Package ‘mSimCC’

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Type Package

Title Micro Simulation Model for Cervical Cancer Prevention

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Description Micro simulation model to reproduce natural history of cervical cancer and cost-effectiveness evaluation of prevention strategies. See Georgalis L, de Sanjose S, Esnaola M, Bosch F X, Diaz M (2016) <doi:10.1097/CEJ.0000000000000202> for more details.

License GPL (>= 2)

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LazyData true

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`mSimCC-package` *Microsimulation model for cervical cancer prevention*

Description

Microsimulation model to reproduce natural history of cervical cancer and cost-effectiveness evaluation of prevention strategies.

Details

Package:	mSimCC
Type:	Package
Version:	0.0.3
Date:	2023-08-21
License:	GPL version 2 or newer
LazyLoad:	yes

Author(s)

David Moriña (Universitat de Barcelona), Pedro Puig (Universitat Autònoma de Barcelona) and Mireia Diaz (Institut Català d'Oncologia)

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References

Georgalis L, de Sanjosé S, Esnaola M, Bosch F X, Diaz M. Present and future of cervical cancer prevention in Spain: a cost-effectiveness analysis. European Journal of Cancer Prevention 2016;**25**(5):430-439.

Moriña D, de Sanjosé S, Diaz M. Impact of model calibration on cost-effectiveness analysis of cervical cancer prevention 2017;**7**.

See Also

`mSimCC-package`, `bCohort`, `microsim`, `costs`, `le`, `plotCIN1Incidence`, `plotCIN2Incidence`, `plotCIN3Incidence`, `plotIncidence`, `plotMortality`, `plotPrevalence`, `qalys`, `yls` bCohort — *Aggregate data from several microsimulated cohorts*

Description

This function aggregates data from several microsimulated cohorts.

Usage

```
bCohort(ind)
```

Arguments

ind	microsimulated cohort obtained using `microsim`.

Value

Data frame with health states as columns and ages as rows.

Author(s)

David Moriña (Universitat de Barcelona), Pedro Puig (Universitat Autònoma de Barcelona) and Mireia Diaz (Institut Català d'Oncologia)

References

Georgalis L, de Sanjosé S, Esnaola M, Bosch F X, Diaz M. Present and future of cervical cancer prevention in Spain: a cost-effectiveness analysis. European Journal of Cancer Prevention 2016;**25**(5):430-439.

Moriña D, de Sanjosé S, Diaz M. Impact of model calibration on cost-effectiveness analysis of cervical cancer prevention 2017;**7**.

See Also

`mSimCC-package`, `microsim`, `costs`, `le`, `plotCIN1Incidence`, `plotCIN2Incidence`, `plotCIN3Incidence`, `plotIncidence`, `plotMortality`, `plotPrevalence`, `qalys`, `yls`

Examples

```
data(probs)
nsim      <- 3
p.men     <- 0
size      <- 20
min.age   <- 10
max.age   <- 84

#### Natural history
hn <- microsim(seed=1234, nsim, probs, abs_states=c(10, 11), sympt_states=c(5, 6, 7, 8),
```

```
                    prob_sympt=c(0.11, 0.23, 0.66, 0.9),
                     size, p.men, min.age, max.age,
                 utilityCoefs = c(1, 1, 0.987, 0.87, 0.87, 0.76, 0.67, 0.67, 0.67, 0.938, 0, 0),
                     costCoefs.md = c(0, 0, 254.1, 1495.9, 1495.9, 5546.8, 12426.4, 23123.4,
                                      34016.6, 0, 0, 0),
                costCoefs.nmd = c(0, 0, 81.4, 194.1, 194.1, 219.1, 219.1, 219.1, 219.1, 0, 0, 0),
                     costCoefs.i = c(0, 0, 0, 0, 0, 0, 0, 0, 0, 0, 0, 0), disc=3,
                     treatProbs=c(0,0,1,1,1,0.9894,0.9422,0.8262,0.5507,0,0,0),
                     nCores=1) ### individual level

hn_c     <- bCohort(hn) ### Aggregated level
```

---

costs *Calculate the costs of a prevention strategy.*

Description

Calculate the costs of a prevention strategy.

Usage

```
costs(scenario, disc=FALSE)
```

Arguments

scenario	microsimulated cohort.
disc	discount rate to be applied. Defaults to FALSE (undiscounted).

Value

Global and per-person costs of the considered prevention strategy.

Author(s)

David Moriña (Universitat de Barcelona), Pedro Puig (Universitat Autònoma de Barcelona) and Mireia Diaz (Institut Català d'Oncologia)

References

Georgalis L, de Sanjosé S, Esnaola M, Bosch F X, Diaz M. Present and future of cervical cancer prevention in Spain: a cost-effectiveness analysis. European Journal of Cancer Prevention 2016;**25**(5):430-439.

Moriña D, de Sanjosé S, Diaz M. Impact of model calibration on cost-effectiveness analysis of cervical cancer prevention 2017;**7**.

See Also

mSimCC-package, microsim, bCohort, le, plotCIN1Incidence, plotCIN2Incidence, plotCIN3Incidence, plotIncidence, plotMortality, plotPrevalence, qalys, yls

Examples

```
data(probs)
nsim       <- 3
p.men      <- 0
size       <- 20
min.age    <- 10
max.age    <- 84

#### Natural history
hn <- microsim(seed=1234, nsim, probs, abs_states=c(10, 11), sympt_states=c(5, 6, 7, 8),
               prob_sympt=c(0.11, 0.23, 0.66, 0.9),
                size, p.men, min.age, max.age,
            utilityCoefs = c(1, 1, 0.987, 0.87, 0.87, 0.76, 0.67, 0.67, 0.67, 0.938, 0, 0),
                costCoefs.md = c(0, 0, 254.1, 1495.9, 1495.9, 5546.8, 12426.4, 23123.4,
                                 34016.6, 0, 0, 0),
           costCoefs.nmd = c(0, 0, 81.4, 194.1, 194.1, 219.1, 219.1, 219.1, 219.1, 0, 0, 0),
                costCoefs.i = c(0, 0, 0, 0, 0, 0, 0, 0, 0, 0, 0, 0), disc=3,
                treatProbs=c(0,0,1,1,1,0.9894,0.9422,0.8262,0.5507,0,0,0),
                nCores=1) ### individual level

costs(hn)
```

---

le — *Calculates life expectancy for a prevention strategy*

Description

Aggregates data from a microsimulated cohort.

Usage

```
le(scenario, disc=FALSE)
```

Arguments

`scenario`	microsimulated cohort.
`disc`	discount rate to be applied. Defaults to `FALSE` (undiscounted).

Value

Global and per-person life expectancy of the considered prevention strategy.

Author(s)

David Moriña (Universitat de Barcelona), Pedro Puig (Universitat Autònoma de Barcelona) and Mireia Diaz (Institut Català d’Oncologia)

References

Georgalis L, de Sanjosé S, Esnaola M, Bosch F X, Diaz M. Present and future of cervical cancer prevention in Spain: a cost-effectiveness analysis. European Journal of Cancer Prevention 2016;**25**(5):430-439.

Moriña D, de Sanjosé S, Diaz M. Impact of model calibration on cost-effectiveness analysis of cervical cancer prevention 2017;**7**.

See Also

mSimCC-package, microsim, costs, bCohort, plotCIN1Incidence, plotCIN2Incidence, plotCIN3Incidence, plotIncidence, plotMortality, plotPrevalence, qalys, yls

Examples

```
data(probs)
nsim       <- 3
p.men      <- 0
size       <- 20
min.age    <- 10
max.age    <- 84

#### Natural history
hn <- microsim(seed=1234, nsim, probs, abs_states=c(10, 11), sympt_states=c(5, 6, 7, 8),
               prob_sympt=c(0.11, 0.23, 0.66, 0.9),
                size, p.men, min.age, max.age,
            utilityCoefs = c(1, 1, 0.987, 0.87, 0.87, 0.76, 0.67, 0.67, 0.67, 0.938, 0, 0),
                costCoefs.md = c(0, 0, 254.1, 1495.9, 1495.9, 5546.8, 12426.4, 23123.4,
                                 34016.6, 0, 0, 0),
           costCoefs.nmd = c(0, 0, 81.4, 194.1, 194.1, 219.1, 219.1, 219.1, 219.1, 0, 0, 0),
                costCoefs.i = c(0, 0, 0, 0, 0, 0, 0, 0, 0, 0, 0, 0), disc=3,
                treatProbs=c(0,0,1,1,1,0.9894,0.9422,0.8262,0.5507,0,0,0),
                nCores=1) ### individual level

le(hn) ### Aggregated level
```

---

microsim *Generate microsimulated cohorts*

Description

Generates several microsimulated cohorts with desired specifications.

Usage

```
microsim(seed=1234, nsim, transition, abs_states, sympt_states, prob_sympt, size,
           p_men, min_age, max_age, utilityCoefs, costCoefs.md, costCoefs.nmd,
       costCoefs.i, disc=3, vacc=FALSE, vacc.age=NULL, ndoses=NULL, vacc.cov=NULL,
           vacc.eff=NULL, vacc.type=NULL, vacc.prop=NULL, vaccprice.md=NULL,
```

```
    vaccprice.nmd=NULL, vaccprice.i=NULL, screening=FALSE, screenType=0,
    scrSchema=0, screenPeriod=NULL, cytoType=NULL, screenPrice.md=NULL,
    screenPrice.nmd=NULL, screenPrice.i=NULL, colpoPrice.md=NULL,
    colpoPrice.nmd=NULL, colpoPrice.i=NULL, hpvTestPrice.md=NULL,
    hpvTestPrice.nmd=NULL, hpvTestPrice.i=NULL, cytoHpvPrice.md=NULL,
    cytoHpvPrice.nmd=NULL, cytoHpvPrice.i=NULL, biopsPrice.md=NULL,
biopsPrice.nmd=NULL, biopsPrice.i=NULL, screenCoverage=NULL, screenSensi=NULL,
  screenSensi2=NULL, screenSensi3=NULL, colpoSensi=NULL, biopSensi=NULL,
    hpvTestSensi=NULL, treatProbs, nAnnualVisits=0, nAnnualVisitsLSIL=0,
    nAnnualVisitsHSIL=0, cytoHPVPeriod=0, cytoHPVPostColpo=0,
  cytoHPVPostBiop=NULL, cytoLSILperiod=0, cytoHSILperiod=0, switchAge=0,
    C_period=NULL, hpvPeriod=0, nCores=1)
```

Arguments

seed	seed to be used in the simulation. Default value is 1234.
nsim	number of cohorts to be simulated.
transition	transition probabilities matrix.
abs_states	vector with the absorbing states.
sympt_states	vector with the health states that might present symptoms.
prob_sympt	vector with the probability of presenting symptoms for each health state that might present symptoms. Should have the same length of sympt_states.
size	number of individuals on each simulated cohort.
p_men	proportion of men in the simulated cohorts.
min_age	lowest age in the cohort.
max_age	largest age in the cohort.
utilityCoefs	vector with the utilities for each health state.
costCoefs.md	vector with the direct medical costs for each health state.
costCoefs.nmd	vector with the direct non medical costs for each health state.
costCoefs.i	vector with the indirect costs for each health state.
disc	discount rate in percentage. Default value is 3.
vacc	boolean value specifying if the considered scenario includes vaccination. Default value is FALSE.
vacc.age	vector with ages at vaccination if the considered scenario includes vaccination. Default value is NULL.
ndoses	number of doses of vaccine if the considered scenario includes vaccination. Default value is NULL.
vacc.cov	vaccine coverage if the considered scenario includes vaccination. Default value is NULL.
vacc.eff	vaccine effectivity if the considered scenario includes vaccination. Default value is NULL.

- `vacc.type` type of vaccine if the considered scenario includes vaccination, character with values `biv` for bivalent, `quad` for quadrivalent and `nona` for nonavalent vaccines. Default value is `NULL`.
- `vacc.prop` proportion of vaccinated women on each age group if the considered scenario includes vaccination. Default value is `NULL`.
- `vaccprice.md` vaccine direct medical costs if the considered scenario includes vaccination. Default value is `NULL`.
- `vaccprice.nmd` vaccine direct non medical costs if the considered scenario includes vaccination. Default value is `NULL`.
- `vaccprice.i` vaccine indirect if the considered scenario includes vaccination. Default value is `NULL`.
- `screening` boolean specifying if the considered scenario includes screening of any type. Default value is `FALSE`.
- `screenType` type of screening. `1` stands for organized screening, `2` stands for opportunistic screening. Default value is `0` (no screening).
- `scrSchema` screening schema. `1` stands for cytology alone with repeat cytology for triage, `2` stands for cytology with HPV triage, `3` stands for HPV with cytology triage and `4` stands for HPV genotyping with cytology triage. Default value is `0` (no screening).
- `screenPeriod` screening period (in years). Default value is `NULL` (no screening).
- `cytoType` type of cytology. `0` stands for conventional cytology, `1` stands for Liquid Based Cytology (LBC). Default value is `NULL` (no cytology).
- `screenPrice.md` medical direct cost of cytology. Default value is `NULL`.
- `screenPrice.nmd` non-medical direct cost of cytology. Default value is `NULL`.
- `screenPrice.i` indirect cost of cytology. Default value is `NULL`.
- `colpoPrice.md` medical direct cost of colposcopy. Default value is `NULL`.
- `colpoPrice.nmd` non-medical direct cost of colposcopy. Default value is `NULL`.
- `colpoPrice.i` indirect cost of colposcopy. Default value is `NULL`.
- `hpvTestPrice.md` medical direct cost of HPV test. Default value is `NULL`.
- `hpvTestPrice.nmd` non-medical direct cost of HPV test. Default value is `NULL`.
- `hpvTestPrice.i` indirect cost of HPV test. Default value is `NULL`.
- `cytoHpvPrice.md` medical direct cost of HPV reflex test, in case `cytoType=1`. Default value is `NULL`.
- `cytoHpvPrice.nmd` non-medical direct cost of HPV reflex test, in case `cytoType=1`. Default value is `NULL`.
- `cytoHpvPrice.i` indirect cost of HPV reflex test, in case `cytoType=1`. Default value is `NULL`.
- `biopsPrice.md` medical direct cost of biopsy. Default value is `NULL`.

`biopsPrice.nmd` non-medical direct cost of biopsy. Default value is `NULL`.

`biopsPrice.i` indirect cost of biopsy. Default value is `NULL`.

`screenCoverage` cytology coverage for each age group. Default value is `NULL`.

`screenSensi` cytology sensitivity for each age group. Default value is `NULL`.

`screenSensi2` cytology sensitivity after cytology for each age group. Default value is `NULL`.

`screenSensi3` cytology sensitivity after HPV test for each age group. Default value is `NULL`.

`colpoSensi` colposcopy sensitivity for each age group. Default value is `NULL`.

`biopSensi` biopsy sensitivity for each age group. Default value is `NULL`.

`hpvTestSensi` HPV test sensitivity for each age group. Default value is `NULL`.

`treatProbs` probability of recuperation after treatment for each FIGO I - FIGO IV states.

`nAnnualVisits` number of annual visits after colposcopy for screening schema `1`. Default value is `0`.

`nAnnualVisitsLSIL` number of annual visits after LSIL for screening schema `2`. Default value is `0`.

`nAnnualVisitsHSIL` number of annual visits after HSIL for screening schema `2`. Default value is `0`.

`cytoHPVPeriod` cytology and HPV test protocol period for screening schemas `3` and `4`. Default value is `0`.

`cytoHPVPostColpo` cytology and HPV test protocol period after colposcopy protocol for screening schemas `3` and `4`. Default value is `0`.

`cytoHPVPostBiop` cytology and HPV test protocol period after biopsy protocol for screening schemas `2`. Default value is `NULL`.

`cytoLSILperiod` period for cytology after LSIL detection for screening schame `2`. Default value is `0`.

`cytoHSILperiod` period for cytology after HSIL detection for screening schame `2`. Default value is `0`.

`switchAge` age at which screening protocol changes for screening schemas `3` and `4`. Default value is `0`.

`C_period` vector with screening periods (in years) before and after switch age for screening schemas `3` and `4`. Default value is `NULL`.

`hpvPeriod` period for HPV test in screening schema `2`. Default value is `0`.

`nCores` number of cores of the computer. Default value is `1`.

Value

Data frame containing the simulated cohorts and the individual history for each person in each simulated cohort.

Author(s)

David Moriña (Universitat de Barcelona), Pedro Puig (Universitat Autònoma de Barcelona) and Mireia Diaz (Institut Català d'Oncologia)

References

Georgalis L, de Sanjosé S, Esnaola M, Bosch F X, Diaz M. Present and future of cervical cancer prevention in Spain: a cost-effectiveness analysis. European Journal of Cancer Prevention 2016;**25**(5):430-439.

Moriña D, de Sanjosé S, Diaz M. Impact of model calibration on cost-effectiveness analysis of cervical cancer prevention 2017;**7**.

See Also

`mSimCC-package`, `bCohort`, `costs`, `le`, `plotCIN1Incidence`, `plotCIN2Incidence`, `plotCIN3Incidence`, `plotIncidence`, `plotMortality`, `plotPrevalence`, `qalys`, `yls`

Examples

```
data(probs)
nsim       <- 3
p.men      <- 0
size       <- 20
min.age    <- 10
max.age    <- 84

#### Natural history
hn <- microsim(seed=1234, nsim, probs, abs_states=c(10, 11), sympt_states=c(5, 6, 7, 8),
               prob_sympt=c(0.11, 0.23, 0.66, 0.9),
                size, p.men, min.age, max.age,
            utilityCoefs = c(1, 1, 0.987, 0.87, 0.87, 0.76, 0.67, 0.67, 0.67, 0.938, 0, 0),
                costCoefs.md = c(0, 0, 254.1, 1495.9, 1495.9, 5546.8, 12426.4, 23123.4,
                                 34016.6, 0, 0, 0),
           costCoefs.nmd = c(0, 0, 81.4, 194.1, 194.1, 219.1, 219.1, 219.1, 219.1, 0, 0, 0),
                costCoefs.i = c(0, 0, 0, 0, 0, 0, 0, 0, 0, 0, 0, 0), disc=3,
                treatProbs=c(0,0,1,1,1,0.9894,0.9422,0.8262,0.5507,0,0,0),
                nCores=1) ### individual level
```

`plotCIN1Incidence` *Calculates and plots the CIN1 incidence.*

Description

Calculates and plots the CIN1 incidence for one or several prevention strategies.

Usage

```
plotCIN1Incidence(..., current=NULL, labels=NULL)
```

Arguments

`...`	one or several microsimulated cohort corresponding to one or several microsimulated cohorts.
`current`	real CIN 1 incidence in the population of interest.
`labels`	labels to be used in the plot.

Value

Returns a list with CIN 1 incidence for each age group.

Author(s)

David Moriña (Universitat de Barcelona), Pedro Puig (Universitat Autònoma de Barcelona) and Mireia Diaz (Institut Català d'Oncologia)

References

Georgalis L, de Sanjosé S, Esnaola M, Bosch F X, Diaz M. Present and future of cervical cancer prevention in Spain: a cost-effectiveness analysis. European Journal of Cancer Prevention 2016;**25**(5):430-439.

Moriña D, de Sanjosé S, Diaz M. Impact of model calibration on cost-effectiveness analysis of cervical cancer prevention 2017;**7**.

See Also

`mSimCC-package`, `microsim`, `costs`, `le`, `bCohort`, `plotCIN2Incidence`, `plotCIN3Incidence`, `plotIncidence`, `plotMortality`, `plotPrevalence`, `qalys`, `yls`

Examples

```
data(probs)
nsim      <- 3
p.men     <- 0
size      <- 20
min.age   <- 10
max.age   <- 84

#### Natural history
hn <- microsim(seed=1234, nsim, probs, abs_states=c(10, 11), sympt_states=c(5, 6, 7, 8),
               prob_sympt=c(0.11, 0.23, 0.66, 0.9),
                size, p.men, min.age, max.age,
            utilityCoefs = c(1, 1, 0.987, 0.87, 0.87, 0.76, 0.67, 0.67, 0.67, 0.938, 0, 0),
                costCoefs.md = c(0, 0, 254.1, 1495.9, 1495.9, 5546.8, 12426.4, 23123.4,
                                 34016.6, 0, 0, 0),
           costCoefs.nmd = c(0, 0, 81.4, 194.1, 194.1, 219.1, 219.1, 219.1, 219.1, 0, 0, 0),
                costCoefs.i = c(0, 0, 0, 0, 0, 0, 0, 0, 0, 0, 0, 0), disc=3,
                treatProbs=c(0,0,1,1,1,0.9894,0.9422,0.8262,0.5507,0,0,0),
                nCores=1) ### individual level
hn_c <- bCohort(hn)
plotCIN1Incidence(hn_c) ### Aggregated level
```

`plotCIN2Incidence` *Calculates and plots the CIN2 incidence.*

Description

Calculates and plots the CIN2 incidence for one or several prevention strategies.

Usage

```
plotCIN2Incidence(..., current=NULL, labels=NULL)
```

Arguments

`...`	one or several microsimulated cohort corresponding to one or several microsimulated cohorts.
`current`	real CIN 2 incidence in the population of interest.
`labels`	labels to be used in the plot.

Value

Returns a list with CIN 2 incidence for each age group.

Author(s)

David Moriña (Universitat de Barcelona), Pedro Puig (Universitat Autònoma de Barcelona) and Mireia Diaz (Institut Català d'Oncologia)

References

Georgalis L, de Sanjosé S, Esnaola M, Bosch F X, Diaz M. Present and future of cervical cancer prevention in Spain: a cost-effectiveness analysis. European Journal of Cancer Prevention 2016;**25**(5):430-439.

Moriña D, de Sanjosé S, Diaz M. Impact of model calibration on cost-effectiveness analysis of cervical cancer prevention 2017;**7**.

See Also

`mSimCC-package`, `microsim`, `costs`, `le`, `bCohort`, `plotCIN1Incidence`, `plotCIN3Incidence`, `plotIncidence`, `plotMortality`, `plotPrevalence`, `qalys`, `yls`

Examples

```
data(probs)
nsim       <- 3
p.men      <- 0
size       <- 20
min.age    <- 10
max.age    <- 84
```

```
#### Natural history
hn <- microsim(seed=1234, nsim, probs, abs_states=c(10, 11), sympt_states=c(5, 6, 7, 8),
               prob_sympt=c(0.11, 0.23, 0.66, 0.9),
                size, p.men, min.age, max.age,
            utilityCoefs = c(1, 1, 0.987, 0.87, 0.87, 0.76, 0.67, 0.67, 0.67, 0.938, 0, 0),
                costCoefs.md = c(0, 0, 254.1, 1495.9, 1495.9, 5546.8, 12426.4, 23123.4,
                                 34016.6, 0, 0, 0),
           costCoefs.nmd = c(0, 0, 81.4, 194.1, 194.1, 219.1, 219.1, 219.1, 219.1, 0, 0, 0),
                costCoefs.i = c(0, 0, 0, 0, 0, 0, 0, 0, 0, 0, 0, 0), disc=3,
                treatProbs=c(0,0,1,1,1,0.9894,0.9422,0.8262,0.5507,0,0,0),
                nCores=1) ### individual level
hn_c <- bCohort(hn)
plotCIN2Incidence(hn_c) ### Aggregated level
```

`plotCIN3Incidence` *Calculates and plots the CIN3 incidence.*

Description

Calculates and plots the CIN3 incidence for one or several prevention strategies.

Usage

```
plotCIN3Incidence(..., current=NULL, labels=NULL)
```

Arguments

`...`	one or several microsimulated cohort corresponding to one or several microsimulated cohorts.
`current`	real CIN 3 incidence in the population of interest.
`labels`	labels to be used in the plot.

Value

Returns a list with CIN 3 incidence for each age group.

Author(s)

David Moriña (Universitat de Barcelona), Pedro Puig (Universitat Autònoma de Barcelona) and Mireia Diaz (Institut Català d'Oncologia)

References

Georgalis L, de Sanjosé S, Esnaola M, Bosch F X, Diaz M. Present and future of cervical cancer prevention in Spain: a cost-effectiveness analysis. European Journal of Cancer Prevention 2016;**25**(5):430-439.

Moriña D, de Sanjosé S, Diaz M. Impact of model calibration on cost-effectiveness analysis of cervical cancer prevention 2017;**7**.

See Also

mSimCC-package, microsim, costs, le, bCohort, plotCIN2Incidence, plotCIN1Incidence, plotIncidence, plotMortality, plotPrevalence, qalys, yls

Examples

```
data(probs)
nsim       <- 3
p.men      <- 0
size       <- 20
min.age    <- 10
max.age    <- 84

#### Natural history
hn <- microsim(seed=1234, nsim, probs, abs_states=c(10, 11), sympt_states=c(5, 6, 7, 8),
               prob_sympt=c(0.11, 0.23, 0.66, 0.9),
                size, p.men, min.age, max.age,
            utilityCoefs = c(1, 1, 0.987, 0.87, 0.87, 0.76, 0.67, 0.67, 0.67, 0.938, 0, 0),
                costCoefs.md = c(0, 0, 254.1, 1495.9, 1495.9, 5546.8, 12426.4, 23123.4,
                                 34016.6, 0, 0, 0),
           costCoefs.nmd = c(0, 0, 81.4, 194.1, 194.1, 219.1, 219.1, 219.1, 219.1, 0, 0, 0),
                costCoefs.i = c(0, 0, 0, 0, 0, 0, 0, 0, 0, 0, 0, 0), disc=3,
                treatProbs=c(0,0,1,1,1,0.9894,0.9422,0.8262,0.5507,0,0,0),
                nCores=1) ### individual level
hn_c <- bCohort(hn)
plotCIN3Incidence(hn_c) ### Aggregated level
```

---

plotIncidence — *Calculates and plots the cervical cancer incidence.*

Description

Calculates and plots the cervical cancer incidence for one or several prevention strategies.

Usage

```
plotIncidence(..., current=NULL, labels=NULL)
```

Arguments

`...`	one or several microsimulated cohort corresponding to one or several microsimulated cohorts.
`current`	real cervical cancer incidence in the population of interest.
`labels`	labels to be used in the plot.

Value

Returns a list with cervical cancer incidence for each age group.

Author(s)

David Moriña (Universitat de Barcelona), Pedro Puig (Universitat Autònoma de Barcelona) and Mireia Diaz (Institut Català d'Oncologia)

References

Georgalis L, de Sanjosé S, Esnaola M, Bosch F X, Diaz M. Present and future of cervical cancer prevention in Spain: a cost-effectiveness analysis. European Journal of Cancer Prevention 2016;**25**(5):430-439.

Moriña D, de Sanjosé S, Diaz M. Impact of model calibration on cost-effectiveness analysis of cervical cancer prevention 2017;**7**.

See Also

`mSimCC-package`, `microsim`, `costs`, `le`, `bCohort`, `plotCIN2Incidence`, `plotCIN1Incidence`, `plotCIN3Incidence`, `plotMortality`, `plotPrevalence`, `qalys`, `yls`

Examples

```
data(probs)
nsim       <- 3
p.men      <- 0
size       <- 20
min.age    <- 10
max.age    <- 84

#### Natural history
hn <- microsim(seed=1234, nsim, probs, abs_states=c(10, 11), sympt_states=c(5, 6, 7, 8),
               prob_sympt=c(0.11, 0.23, 0.66, 0.9),
                size, p.men, min.age, max.age,
            utilityCoefs = c(1, 1, 0.987, 0.87, 0.87, 0.76, 0.67, 0.67, 0.67, 0.938, 0, 0),
                costCoefs.md = c(0, 0, 254.1, 1495.9, 1495.9, 5546.8, 12426.4, 23123.4,
                                 34016.6, 0, 0, 0),
           costCoefs.nmd = c(0, 0, 81.4, 194.1, 194.1, 219.1, 219.1, 219.1, 219.1, 0, 0, 0),
                costCoefs.i = c(0, 0, 0, 0, 0, 0, 0, 0, 0, 0, 0, 0), disc=3,
                treatProbs=c(0,0,1,1,1,0.9894,0.9422,0.8262,0.5507,0,0,0),
                nCores=1) ### individual level
hn_c <- bCohort(hn)
plotIncidence(hn_c) ### Aggregated level
```

`plotMortality` *Calculates and plots the cervical cancer mortality.*

Description

Calculates and plots the cervical cancer mortality for one or several prevention strategies.

Usage

```
plotMortality(..., current=NULL, labels=NULL)
```

Arguments

`...`	one or several microsimulated cohort corresponding to one or several microsimulated cohorts.
`current`	real cervical cancer mortality in the population of interest.
`labels`	labels to be used in the plot.

Value

Returns a list with cervical cancer mortality for each age group.

Author(s)

David Moriña (Universitat de Barcelona), Pedro Puig (Universitat Autònoma de Barcelona) and Mireia Diaz (Institut Català d'Oncologia)

References

Georgalis L, de Sanjosé S, Esnaola M, Bosch F X, Diaz M. Present and future of cervical cancer prevention in Spain: a cost-effectiveness analysis. European Journal of Cancer Prevention 2016;**25**(5):430-439.

Moriña D, de Sanjosé S, Diaz M. Impact of model calibration on cost-effectiveness analysis of cervical cancer prevention 2017;**7**.

See Also

`mSimCC-package`, `microsim`, `costs`, `le`, `bCohort`, `plotCIN2Incidence`, `plotCIN1Incidence`, `plotCIN3Incidence`, `plotMortality`, `plotPrevalence`, `qalys`, `yls`

Examples

```
data(probs)
nsim       <- 3
p.men      <- 0
size       <- 20
min.age    <- 10
max.age    <- 84

#### Natural history
hn <- microsim(seed=1234, nsim, probs, abs_states=c(10, 11), sympt_states=c(5, 6, 7, 8),
               prob_sympt=c(0.11, 0.23, 0.66, 0.9),
                size, p.men, min.age, max.age,
            utilityCoefs = c(1, 1, 0.987, 0.87, 0.87, 0.76, 0.67, 0.67, 0.67, 0.938, 0, 0),
                costCoefs.md = c(0, 0, 254.1, 1495.9, 1495.9, 5546.8, 12426.4, 23123.4,
                                 34016.6, 0, 0, 0),
           costCoefs.nmd = c(0, 0, 81.4, 194.1, 194.1, 219.1, 219.1, 219.1, 219.1, 0, 0, 0),
                costCoefs.i = c(0, 0, 0, 0, 0, 0, 0, 0, 0, 0, 0, 0), disc=3,
```

```
                treatProbs=c(0,0,1,1,1,0.9894,0.9422,0.8262,0.5507,0,0,0),
                nCores=1) ### individual level
hn_c <- bCohort(hn)
plotMortality(hn_c) ### Aggregated level
```

`plotPrevalence` *Calculates and plots the HPV prevalence.*

Description

Calculates and plots the HPV prevalence for one or several prevention strategies.

Usage

```
plotPrevalence(..., current=NULL, labels=NULL)
```

Arguments

`...`	one or several microsimulated cohort corresponding to one or several microsimulated cohorts.
`current`	real HPV prevalence in the population of interest.
`labels`	labels to be used in the plot.

Value

Returns a list with HPV prevalence for each age group.

Author(s)

David Moriña (Universitat de Barcelona), Pedro Puig (Universitat Autònoma de Barcelona) and Mireia Diaz (Institut Català d'Oncologia)

References

Georgalis L, de Sanjosé S, Esnaola M, Bosch F X, Diaz M. Present and future of cervical cancer prevention in Spain: a cost-effectiveness analysis. European Journal of Cancer Prevention 2016;**25**(5):430-439.

Moriña D, de Sanjosé S, Diaz M. Impact of model calibration on cost-effectiveness analysis of cervical cancer prevention 2017;**7**.

See Also

`mSimCC-package`, `microsim`, `costs`, `le`, `bCohort`, `plotCIN2Incidence`, `plotCIN1Incidence`, `plotCIN3Incidence`, `plotMortality`, `plotIncidence`, `qalys`, `yls`

Examples

```
data(probs)
nsim      <- 3
p.men     <- 0
size      <- 20
min.age   <- 10
max.age   <- 84

#### Natural history
hn <- microsim(seed=1234, nsim, probs, abs_states=c(10, 11), sympt_states=c(5, 6, 7, 8),
               prob_sympt=c(0.11, 0.23, 0.66, 0.9),
                size, p.men, min.age, max.age,
            utilityCoefs = c(1, 1, 0.987, 0.87, 0.87, 0.76, 0.67, 0.67, 0.67, 0.938, 0, 0),
                costCoefs.md = c(0, 0, 254.1, 1495.9, 1495.9, 5546.8, 12426.4, 23123.4,
                                 34016.6, 0, 0, 0),
           costCoefs.nmd = c(0, 0, 81.4, 194.1, 194.1, 219.1, 219.1, 219.1, 219.1, 0, 0, 0),
                costCoefs.i = c(0, 0, 0, 0, 0, 0, 0, 0, 0, 0, 0, 0), disc=3,
                treatProbs=c(0,0,1,1,1,0.9894,0.9422,0.8262,0.5507,0,0,0),
                nCores=1) ### individual level
hn_c <- bCohort(hn)
plotPrevalence(hn_c) ### Aggregated level
```

`probs` *Transition probabilities matrix for Spanish population*

Description

This data corresponds to a transition probabilities matrix calibrated for the Spanish population.

Usage

```
probs
```

Format

A data frame with 180 rows and 13 columns.

`qalys` *Aggregate data from a microsimulated cohort*

Description

Aggregates data from a microsimulated cohort.

Usage

```
qalys(scenario, disc=FALSE)
```

Arguments

`scenario`	microsimulated cohort.
`disc`	discount rate to be applied. Defaults to `FALSE` (undiscounted).

Value

Global and per-person QALYs of the considered prevention strategy.

Author(s)

David Moriña (Universitat de Barcelona), Pedro Puig (Universitat Autònoma de Barcelona) and Mireia Diaz (Institut Català d'Oncologia)

References

Georgalis L, de Sanjosé S, Esnaola M, Bosch F X, Diaz M. Present and future of cervical cancer prevention in Spain: a cost-effectiveness analysis. European Journal of Cancer Prevention 2016;**25**(5):430-439.

Moriña D, de Sanjosé S, Diaz M. Impact of model calibration on cost-effectiveness analysis of cervical cancer prevention 2017;**7**.

See Also

`mSimCC-package`, `microsim`, `costs`, `le`, `plotCIN1Incidence`, `plotCIN2Incidence`, `plotCIN3Incidence`, `plotIncidence`, `plotMortality`, `plotPrevalence`, `bCohort`, `yls`

Examples

```
data(probs)
nsim       <- 3
p.men      <- 0
size       <- 20
min.age    <- 10
max.age    <- 84

#### Natural history
hn <- microsim(seed=1234, nsim, probs, abs_states=c(10, 11), sympt_states=c(5, 6, 7, 8),
               prob_sympt=c(0.11, 0.23, 0.66, 0.9),
                size, p.men, min.age, max.age,
            utilityCoefs = c(1, 1, 0.987, 0.87, 0.87, 0.76, 0.67, 0.67, 0.67, 0.938, 0, 0),
                costCoefs.md = c(0, 0, 254.1, 1495.9, 1495.9, 5546.8, 12426.4, 23123.4,
                                 34016.6, 0, 0, 0),
           costCoefs.nmd = c(0, 0, 81.4, 194.1, 194.1, 219.1, 219.1, 219.1, 219.1, 0, 0, 0),
                costCoefs.i = c(0, 0, 0, 0, 0, 0, 0, 0, 0, 0, 0, 0), disc=3,
                treatProbs=c(0,0,1,1,1,0.9894,0.9422,0.8262,0.5507,0,0,0),
                nCores=1) ### individual level

qalys(hn)
```

yls *Aggregate data from a microsimulated cohort*

Description

Aggregates data from a microsimulated cohort.

Usage

```
yls(scenario1, scenario2, disc = FALSE)
```

Arguments

scenario1	microsimulated cohort.
scenario2	microsimulated cohort.
disc	discount rate to be applied. Defaults to FALSE (undiscounted).

Value

Years of life saved due to strategy scenario1 compared to scenario2.

Author(s)

David Moriña (Universitat de Barcelona), Pedro Puig (Universitat Autònoma de Barcelona) and Mireia Diaz (Institut Català d'Oncologia)

References

Georgalis L, de Sanjosé S, Esnaola M, Bosch F X, Diaz M. Present and future of cervical cancer prevention in Spain: a cost-effectiveness analysis. European Journal of Cancer Prevention 2016;**25**(5):430-439.

Moriña D, de Sanjosé S, Diaz M. Impact of model calibration on cost-effectiveness analysis of cervical cancer prevention 2017;**7**.

See Also

mSimCC-package, microsim, costs, le, plotCIN1Incidence, plotCIN2Incidence, plotCIN3Incidence, plotIncidence, plotMortality, plotPrevalence, qalys, bCohort

Examples

```
data(probs)
nsim       <- 3
p.men      <- 0
size       <- 20
min.age    <- 10
max.age    <- 84
```

```
#### Natural history
hn <- microsim(seed=1234, nsim, probs, abs_states=c(10, 11), sympt_states=c(5, 6, 7, 8),
               prob_sympt=c(0.11, 0.23, 0.66, 0.9),
                size, p.men, min.age, max.age,
            utilityCoefs = c(1, 1, 0.987, 0.87, 0.87, 0.76, 0.67, 0.67, 0.67, 0.938, 0, 0),
                costCoefs.md = c(0, 0, 254.1, 1495.9, 1495.9, 5546.8, 12426.4, 23123.4,
                                 34016.6, 0, 0, 0),
           costCoefs.nmd = c(0, 0, 81.4, 194.1, 194.1, 219.1, 219.1, 219.1, 219.1, 0, 0, 0),
                costCoefs.i = c(0, 0, 0, 0, 0, 0, 0, 0, 0, 0, 0, 0), disc=3,
                treatProbs=c(0,0,1,1,1,0.9894,0.9422,0.8262,0.5507,0,0,0),
                nCores=1)

vacc12 <- microsim(seed=1234, nsim, probs, abs_states=c(10, 11), sympt_states=c(5, 6, 7, 8),
                   prob_sympt=c(0.11, 0.23, 0.66, 0.9),
                   size, p.men, min.age, max.age,
             utilityCoefs = c(1, 1, 0.987, 0.87, 0.87, 0.76, 0.67, 0.67, 0.67, 0.938, 0, 0),
                  costCoefs.md = c(0, 0, 254.1, 1495.9, 1495.9, 5546.8, 12426.4, 23123.4,
                                   34016.6, 0, 0, 0),
                  costCoefs.nmd = c(0, 0, 81.4, 194.1, 194.1, 219.1, 219.1, 219.1, 219.1,
                                    0, 0, 0),
                  costCoefs.i = c(0, 0, 0, 0, 0, 0, 0, 0, 0, 0, 0, 0), disc=3, vacc=TRUE,
                   vacc.age=12, vacc.prop=1, ndoses=3,
                   vacc.cov=0.828, vacc.eff=1, vacc.type="biv", vaccprice.md=33.6,
                   vaccprice.nmd=0, vaccprice.i=0,
                   treatProbs=c(0,0,1,1,1,0.9894,0.9422,0.8262,0.5507,0,0,0), nCores=1)
yls(hn, vacc12)
```

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