Package ‘cystiSim’

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Title Agent-Based Model for Taenia_solium Transmission and Control
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Description The cystiSim package provides an agent-based model for Taenia solium transmission and control. cystiSim was developed within the framework of CYSTINET, the European Network on taeniosis/cysticercosis, COST ACTION TD1302.

URL https://github.com/brechtdv/cystiSim
BugReports https://github.com/brechtdv/cystiSim/issues
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The cystiSim model allows simulating *Taenia solium* taeniosis/cysticercosis transmission in a virtual population of humans and pigs. It also allows evaluating the possible effects of human mass drug administration, pig mass drug administration, and pig vaccination. **cystiSim** was developed within the framework of CYSTINET, the European Network on taeniosis/cysticercosis, COST ACTION TD1302 ([http://www.cystinet.org/](http://www.cystinet.org/)).

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Available functions in the **cystiSim** package:

- **baseline**
  - `random_baseline_man` Generate a random baseline human population.
  - `random_baseline_pig` Generate a random baseline pig population.

- **model—S3 class 'cystiRun'**
  - `fit` Fit parameters of a cystiRun model.
  - `initiate` Initiate a cystiRun model.
  - `update` Update a cystiRun model.

- **interventions**
  - `do_man_mda` Do human mass drug administration.
  - `do_pig_mda` Do pig mass drug administration.
**do_pig_vac**  Do pig vaccination.
**do_pig_mda_vac**  Do pig mass drug administration AND vaccination.

**simulate—S3 class ’cystiSim’**

- **cystiSim**  Simulate multiple cystiRun models.
- **report**  Generate a PDF report for a cystiSim object.
- **elim**  Derive when elimination occurred in a cystiSim object.

For more details and examples, please visit the cystiSim Wiki pages on [https://github.com/brechtdv/cystiSim/wiki](https://github.com/brechtdv/cystiSim/wiki).

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**baseline**

**Random baseline populations**

**Description**

Generate random baseline human and pig populations.

**Usage**

- `random_baseline_man(n, p)`
- `random_baseline_pig(n, p, p.high)`

**Arguments**

- **n**  Number of individuals to simulate.
- **p**  Proportion of individuals infected with a mature parasite.
- **p.high**  Proportion of infected pigs with high infection intensity.

**Note**

For more details and examples, please visit the cystiSim Wiki pages on [https://github.com/brechtdv/cystiSim/wiki](https://github.com/brechtdv/cystiSim/wiki).

**Author(s)**

<brechtdv@gmail.com>
Description

Functions to initiate, update and explore 'cystiRun' objects. A 'cystiRun' object corresponds to a single run of a cystiSim model.

Usage

initiate(man, pig, ph2m, pl2m, m2p, e2p, age.coef = c(0, 0), slaughter = slaughter_nbinom, slaughter.args = list(min = 6, max = 36, size = 0.70, mu = 80))

## S3 method for class 'cystiRun'
update(object, n = 1200, verbose = TRUE, ...)

## S3 method for class 'cystiRun'
print(x, from = 200, to = NA, ...)

## S3 method for class 'cystiRun'
plot(x, y = NULL, show = c("PC", "PR", "HT", "EN"), start = 0, from = 1, to = NA, ...)

prevalence(z)

Arguments

<table>
<thead>
<tr>
<th>Argument</th>
<th>Description</th>
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</thead>
<tbody>
<tr>
<td>man</td>
<td>Human population dataframe.</td>
</tr>
<tr>
<td>pig</td>
<td>Pig population dataframe.</td>
</tr>
<tr>
<td>ph2m</td>
<td>Pig (Heavy infection) to Man transmission probability.</td>
</tr>
<tr>
<td>pl2m</td>
<td>Pig (Light infection) to Man transmission probability.</td>
</tr>
<tr>
<td>m2p</td>
<td>Man to Pig transmission probability.</td>
</tr>
<tr>
<td>e2p</td>
<td>Environment to Pig transmission probability.</td>
</tr>
<tr>
<td>age.coef</td>
<td>Optional intercept and slope for the association between age and taeniosis.</td>
</tr>
<tr>
<td>slaughter</td>
<td>Function that defines the slaughter probability of pigs.</td>
</tr>
<tr>
<td>slaughter.args</td>
<td>Arguments to be passed to the slaughter function.</td>
</tr>
<tr>
<td>object</td>
<td>Object of class 'cystiRun'.</td>
</tr>
<tr>
<td>n</td>
<td>Number of iterations (months).</td>
</tr>
<tr>
<td>verbose</td>
<td>If TRUE, a progress bar is shown.</td>
</tr>
<tr>
<td>x</td>
<td>Object of class 'cystiRun'.</td>
</tr>
<tr>
<td>y</td>
<td>Currently ignored.</td>
</tr>
</tbody>
</table>
cystiRun

- **z** Vector of infection indicators.
- **start** Origin of plot.
- **from** First iteration to be used in output.
- **to** Last iteration to be used in output. The default value NA corresponds to the last available iteration.
- **show** Which output should be plotted?
- **...** Arguments to be passed on to generic function.

**Value**

initiate and update return an object of S3 class `cystiRun`.

**Note**

For more details and examples, please visit the cystiSim Wiki pages on https://github.com/brechtdv/cystiSim/wiki.

**Author(s)**

<brechtdv@gmail.com>

**See Also**

Intervention functions: `do_man_mda`, `do_pig_mda`, `do_pig_vac`, `do_pig_mda_vac`

**Examples**

```r
## we will use the built-in Mbeya dataset
prevalence(pig_mbeya$cysti)
prevalence(man_mbeya$taenia)

## define transmission probabilities
ph2m <- 0.000174918
pl2m <- 0.000149501
m2p <- 6.85E-05
e2p <- 0.00022611

## first initiate the 'cystiRun' object
mod <- initiate(man_mbeya, pig_mbeya, ph2m, pl2m, m2p, e2p)

## update the model 240 cycles (=20 years)
## this is a burn-in period, needed to obtain steady state
mod <- update(mod, 240)

## apply human mass drug administration
mod <- do_man_mda(mod, efficacy = 0.70, coverage = 0.80)

## apply pig mass drug administration
mod <- do_pig_mda(mod, efficacy = 0.90, coverage = 0.90)
```
# cystiSim

--

**Description**

Functions to initiate and explore `cystiSim` objects. A `cystiSim` object corresponds to multiple runs of a `cystiSim` model.

**Usage**

```r
cystiSim(n = 100, mod, main = NULL)
report(x, ...)
## S3 method for class 'cystiSim'
print(x, ...)
## S3 method for class 'cystiSim'
summary(object, round = 3, ...)
## S3 method for class 'cystiSim'
plot(x, y, annotate = TRUE, ...)
## S3 method for class 'cystiSim'
report(x, name = "cystiSim", ...)
## S3 method for class 'cystiSim'
elim(x, show = c("m", "y"), ...)
```

**Arguments**

- `n`: Number of iterations (months).
- `mod`: `cystiSim` model.
- `main`: `cystiSim` model label.
- `x`: Object of class `cystiSim`.
- `object`: Object of class `cystiSim`.
- `y`: Currently ignored.
- `round`: Number of decimal digits to be printed.
- `annotate`: Should plot be annotated with summary information?

```r
c # update the model 120 more cycles (=10 years)
mod <- update(mod, 120)

# plot the cycles
plot(mod, from = 200, start = 40)
```
cystiSim

name            Report name.
show            Show time till elimination in terms of months or years?
...             Other arguments to be passed to generics.

Value

cystiSim returns an object of S3 class 'cystSim'.

Note

For more details and examples, please visit the cystiSim Wiki pages on https://github.com/berhtdv/cystiSim/wiki.

Author(s)

<berhtdv@gmail.com>

See Also

cystiRun

Examples

## Not run:

## we will use the built-in Mbeya dataset
define(pig_mbeya$cysti)
define(man_mbeya$taenia)

## define transmission probabilities
ph2m <- 0.000174918
pl2m <- 0.000149501
m2p <- 6.85E-05
e2p <- 0.00022611

## set seed for reproducibility
set.seed(264)

## need to define coverage and efficacy of all interventions
cov_man_mda <- 0.80
cov_pig_mda <- 0.90
cov_pig_vac <- NULL
eff_man_mda <- 0.70
eff_pig_mda <- 0.90
eff_pig_vac <- NULL

## run the simulations
sim <-
cystiSim(
  n = 10,
  main = "example",
)
do_man_mda

mod = {
  initiate(man_mbeya, pig_mbeya, ph2m, pl2m, m2p, e2p) %>%
  update(240) %>%
  do_man_mda(coverage = cov_man_mda, efficacy = eff_man_mda) %>%
  do_pig_mda(coverage = cov_pig_mda, efficacy = eff_pig_mda) %>%
  update(120)
}

## summarize results
summary(sim)

## plot simulations (mean and uncertainty interval)
plot(sim)

## create PDF report and plot
report(sim)

## End(Not run)

do_man_mda Do human mass drug administration(MDA)

Description

Intervention function that mimics the possible effects of human mass drug administration.

Usage

do_man_mda(x, coverage, efficacy, min.age = 0, max.age = Inf)

Arguments

  x      cystiRun object.
  coverage Presumed coverage of drug administration within eligible population, expressed
           as a decimal value.
  efficacy Presumed efficacy of tapeworm treatment, expressed as a decimal value.
  min.age Minimum age for MDA, in months. Defaults to 0, i.e., no lower age limit.
  max.age Maximum age for MDA, in months. Defaults to Inf, i.e., no upper age limit.

Note

For more details and examples, please visit the cystiSim Wiki pages on https://github.com/brechtdv/cystiSim/wiki.

Author(s)

<brechtdv@gmail.com>
**do_pig_mda**

**See Also**

Other interventions: `do_pig_mda`, `do_pig_vac`, `do_pig_mda_vac`

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**do_pig_mda**  
*Do pig mass drug administration (MDA)*

**Description**

Intervention function that mimics the possible effects of pig mass drug administration.

**Usage**

```
do_pig_mda(x, coverage, efficacy, immunity = 3, min.age = 1, max.age = Inf)
```

**Arguments**

- `x`: cystiRun object.
- `coverage`: Presumed coverage of drug treatment within eligible population, expressed as a decimal value.
- `efficacy`: Presumed efficacy of drug treatment, expressed as a decimal value.
- `immunity`: Presumed duration of immunity following drug treatment of an infected pig. Defaults to 3 months.
- `min.age`: Minimum age for drug treatment, in months. Defaults to 1 month.
- `max.age`: Maximum age for drug treatment, in months. Defaults to Inf, i.e., no upper age limit.

**Note**

For more details and examples, please visit the [cystiSim Wiki](https://github.com/brechtdv/cystiSim/wiki).

**Author(s)**

<brechtdv@gmail.com>

**See Also**

Other interventions: `do_man_mda`, `do_pig_vac`, `do_pig_mda_vac`
do_pig_mda_vac

**Do pig mass drug administration (MDA) and vaccination**

**Description**

Intervention function that mimics the possible effects of combined pig mass drug administration and vaccination.

**Usage**

```r
do_pig_mda_vac(x, coverage, efficacy.mda, efficacy.vac, 
    immunity.mda = 3, immunity.vac = Inf, interval = 4, 
    min.age = 1, max.age = Inf)
```

**Arguments**

- `x` cystiRun object.
- `coverage` Presumed coverage within eligible population, expressed as a decimal value.
- `efficacy.mda` Presumed efficacy of drug treatment, expressed as a decimal value.
- `efficacy.vac` Presumed efficacy of vaccine, expressed as a decimal value.
- `immunity.mda` Presumed duration of immunity following drug treatment of an infected pig. Defaults to 3 months.
- `immunity.vac` Presumed duration of immunity following successful vaccination. Defaults to Inf.
- `interval` Maximum interval between two consecutive shots for immunity. Defaults to 4 months.
- `min.age` Minimum age for intervention, in months. Defaults to 1 month.
- `max.age` Maximum age for intervention, in months. Defaults to Inf, i.e., no upper age limit.

**Note**

For more details and examples, please visit the cystiSim Wiki pages on [https://github.com/brechtdv/cystiSim/wiki](https://github.com/brechtdv/cystiSim/wiki).

**Author(s)**

<brechtdv@gmail.com>

**See Also**

Other interventions: do_man_mda, do_pig_mda, do_pig_vac
do_pig_vac

---

**do_pig_vac**  
*Do pig vaccination*

### Description

Intervention function that mimics the possible effects of pig vaccination.

### Usage

```r
do_pig_vac(x, coverage, efficacy, immunity = Inf, interval = 4,
            min.age = 1, max.age = Inf)
```

### Arguments

- **x**  
  cystiRun object.

- **coverage**  
  Presumed coverage of vaccination within eligible population, expressed as a decimal value.

- **efficacy**  
  Presumed efficacy of vaccine, expressed as a decimal value.

- **immunity**  
  Presumed duration of immunity following successful vaccination. Defaults to Inf.

- **interval**  
  Maximum interval between two consecutive shots for immunity. Defaults to 4 months.

- **min.age**  
  Minimum age for vaccination, in months. Defaults to 1 month.

- **max.age**  
  Maximum age for vaccination, in months. Defaults to Inf, i.e., no upper age limit.

### Note

For more details and examples, please visit the **cystiSim** Wiki pages on [https://github.com/brechtdv/cystisim/wiki](https://github.com/brechtdv/cystisim/wiki).

### Author(s)

<<brechtdv@gmail.com>>

### See Also

Other interventions:  
- `do_man_mda`
- `do_pig_mda`
- `do_pig_mda_vac`
fit

Fit cystiSim parameters

Description

This function simulates random cystiSim parameters, and return those scenarios that result in a baseline prevalence close to the specified target.

Usage

```r
fit(n.sim, n.update, target, limit,
    man, pig, ph2m, pl2m, m2p, e2p, age.coef = c(0, 0),
    slaughter = slaughter_nbinom,
    slaughter.args = list(min = 6, max = 36, size = 0.70, mu = 80))
```

Arguments

- `n.sim` Desired number of retained scenarios.
- `n.update` Number of updates of the baseline model.
- `target` Named list of target prevalences for `ht`, `pc` and/or `pi`
- `limit` Maximum tolerated deviance.
- `man` Human population dataframe.
- `pig` Pig population dataframe.
- `ph2m` Pig (Heavy infection) to Man transmission probability.
- `pl2m` Pig (Light infection) to Man transmission probability.
- `m2p` Man to Pig transmission probability.
- `e2p` Environment to Pig transmission probability.
- `age.coef` Optional intercept and slope for the association between age and taeniosis.
- `slaughter` Function that defines the slaughter probability of pigs.
- `slaughter.args` Arguments to be passed to the slaughter function.

Details

The abbreviations used:

- `ht`...Human Taeniosis prevalence
- `pc`...Porcine Cysticercosis prevalence
- `pi`...Pig Intensity proportion (i.e., proportion heavily infection pigs)

Note

For more details and examples, please visit the cystiSim Wiki pages on https://github.com/brechtdv/cystiSim/wiki.
**man_mbeya**

**Description**

Default baseline dataframe.

**Usage**

```r
data("man_mbeya")
```

**Format**

A data frame with 6000 observations on the following 7 variables.

- **age**  a numeric vector
- **sex**  a factor with levels female male
- **taenia**  a numeric vector
- **taenia_immature**  a numeric vector
- **time_since_infection**  a numeric vector
- **environment**  a numeric vector
- **time_since_contamination**  a numeric vector

**Note**

For more details and examples, please visit the **cystiSim** Wiki pages on [https://github.com/brechtdv/cystiSim/wiki](https://github.com/brechtdv/cystiSim/wiki).

**man_mbozi**

**Description**

Default baseline dataframe.

**Usage**

```r
data("man_mbozi")
```
**Format**

A data frame with 6000 observations on the following 7 variables.

- **age**: a numeric vector
- **sex**: a factor with levels `female` `male`
- **taenia**: a numeric vector
- **taenia_immature**: a numeric vector
- **time_since_infection**: a numeric vector
- **environment**: a numeric vector
- **time_since_contamination**: a numeric vector

**Note**

For more details and examples, please visit the [cystiSim Wiki pages on](https://github.com/brechtdv/cystisim/wiki).

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**pig_mbeya**

**Mbeya pig population**

---

**Description**

Default baseline dataframe.

**Usage**

```r
data("pig_mbeya")
```

**Format**

A data frame with 498 observations on the following 8 variables.

- **age**: a numeric vector
- **cysti**: a numeric vector
- **cysti_immature**: a numeric vector
- **time_since_infection**: a numeric vector
- **intensity**: a factor with levels `P` `H` `L`
- **immunity**: a numeric vector
- **time_since_vaccination**: a logical vector
- **slaughtered**: a numeric vector

**Note**

For more details and examples, please visit the [cystiSim Wiki pages on](https://github.com/brechtdv/cystisim/wiki).
pig_mbozi

**Description**
Default baseline dataframe.

**Usage**
data("pig_mbozi")

**Format**
A data frame with 498 observations on the following 8 variables.
- `age` a numeric vector
- `cysti` a numeric vector
- `cysti_immature` a numeric vector
- `time_since_infection` a numeric vector
- `intensity` a factor with levels 0 H L
- `immunity` a numeric vector
- `time_since_vaccination` a logical vector
- `slaughtered` a numeric vector

**Note**
For more details and examples, please visit the cystiSim Wiki pages on [https://github.com/brechtdv/cystiSim/wiki](https://github.com/brechtdv/cystiSim/wiki).

slaughter

**Pig slaughter functions**

**Description**
These functions simulate age-dependent slaughter of pigs. The default function is `slaughter_nbinom`.

**Usage**
- `slaughter_binom(age, min, max, p)`
- `slaughter_nbinom(age, min, max, size, mu)`
Arguments

- **age**: Age of the pigs.
- **min**: Minimum age at slaughter, i.e., $Pr(slaughter < \text{min}) = 0$.
- **max**: Age at which all pigs are definitely slaughtered, i.e., $Pr(slaughter \geq \text{max}) = 1$.
- **p**: Binomial probability of slaughter.
- **size**: Size of Negative Binomial distribution of age-specific slaughter probability.
- **mu**: Mean of Negative Binomial distribution of age-specific slaughter probability.

Note

For more details and examples, please visit the **cystiSim** Wiki pages on [https://github.com/brechtdv/cystiSim/wiki](https://github.com/brechtdv/cystiSim/wiki).

Author(s)

<brechtdv@gmail.com>
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