

Package: hrp2malaRia (via r-universe)

October 4, 2026

Type Package

Title pfhrp2 gene deletion malaria modelling

Version 0.1.3

Date 2023-01-25

Author OJ Watson

Maintainer <oj.watson@hotmail.co.uk>

Description Individual based malaria transmission model.

Depends R (>= 3.1.0)

Imports ggplot2, reshape2, shiny

Suggests context, testthat (>= 3.0.0)

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LazyData TRUE

RoxygenNote 7.1.2

Encoding UTF-8

Remotes mrc-ide/context

Config/testthat/edition 3

Config/pak/sysreqs cmake make libicu-dev libuv1-dev zlib1g-dev

Repository https://plasmogenepi.r-universe.dev

Date/Publication 2025-07-24 12:14:11 UTC

RemoteUrl https://github.com/OJWatson/hrp2malaRia

RemoteRef HEAD

RemoteSha b01fb0a47355d5a278dee47050c48a9bf7edeeeb

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DRC	<i>DRC Seaosnal data to match regions from Parr et al. 2016 JID</i>
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Description

DRC Seaosnal data to match regions from Parr et al. 2016 JID

Usage

data(DRC)

Format

An object of class `data.frame` with 8 rows and 26 columns.

eq.0	<i>Equilibrium conditions for model. Also stored internally for model use when package is not loaded</i>
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Description

Equilibrium conditions for model. Also stored internally for model use when package is not loaded

Usage

data(eq.0)

Format

An object of class `list` of length 4.

hrp2_Simulation

*Individual Based Malaria Simulator***Description**

hrp2_Simulation simulates an individual based malaria system considering multiplicity of infection and infection status of individuals.

Usage

```
hrp2_Simulation(
  ID = NULL,
  saved.rds = NULL,
  root = NULL,
  direct.input = NULL,
  years = 0.5,
  time.step = 1,
  states = c(1, 2, 3, 4, 5, 6),
  storage = 50,
  storage_capture = 30,
  just_storage_results = FALSE,
  N = 1000,
  max.age = 60,
  strains.0 = 10,
  desired.freq = NULL,
  d.death = 21,
  EIR = 20/365,
  a.0 = 8 * 365,
  rho = 0.85,
  zeta.sd = 1.67,
  omega = 0.8405912,
  theta = 1,
  ft = 0.4,
  rdt.det = 1,
  rdt.nonadherence = 0,
  microscopy.use = 0,
  include.nmf = FALSE,
  fever.age.breaks = c(-0.1, 1, 2, 3, 4, 5, 7, 9, 11, 13, 15, 20, 25, 30, 101),
  annual.nmf.per.age.bracket = c(2.235, 1.841, 1.503, 1.175, 0.928, 0.67, 0.486, 0.512,
    0.475, 0.429, 0.652, 0.747, 0.804, 0.789),
  nmf.multiplier = 1,
  ss = NULL,
  fitness = 1,
  mu.0 = 0.132,
  beta = c(0.05879106, 0.07108894),
  a.k = 0.30677,
  delay.mos = 10,
```

```

delay.gam = 12,
d.E = 12,
d.I = 200,
d.T = 5,
d.D = 5,
d.U = 110,
d.P = 25,
d.A = d.I - d.D,
d.l = 0.160527,
d.ID = 10 * 365,
I.D0 = 1.577533,
k.D = 0.476614,
u.D = 9.44512,
a.D = 8001.99,
f.D0 = 0.007055,
g.D = 4.8183,
b.0 = 0.590076,
b.1 = 0.5,
d.B = 10 * 365,
I.B0 = 43.8787,
k.B = 2.15506,
u.B = 7.19919,
phi.0 = 0.791666,
phi.1 = 0.000737,
d.CA = 10950,
I.C0 = 18.02366,
k.C = 2.36949,
u.C = 6.06349,
P.M = 0.774368,
d.CM = 67.6952,
g.1 = 1.82425,
c.S = 0,
c.D = 0.0676909,
c.T = 0.322 * c.D,
c.U = 0.0062,
c.A = 0,
c.P = 0
)

```

Arguments

ID	ID of model run saved object when using didehpc tools. Default = NULL
saved.rds	File path for saved model run as rds. Default = NULL. Takes priority over ID/root
root	Name of context root when using didehpc tools to submit and save model runs. Default = NULL.
direct.input	R object for old model run to be restarted. Default = NULL. Takes priority over saved.rds and ID/root

years	Length of Simulation (years). Default = 0.5
time.step	Simulation time interval considered in days. Has to be 1.
states	Vector of the compartmental states. Default = c(1, 2, 3, 4, 5, 6), which are c("S","D","A","U","T","P")
storage	Number of last time steps to store. If storage = 0 (default), then all results are stored
storage_capture	Number of previous time steps used to calculate mean measures for series. Default = 30
just_storage_results	Boolean for keeping just the storage results. ## Demographic paramaters
N	Population Size. Default = 1000
max.age	Maximum age (years). Default = 100
strains.0	Ratio of wild type strains to hrp2 at initialisation. Must be an integer. Default = 10
desired.freq	Desired hrp2 deletion frequency to be enforced when a previous simulation is reloaded
d.death	Average life expectancy (years). Deafult = 21 ## Epidemiological Parameters
EIR	Maximum EIR / day. Default = 20/365,
a.0	Age-dependent biting parameter (days). Default = 8*365
rho	Age-dependent biting parameter (days). Default = 0.85
zeta.sd	sd of lognormal distribution used to generate indiviudal specific biting. Default = 1.67
omega	BM age scaling parameter. Default = 0.75 ## Entomological parameters
theta	Seasonal effects. Default = 1
ft	Probability of receiving assesment. Default = 0.4
rdt.det	Probability of detecting malaria given mono infection of hrp2' strains. Default = 1
rdt.nonadherence	Probability of non adherence to test result. Default = 0, i.e. perfect adherence
microscopy.use	Probability of microscopy use. Default = 0, i.e. no microscopy
include.nmf	Boolean detailing whether to include nmf section. Default = FALSE
fever.age.breaks	Age breaks for fevers
annual.nmf.per.age.bracket	Annual number of non malarial fevers for each age bracket in fever.age.breaks. Default is mean across 5 representative surveys from Burundi 2012, Liberia 2009/2011 and Nigeria 2010/2015
nmf.multiplier	Multiplication for annual.nmf.per.age.bracket to introduce sensitivity. Default = 1 ## delays and durations
ss	Seasonal fourier terms for rainfall. 7 needed (intercept and first 3 cos and sin terms). Default = NULL

fitness	Relative fitness of hrp2 deletions. Default = 1, i.e. no fitness cost. ## Diagnostics and nmf
mu.0	Baseline mosquito mortality. Default = 0.132
beta	Birthrate in form of $y = \text{beta}[1] * \text{EIR} + \text{beta}[2]$. Default = $c(0.0572289, 0.0696121)$
a.k	Daily biting rate. Default = 0.30667
delay.mos	Mosquito extrinsic incubation period (days). Default = 10
delay.gam	Delay from emergence of blood-stage parasites to onward infectivity (days). Default = 12.5
d.E	Latent period delay in pre-erythrocytic stage (days). Default = 12
d.I	Patent infection duration with no immunity (including disease) (days). Default = 200
d.T	Clinical disease duration with treatment (days). Default = 5
d.D	Clinical disease duration without treatment (days). Default = 5
d.U	Sub-patent infection duration (days). Default = 100
d.P	Prophylaxis with SP following treatment duration (days). Default = 25
d.A	Asymptomatic infection duration (days). Default = $d.I - d.D$ ## Pre-erythrocytic immunity parameters
d.1	= 0.161 Probability with maximum immunity
d.ID	= $10 * 365$ Inverse of decay rate
I.D0	Scale parameter. Default = 1.58
k.D	Shape parameter. Default = 0.477
u.D	Duration in which immunity is not boosted (days). Default = 9.45
a.D	Scale parameter relating age to immunity (days). Default = $21.923 * 365$
f.D0	Parameter relating age to immunity. Default = 0.0071
g.D	Shape parameter relating age to immunity. Default = 4.81 ## Blood stage immunity parameters
b.0	Probability with no immunity. Default = 0.590
b.1	Maximum relative reduction. Default = 0.5
d.B	Inverse of decay rate (days). Default = $10 * 365$
I.B0	Scale parameter. Default = 43.9
k.B	Shape parameter. Default = 2.16
u.B	Duration in which immunity is not boosted (days). Default = 7.2 ## Acquired and maternal immunity parameters
phi.0	Probability with no immunity. Default = 0.7916
phi.1	Maximum relative reduction. Default = 0.00074
d.CA	Inverse of decay rate (days). Default = $30 * 365$
I.C0	Scale parameter. Default = 18.0
k.C	Shape parameter. Default = 2.37
u.C	Duration in which immunity is not boosted (days). Default = 6.06

P.M	New-born immunity relative to mother's. Default = 0.774
d.CM	Inverse of decay rate of maternal immunity (days). Default = 67.7 ## contributions to infectious reservoir by state and age
g.1	Relates infectiousness probability of detection. Default = 1.82 ## Other params to do with reloading model runs
c.S	Contribution from S. Default = 0
c.D	Contribution from D. Default = 0.068
c.T	Contribution from T. Default = 0.32 * c.D
c.U	Contribution from U. Default = 0.0062
c.A	Contribution from A. Default = $c.U + (c.D - c.U) * q^{g.1}$, where q is the probability of detection of parasites as calculated using pre-erythrocytic immunity and age
c.P	Contribution from P. Default = 0

Details

The simulator considers individuals to progress through the Griffin 2016 model.

The model also introduces a further acknowledgement of the hrp2 strains present in hosts, and the effects of this on detection.

The model first allocates a fixed length for all storage and proceeds in a ring like fashion allowing for delays to be incorporated.

Simulation parameters

Value

Result a list of 59 elements including the following Time - Vector of time steps considered Status - Matrix of individuals' infection status by Time Last_Infection_Time - Vector of individual's last infection Last_Bite_Time - Vector of individual's last bite Age - Vector of individual's ages N.Sens - Matrix of individuals' MOI of RDT sensitive strains by Time N.Dels - Matrix of individuals' MOI of RDT resistant strains by Time I.B - Vector of individual's blood stage immunity I.CA - Vector of individual's acquired immunity I.CM - Vector of individual's maternal immunity I.D - Vector of individual's pre-erythrocytic immunity Counter - Simulation step counter d.EIR - daily EIR in individuals > 18 years I.Reservoir - Vector of each strains weighted contribution to the last step's I.Reservoir Sv - Susceptible mosquito population Ev - Exposed mosquito population Iv - Infected mosquito population Prev - Daily prevalence N.Sens/N.Dels - sum of sensitive to diagnostic and deletion strains Incidence - Clinical cases / population / per day Mono - monoinfected individual proportions FOIv - Force of infection to vectorsf S. ... - Series storage of various of the above

hrp2malaria_package	<i>hrp2malaria: Individual multiplicity of infection malaria model</i>
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Description

hrp2malaria: Individual multiplicity of infection malaria model

Author(s)

OJ Watson <oj.watson@hotmail.co.uk>

run_seasonality_shiny	<i>Seasonality Shiny</i>
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Description

run_seasonality_shiny runs a shiny app that displays the outcomes of the seasonality investigation. The shiny shows how the bias in the observed prevalence of pfhrp2 deletions changes for each level 1 admin region changes throughout the transmission season

Usage

run_seasonality_shiny()

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