

# Package ‘cystiSim’

October 12, 2022

**Title** Agent-Based Model for Taenia\_solium Transmission and Control

**Version** 0.1.0

**Date** 2016-05-15

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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>

**Depends** R (>= 3.3.0), ggplot2

**Imports** magrittr, knitr, graphics, grDevices, stats, utils

**License** GPL (>= 2)

**LazyData** true

**NeedsCompilation** no

**Repository** CRAN

**Date/Publication** 2016-05-15 21:46:33

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cystiSim-package	<i>Agent-based model for Taenia solium transmission and control.</i>
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## Description

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/>).

## Details

Package:	cystiSim
Version:	0.1.0
Date:	2016-05-15
Authors:	Brecht Devleesschauwer, Uffe Christian Braae
Maintainer:	<brechtdv@gmail.com>
URL:	<a href="https://github.com/brechtdv/cystiSim">https://github.com/brechtdv/cystiSim</a>
BugReports:	<a href="https://github.com/brechtdv/cystiSim/issues">https://github.com/brechtdv/cystiSim/issues</a>
Depends:	R (>= 3.3.0), ggplot2
Imports:	magrittr, knitr
License:	GPL (>= 2)
LazyLoad:	yes

Available functions in the **cystiSim** package:

### baseline

<code>random_baseline_man</code>	Generate a random baseline human population.
<code>random_baseline_pig</code>	Generate a random baseline pig population.

### model—S3 class 'cystiRun'

<code>fit</code>	Fit parameters of a cystiRun model.
<code>initiate</code>	Initiate a cystiRun model.
<code>update</code>	Update a cystiRun model.

### interventions

<code>do_man_mda</code>	Do human mass drug administration.
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<code>do_pig_mda</code>	Do pig mass drug administration.
<code>do_pig_vac</code>	Do pig vaccination.
<code>do_pig_mda_vac</code>	Do pig mass drug administration AND vaccination.
<b>simulate</b> —S3 class 'cystiSim'	
<code>cystiSim</code>	Simulate multiple cystiRun models.
<code>report</code>	Generate a PDF report for a cystiSim object.
<code>elim</code>	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>.

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baseline	<i>Random baseline populations</i>
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## 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>.

## Author(s)

<brechtdv@gmail.com>

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cystiRun                      *'cystiRun' object*

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## 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

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.
object	Object of class 'cystiRun'.
n	Number of iterations (months).
verbose	If TRUE, a progress bar is shown.
x	Object of class 'cystiRun'.
y	Currently ignored.

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**

```
## 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)
```

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

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

---

cystiSim

*'cystiSim' object*


---

## Description

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

## Usage

```
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?

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 'cystiSim'.

**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**

[cystiRun](#)

**Examples**

```
## Not run:

## 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

## 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",
```

```

    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>



**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 pages on <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**

```
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>.

**Author(s)**

<brechtdv@gmail.com>

**See Also**

Other interventions: [do\\_man\\_mda](#), [do\\_pig\\_mda](#), [do\\_pig\\_vac](#)

---

`do_pig_vac`*Do pig vaccination*

---

**Description**

Intervention function that mimics the possible effects of pig vaccination.

**Usage**

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

**Arguments**

<code>x</code>	cystiRun object.
<code>coverage</code>	Presumed coverage of vaccination within eligible population, expressed as a decimal value.
<code>efficacy</code>	Presumed efficacy of vaccine, expressed as a decimal value.
<code>immunity</code>	Presumed duration of immunity following successful vaccination. Defaults to Inf.
<code>interval</code>	Maximum interval between two consecutive shots for immunity. Defaults to 4 months.
<code>min.age</code>	Minimum age for vaccination, in months. Defaults to 1 month.
<code>max.age</code>	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>.

**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

```
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>.

**Author(s)**

<brechtdv@gmail.com>

---

man_mbeya	<i>Mbeya human population</i>
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---

**Description**

Default baseline dataframe.

**Usage**

```
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>.

---

man_mbozi	<i>Mbozi human population</i>
-----------	-------------------------------

---

**Description**

Default baseline dataframe.

**Usage**

```
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/brechtvd/cystiSim/wiki>.

---

pig_mbeya	<i>Mbeya pig population</i>
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---

**Description**

Default baseline dataframe.

**Usage**

```
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 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/brechtvd/cystiSim/wiki>.

---

pig_mbozi	<i>Mbozi pig population</i>
-----------	-----------------------------

---

**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/brechtvd/cystiSim/wiki>.

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slaughter	<i>Pig slaughter functions</i>
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---

**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., $Pr(\text{slaughter} < \text{min}) = 0$ .
max	Age at which all pigs are definitely slaughtered, i.e., $Pr(\text{slaughter} \geq \text{max}) = 1$ .
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>.

**Author(s)**

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