
disc.cost	Number (optional): discounting for cancer cost.
disc.ben	Number (optional): discounting for...
discounting	Logical: should discounting be applied?

## 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=F], use.names=F), 9)
cohort <- unlist(data.popproj[iso3=="AFG", "2020"], use.names=F)
incidence <- unlist(data.incidence[iso3=="AFG", as.character(0:100)], with=F], use.names=F)
mortality_cecx <- unlist(data.mortall[iso3=="AFG", as.character(0:100)], with=F], use.names=F)
prevalence <- unlist(data.cecx_5y_prevalence[iso3=="AFG", as.character(0:100)], with=F], use.names=F)
agevac <- 9
coverage <- 0.8
campaigns <- -1
vaccine_efficacy_nosexdebut <- 0.95
vaccine_efficacy_sexdebut <- 0
daly.canc.diag <- 0.002
daly.canc.seq <- 0.002
daly.canc.control <- 0.05
daly.canc.metastatic <- 0.05
daly.canc.terminal <- 0.1
cost_cancer <- 100
```

```
RunCohort(lifetab, cohort, incidence, mortality_cecx, prevalence, agevac, coverage, campaigns,
vaccine_efficacy_nosexdebut, vaccine_efficacy_sexdebut, daly.canc.diag, daly.canc.seq, daly.canc.control,
daly.canc.metastatic, daly.canc.terminal, 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, disc.cost = 0.03, disc.ben = 0.03,
cov = 1, agevac = 10, agecohort = 10, cohort = -1,
canc.cost = "unadj", canc.inc = "2018", daly.canc.diag = 0.288,
daly.canc.control = 0.049, daly.canc.metastatic = 0.451,
daly.canc.terminal = 0.54, sens = -1, unwp_mortality = FALSE,
year_born = -1, year_vac = -1, campaigns = -1,
analyseCosts = FALSE, discounting = TRUE, run_batch = FALSE,
psadat = -1)
```

**Arguments**

country_iso3	Character string (required): ISO3 code of the country
disc.cost	Number (optional): Discounting for costs (only if discounting=TRUE)
disc.ben	Number (optional): Discounting for ... (only if discounting=TRUE)
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.cost	Character (optional): Is cost of cancer adjusted ("adj") or not ("unadj")
canc.inc	Integer (optional): Reference year for cancer incidence rates (2018 or 2012 or 2008)
daly.canc.diag	Number (optional): Daly weight for cancer diagnosis
daly.canc.control	Number: daly-weight for controlled phase of cervical cancer
daly.canc.metastatic	Number: daly-weight for metastatic phase of cervical cancer
daly.canc.terminal	Number (optional): Daly weight for cancer death
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
discounting	Logical (optional): If TRUE, runs analysis undiscounted and discounted. If FALSE, only uses undiscounted
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=0.88)
RunCountry("AFG", year_vac=2020, agevac=10, cov=0.75, vaceff=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

## \*Topic **datasets**

- [data.cecx\\_1y\\_prevalence, 5](#)
- [data.cecx\\_3y\\_prevalence, 6](#)
- [data.cecx\\_5y\\_prevalence, 7](#)
- [data.costcecx, 7](#)
- [data.countryname, 8](#)
- [data.global, 8](#)
- [data.incidence, 10](#)
- [data.mortall, 10](#)
- [data.mortall.unwpp.mx, 11](#)
- [data.mortcecx, 11](#)
- [data.pop, 12](#)
- [data.popproj, 12](#)
- [data.quality, 13](#)
- [data.sexual\\_debut, 13](#)
- [data.valid, 14](#)

- [ageCoverage, 2](#)
- [analyseCosts, 3](#)

- [BatchRun, 3](#)

- [checkSize, 5](#)

- [data.cecx\\_1y\\_prevalence, 5](#)
- [data.cecx\\_3y\\_prevalence, 6](#)
- [data.cecx\\_5y\\_prevalence, 7](#)
- [data.costcecx, 7](#)
- [data.countryname, 8](#)
- [data.global, 8](#)
- [data.incidence, 10](#)
- [data.mortall, 10](#)
- [data.mortall.unwpp.mx, 11](#)
- [data.mortcecx, 11](#)
- [data.pop, 12](#)
- [data.popproj, 12](#)
- [data.quality, 13](#)
- [data.sexual\\_debut, 13](#)
- [data.valid, 14](#)
- [dtAggregate, 15](#)
- [dtColMatch, 16](#)

- [getISO3, 17](#)

- [lifeTable, 17](#)

- [monetary\\_to\\_number, 18](#)

- [OutputGavi, 18](#)

- [prime, 19](#)
- [prime-package \(prime\), 19](#)
- [propSexDebut, 19](#)

- [RegisterBatchData, 20](#)
- [RegisterBatchDataGavi, 21](#)
- [RunCohort, 22](#)
- [RunCountry, 23](#)

- [writelog, 25](#)