Package: magenta (via r-universe)

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Type Package

Title Individual-Based Simulation Model of Malaria Epidemiology and Genomics

Version 1.3.5

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URL https://ojwatson.github.io/magenta/

BugReports https://github.com/OJWatson/magenta/issues

Description Individual-based simulation model of malaria epidemiology and genomics. magenta extends the imperial malaria model by tracking the infection history of individuals. With this additional genetic characteristics of the parasite can be assessed, including resistance.

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Depends R (>= 2.10)

Imports dde, dplyr, ggplot2, magrittr, odin, progress, Rcpp (>= 0.12.7), redux, reshape2, rlang, statmod, stringdist, stringi

Remotes mrc-ide/odin, mrc-ide/dde

LinkingTo Rcpp, BH

LazyData TRUE

LazyDataCompression xz

RoxygenNote 7.2.3

SystemRequirements C++11

VignetteBuilder knitr

Additional_repositories https://mrc-ide.github.io/drat

Suggests knitr, rmarkdown, testthat, lattice, RColorBrewer, cowplot

Encoding UTF-8

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

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

RemoteRef HEAD

RemoteSha 267650a550cd5b558fba981e600b1c19a07a503b

Contents

`admin_units_seasonal` *Admin level 1 africa seasonal parameters*

Description

These datasets represent the data fitted within the Imperial College Malaria model for relating seasonal profiles to malaria transmission intensity at level 1 admin regions across Africa

Usage

```
admin_units_seasonal
```

Format

A dataframe of 850 observations of 15 variables:

`admin_units_seasonal`: A dataframe of admin units and their seasonal parameters

- country: Country string
- admin1: Admin 1 string
- map_prev_2010: 2010 Atlas map microscopy prevalence in 2-10 year olds
- id: Numeric vector of 1:850
- gaul_code: Numeric vector for gaul code
- a0: Average value of fourier series
- a1: First of partial series cos terms
- b1: First of partial series sine terms
- a2: Second of partial series cos terms
- b2: Second of partial series sine terms
- a3: Third of partial series cos terms
- b3: Third of partial series sine terms
- theta_c: Rainfall normalising constant
- dide_code: DIDE geo plotting code
- ft: Treatment Coverage

---

convert_barcode_vectors

Convert human barcodes to numerics

Description

`convert_barcode_vectors` converts human barcode vectors to nums and calculated COIs.

Usage

```
convert_barcode_vectors(
  sim_save,
  ID,
  sub_patents_included = TRUE,
  ibd = FALSE,
  nl = 24,
  COI_type = "pcr_imperial"
)
```

Arguments

sim_save	Saved output of simulation
ID	Vector of detection immunities for the population
sub_patents_included	Boolean as to whether subpatents are included. Default = TRUE
ibd	Boolean for IBD simulations. Default = FALSE
nl	Numeric for number of loci. Default = 24
COI_type	String for type of COI calculation. Default = "pcr_imperial"
	convert_barcode_vectors

---

drug_create *Create list describing parameters for drug efficacy and prophlyaxis*

Description

Create list describing parameters for drug efficacy and prophlyaxis

Usage

```
drug_create(
  prob_of_lpf = c(1, 0.97, 0.8, 0.55),
  barcode_res_pos = c(0, 1),
  prophylactic_pos = 1,
  dur_P = 25,
  dur_SPC = 5,
  drug_clearance_max_time = 60,
 prophylactic_probability = 1 - pgamma(seq(0, drug_clearance_max_time, 0.2), shape =
    16.8, rate = 16.8/17.9),
 prophylactic_resistant_probability = 1 - pgamma(seq(0, drug_clearance_max_time, 0.2),
    shape = 16.8, rate = 16.8/8.7)
)
```

Arguments

prob_of_lpf	Vector of probabilities for the chance of late parasitological failure (lpf). The vector gives the prob of lpf for each relevent barcode combination for a given drug. E.g. The default is:
	`c(1.0, 0.97, 0.80, 0.55)`
	The vector is length 4, and so 2 barcode positions change the prob of lpf. If the parasite is 0,0 then the prob of lpf is 0 (1-1), but if it was 0,1 it would be 0.2.
barcode_res_pos	Vector for which barcode positions correspond to which drug resistance mechanism. E.g. the default is:
	`c(0,1)`
	Resistance to drug is encoded at barcode position 0 and 1

prophylactic_pos
: Vector for which barcode positions determine the impact of drug resistance in shortening the effective prophylactic period. E.g. the default is `c(1)`, which shows that for the drug, the prophylactic position is encoded in barcode position 1.

dur_P
: Duration of prophylaxis in days. Default = 25.

dur_SPC
: Duration of slow parasite clearance. Default = 5.

drug_clearance_max_time
: Maximum number of days to which to consider waning prophylaxis. Default = 60 days.

prophylactic_probability
: Vector of changing probability of reinfection due to waning prophylaxis. The last element reflects the probability after `drug_clearance_max_time` and the first element is the probability at time = 0 days.

prophylactic_resistant_probability
: Vector of changing probability of reinfection due to waning prophylaxis when challenged by a parasite that is resistant to the partner drug. The last element reflects the probability after `drug_clearance_max_time` and the first element is the probability at time = 0 days.

`drug_create_al` *AL Drug Create*

Description

AL Drug Create

Usage

```
drug_create_al()
```

Note

We have curves of the longest and shortest duration of AL prophylaxis from Bretscher et al. However, we have multiple types of partner drug resistance. At the moment we will say that any loci associated with lumefantrine resistance yield the resistant curve but it may be better to have a distinct curve for each lumefantrine resistant genotype with the T0.5 aligned to the prob of lpf.

drug_create_asaq *ASAQ Drug Create*

Description

ASAQ Drug Create

Usage

```
drug_create_asaq()
```

Note

We have curves of the longest and shortest duration of ASAQ prophylaxis from Bretscher et al. However, we have multiple types of partner drug resistance. At the moment we will say that any loci associated with AQ resistance yield the resistant curve but it may be better to have a distinct curve for each AQ resistant genotype with the T0.5 aligned to the prob of lpf.

drug_create_default_no_resistance *Perfect Drug Create*

Description

Perfect Drug Create

Usage

```
drug_create_default_no_resistance()
```

Note

Perfect Efficacy Drug. Used as default to match deterministic model easily

drug_create_dhappq *DHA-PPQ Drug Create*

Description

DHA-PPQ Drug Create

Usage

```
drug_create_dhappq()
```

drug_list_create *Create drug list*

Description

List for simulating drug usage for resistance/mft variables

Usage

```
drug_list_create(
  resistance_flag = FALSE,
  number_of_resistance_loci = 2,
  artemisinin_loci = c(0),
  cost_of_resistance = c(0.99, 0.99),
  absolute_fitness_cost_flag = FALSE,
  epistatic_logic = NULL,
  number_of_drugs = 1,
  drugs = list(drug_create_default_no_resistance()),
  mft_flag = FALSE,
  temporal_cycling = -1,
  sequential_cycling = -1,
  sequential_update = 3,
  drug_choice = 0,
  partner_drug_ratios = rep(1/number_of_drugs, number_of_drugs)
)
```

Arguments

`resistance_flag`
: Boolean are we simulating resistance

`number_of_resistance_loci`
: Numeric for number of res. loci

`artemisinin_loci`
: Numerics for barcode positions that confer artemisinin resistance

`cost_of_resistance`
: Numeric vector for fitness cost of each resistance loci.

`absolute_fitness_cost_flag`
: Boolean are we simulating fitness costs as absolute (i.e. impactive onward transmission chance) or relative (resistant strains have decreases chance of being onwardly transmitted in mixed infections). Default = FALSE.

`epistatic_logic`
: Is there compensatory relationships. i.e. what loci need to be true for resistance cost to exist. Default of NULL means that this becomes seq_len(number_of_resistance_loci), i.e. only dependent on their own loci. (TODO: Change this to be a list of length norl)

number_of_drugs
: Numeric for number of drugs used

drugs
: List of drugs that are being used, with each list element being created by drug_create.

mft_flag
: Boolean are we doing mft

temporal_cycling
: Numeric for when in years a drug switch occurs

sequential_cycling
: Numeric for what perc. treatment failure before switch

sequential_update
: How long does it take in years for sequential to be implemented

drug_choice
: What's the default drug choice to begin. Default = 0

partner_drug_ratios
: Numeric vector for ratio of first line drugs used

---

drug_table *Drug Efficacy by Genotype Table*

Description

Table of probaility of late parasitological failure (28-day treatment failure) per genoytpe.

Sourced from:

Antimalarial mass drug administration in large populations and the evolution of drug resistance. Tran Dang Nguyen, Thu Nguyen-Anh Tran, Daniel M. Parker, Nicholas J White, Maciej F Boni. bioRxiv 2021.03.08.434496; doi: https://doi.org/10.1101/2021.03.08.434496

Usage

```
drug_table
```

Format

A data.frame of drug efficacies by genotype

`equilibrium_init_create` *Equilibrium initialisation list creation*

Description

`equilibrium_init_create` creates an equilibrium initialisation state to be used within later model runs

Usage

```
equilibrium_init_create(
  age_vector,
  het_brackets,
  ft,
  EIR,
  model_param_list,
  country = NULL,
  admin = NULL,
  quiet = FALSE
)
```

Arguments

`age_vector`	Vector of age brackets.
`het_brackets`	Integer number of biting heteogenity compartments.
`ft`	Numeric for the frequency of people seeking treatment.
`EIR`	Numeric for desired annual EIR.
`model_param_list`	List of epidemiological parameters created by
`country`	String for country of interest. If NULL the seasonal parameters will attempt to be loaded using just the admin unit, however if there is ambiguity in the admin unit an error will be thrown. If both NULL then no seasonality is assumed. Default = NULL.
`admin`	String for admin unit with country for loading seasonal parameters. If country is NULL, the admin unit will attempt to be located,however if there is ambiguity in the admin unit an error will be thrown. If both country and admin are NULL then no seasonality is assumed. Default = NULL.
`quiet`	Whether function should be quiet. If FALSE (default) the returned country and admin are printed.

housekeeping_list_create *Create housekeeping parameter list*

Description

List for simulation housekeeping vars, e.g. quiet prints,

Usage

```
housekeeping_list_create(
  quiet = TRUE,
  quiet_test = TRUE,
  cluster = FALSE,
  clear_up = TRUE
)
```

Arguments

quiet	Boolean for quiet simulation. Default = TRUE
quiet_test	Boolean for quiet testing statement. Default = TRUE
cluster	Boolean for simulation being on cluster. Default = TRUE
clear_up	Boolean for whether to clear up the memory used by the simulation. Default = TRUE

importations *Importation data*

Description

Importation data for admin units in admin_units_seasonal

Usage

```
importations
```

Format

A list of length 18

`importations`: A list of length 18, with each list representing a year. In each year is then a further 2 lists which are:

- incidence: Proportions of incidence that originated from other admin units, i.e. individuals in admin i that moved to admin j and then returned with an infection acquired while in admin j.
- mosquitoFOI: Proportion of the force of infection towards mosquitoes that originated from outside admin units, i.e. the proportion of mosquitoes that are infected from infected individuals who travelled from admin j into admin i.

intervention_grab *Intervention grab*

Description

Intervention grab

Usage

```
intervention_grab(
  country,
  admin,
  year_range,
  final_itn_cov = NULL,
  final_irs_cov = NULL,
  final_ft = NULL
)
```

Arguments

country	Country string
admin	Admin string
year_range	Year range
final_itn_cov	Final ITN coverage
final_irs_cov	Final IRS coverage
final_ft	Final treatment coverage

Details

Grabs ITN, IRS ft from database

N.B. The admin region used for ft can be checked

irs_2000_2015 *IRS for 2000 to 2015*

Description

IRS data for SSSA for 2000 to 2015

Usage

```
irs_2000_2015
```

Format

A dataframe of 5 elements:

`$irs_2000_2015`: A dataframe of admin units and their seasonal parameters

- intervention: String stating IRS
- country: Country string
- admin: Admin string
- year: Numeric year
- value: Value for IRS coverage

`itn_2000_2015` *ITN for 2000 to 2015*

Description

ITN data for SSSA for 2000 to 2015

Usage

```
itn_2000_2015
```

Format

A dataframe of 5 elements:

`itn_2000_2015`: A dataframe of admin units and their seasonal parameters

- intervention: String stating ITN
- country: Country string
- admin: Admin string
- year: Numeric year
- value: Value for ITN coverage

model_param_list_create *Model Parameter List Creation*

Description

model_param_list_create creates list of model parameters to be used within equilibrium_init_create

Usage

```
model_param_list_create(
  eta = 0.0001305,
  rho = 0.85,
  a0 = 2920,
  sigma2 = 1.67,
  max_age = 100 * 365,
  rA = 0.00512821,
  rT = 0.2,
  rD = 0.2,
  rU = 0.00906627,
  rP = 1/25,
  dE = 12,
  delayGam = 12.5,
  cD = 0.0676909,
  cT = 0.322 * cD,
  cU = 0.006203,
  gamma1 = 1.82425,
  d1 = 0.160527,
  dID = 3650,
  ID0 = 1.577533,
  kD = 0.476614,
  uD = 9.44512,
  aD = 8001.99,
  fD0 = 0.007055,
  gammaD = 4.8183,
  alphaA = 0.75735,
  alphaU = 0.185624,
  b0 = 0.590076,
  b1 = 0.5,
  dB = 3650,
  IB0 = 43.8787,
  kB = 2.15506,
  uB = 7.19919,
  phi0 = 0.791666,
  phi1 = 0.000737,
  dCA = 10950,
  IC0 = 18.02366,
```

```
  kC = 2.36949,
  uCA = 6.06349,
  PM = 0.774368,
  dCM = 67.6952,
  delayMos = 10,
  tau1 = 0.69,
  tau2 = 2.31,
  mu0 = 0.132,
  Q0 = 0.92,
  chi = 0.86,
  bites_Bed = 0.89,
  bites_Indoors = 0.97,
  muEL = 0.0338,
  muLL = 0.0348,
  muPL = 0.249,
  dEL = 6.64,
  dLL = 3.72,
  dPL = 0.643,
  gammaL = 13.25,
  km = 11,
  cm = 0.05,
  betaL = 21.2,
  num_int = 4,
  itn_cov = 0,
  irs_cov = 0,
  ITN_IRS_on = -1,
  DY = 365,
  d_ITN0 = 0.41,
  r_ITN0 = 0.56,
  r_ITN1 = 0.24,
  r_IRS0 = 0.6,
  d_IRS0 = 1,
  irs_half_life = 0.5 * DY,
  itn_half_life = 2.64 * DY,
  IRS_interval = 1 * DY,
  ITN_interval = 3 * DY
)
```

Arguments

eta	Death rate for expoential population distribtuion, i.e. 1/Mean Population Age. Default = 0.0001305
rho	Age-dependent biting parameter. Default = 0.85
a0	Age-dependent biting parameter. Default = 2920
sigma2	Variance of the log heterogeneity in biting rates. Default = 1.67
max_age	Maximum age in days. Default = 100*365
rA	Rate of leaving asymptomatic infection. Default = 0.00512821

rT	Rate of leaving treatment. Default = 0.2
rD	Rate of leaving clinical disease. Default = 0.2
rU	Rate of recovering from subpatent infection. Default = 0.00906627
rP	Rate of leaving prophylaxis. Default = 0.05
dE	Latent period of human infection. Default = 12
delayGam	Lag from parasites to infectious gametocytes. Default = 12.5
cD	Untreated disease contribution to infectiousness. Default = 0.0676909
cT	Treated disease contribution to infectiousness. Default = 0.322 * cD
cU	Subpatent disease contribution to infectiousness. Default = 0.006203
gamma1	Parameter for infectiousness of state A. Default = 1.82425
d1	Minimum probability due to maximum immunity. Default = 0.160527
dID	Inverse of decay rate. Default = 3650
ID0	Scale parameter. Default = 1.577533
kD	Shape parameter. Default = 0.476614
uD	Duration in which immunity is not boosted. Default = 9.44512
aD	Scale parameter relating age to immunity. Default = 8001.99
fD0	Time-scale at which immunity changes with age. Default = 0.007055
gammaD	Shape parameter relating age to immunity. Default = 4.8183
alphaA	PCR detection probability parameters state A. Default = 0.757
alphaU	PCR detection probability parameters state U. Default = 0.186
b0	Maximum probability due to no immunity. Default = 0.590076
b1	Maximum relative reduction due to immunity. Default = 0.5
dB	Inverse of decay rate. Default = 3650
IB0	Scale parameter. Default = 43.8787
kB	Shape parameter. Default = 2.15506
uB	Duration in which immunity is not boosted. Default = 7.19919
phi0	Maximum probability due to no immunity. Default = 0.791666
phi1	Maximum relative reduction due to immunity. Default = 0.000737
dCA	Inverse of decay rate. Default = 10950
IC0	Scale parameter. Default = 18.02366
kC	Shape parameter. Default = 2.36949
uCA	Duration in which immunity is not boosted. Default = 6.06349
PM	New-born immunity relative to mother. Default = 0.774368
dCM	Inverse of decay rate of maternal immunity. Default = 67.6952
delayMos	Extrinsic incubation period. Default = 10
tau1	Duration of host seeking, assumed to be constant between species. Default = 0.69

tau2	Duration of mosquito resting after feed. Default = 2.31
mu0	Daily mortality of adult mosquitos. Default = 0.132
Q0	Anthrophagy probability. Default = 0.92
chi	Endophily probability. Default = 0.86
bites_Bed	Percentage of bites indoors and in bed. Default = 0.89
bites_Indoors	Percentage of bites indoors . Default = 0.97
muEL	Per capita daily mortality rate of early stage larvae (low density). Default = 0.0338
muLL	Per capita daily mortality rate of late stage larvae (low density). Default = 0.0348
muPL	Per capita daily mortality rate of pupae. Default = 0.249
dEL	Development time of early stage larvae. Default = 6.64
dLL	Development time of late stage larvae. Default = 3.72
dPL	Development time of pupae. Default = 0.643
gammaL	Relative effect of density dependence on late instars relative to early instars. Default = 13.25
km	Seasonal carrying capacity. Default = 11
cm	Seasonal birth rate. Default = 0.05
betaL	Number of eggs laid per day per mosquito. Default = 21.2
num_int	Number of possible interventions. Default = 4
itn_cov	The proportion of people that use an ITN. Default = 0
irs_cov	The proportion of people living in houses that have been sprayed. Default = 0
ITN_IRS_on	Time of ITN and IRS to be activated. Default = -1, i.e. never.
DY	Duration of year (days). Default = 365
d_ITN0	Probability of dying with an encounter with ITN (max). Default = 0.41
r_ITN0	Probability of repeating behaviour with ITN (max). Default = 0.56
r_ITN1	Probability of repeating behaviour with ITN (min). Default = 0.24
r_IRS0	Probability of repeating behaviour with IRS (min). Default = 0.6
d_IRS0	Probability of dying with an encounter with IRS (max). Default = 1
irs_half_life	IRS half life. Default = 0.5 * DY
itn_half_life	ITN half life. Default = 2.64 * DY
IRS_interval	How long before IRS is repeated, i.e. when IRS decay = 1. Default = 1 * DY
ITN_interval	How long before ITN is repeated, i.e. when IRS decay = 1. Default = 3 * DY

nmf_list_create *Create nmf list*

Description

List for simulating non malarial fever

Usage

```
nmf_list_create(
  nmf_flag = FALSE,
 mean_nmf_frequency = c(148.578, 139.578, 141.564, 155.874, 179.364, 216.192, 233.478,
    268.056, 312.858, 315.564, 285.156, 255.246, 238.302, 216.618),
 nmf_age_brackets = c(-0.1, 365, 730, 1095, 1460, 1825, 2555, 3285, 4015, 4745, 5475,
    7300, 9125, 10950, 36850),
  prob_of_testing_nmf = 0.5
)
```

Arguments

nmf_flag	Boolean are we doing non malarial fevers
mean_nmf_frequency	Vector for mean number of days between fevers for the age bracket considered
nmf_age_brackets	Vector for age brackets
prob_of_testing_nmf	Numeric for probability that a NMF is tested by RDT before being treated with antimalarials.

param_list_simulation_finalizer_create *Parameter List creation for magenta simulation finalizer*

Description

param_list_simulation_finalizer_create creates suitable parameter list for simulation_R for free memory used by a simulation

Usage

```
param_list_simulation_finalizer_create(statePtr)
```

Arguments

statePtr	Pointer for current model state as return by simulation_R$Ptr

param_list_simulation_get_create
Parameter List creation for magenta simulation getting (saving to disk)

Description

param_list_simulation_get_create creates suitable parameter list for simulation_R for continuing a simulation from memory within the active session.

Usage

```
param_list_simulation_get_create(statePtr)
```

Arguments

statePtr	Pointer for current model state as return by simulation_R$Ptr

param_list_simulation_init_create
Parameter List creation for magenta simulation initialisation

Description

param_list_simulation_init_create creates suitable parameter list for simulation_R for the beginning of a simulation. Also takes an argument for feeding in spatial parameters/data.

Usage

```
param_list_simulation_init_create(
  N = 10000,
  eqSS,
  barcode_list,
  spatial_list,
  housekeeping_list,
  drug_list,
  nmf_list,
  vector_adaptation_list,
  mpl
)
```

Arguments

N	Population size. Default = 1e4
eqSS	Output of equilibrium_steady_state_create
barcode_list	List of barcode/genetic parameters
spatial_list	Spatial parmeters to come in
housekeeping_list	Housekeeping parameter list from housekeeping_list_create
drug_list	Drug parameter list from drug_list_create
nmf_list	Non malarial fever parameter list from nmf_list_create
vector_adaptation_list	vector adaptation list from vector_adaptation_list
mpl	model parameter list from model_param_list_create

---

param_list_simulation_saved_init_create

Parameter List creation for loading saved magenta simulation

Description

param_list_simulation_saved_init_create creates suitable parameter list for simulation_R for continuing a simulation from memory within the active session.

Usage

```
param_list_simulation_saved_init_create(savedState)
```

Arguments

savedState	Saved state generated by simulation_R when provided with a param_list_simulation_get_create parameter list

---

param_list_simulation_update_create

Parameter List creation for magenta simulation updating

Description

param_list_simulation_update_create creates suitable parameter list for simulation_R for continuing a simulation from memory within the active session.

Usage

```
param_list_simulation_update_create(
  years = 1,
  ft = 0.4,
  mu_vec = NULL,
  fv_vec = NULL,
  statePtr,
  spatial_list,
  drug_list,
  barcode_list
)
```

Arguments

years	Length of simulation. Default = 1
ft	Treatments seeking value
mu_vec	Vector of mosquito mortalities for each day with years. Default = NULL, which will result in rep(0.132,floor(years*365))
fv_vec	Vector of mosquito bitings for each day with years. Default = NULL, which will result in rep(1/3,floor(years*365))
statePtr	Pointer for current model state as return by simulation_R$Ptr
spatial_list	Spatial list
drug_list	Drug list
barcode_list	Barcode parameter list

---

pipeline *Pipeline for cluster submission*

Description

pipeline steps through creating the parameter list, the equilibrium initialisation and steady state creation before checking and passing suitable parameters to the simulation. This is then saved. If a path to a savedState is provided then this state is loaded and continued.

Usage

```
pipeline(
  EIR = 120,
  ft = 0.4,
  itn_cov = 0,
  irs_cov = 0,
  use_historic_interventions = FALSE,
  survival_percentage = 0.2,
  oocyst_mean = 2.5,
```

```
  oocyst_shape = 1,
  N = 1e+05,
  years = 20,
  update_length = 365,
  country = NULL,
  admin = NULL,
  spatial_type = NULL,
  spatial_incidence_matrix = NULL,
  spatial_mosquitoFOI_matrix = NULL,
  island_imports_plaf_linked_flag = FALSE,
  num_loci = 24,
  ibd_length = 1,
  plaf = rep(0.5, num_loci),
  prob_crossover = rep(0.5, num_loci),
  starting_ibd = 0,
  mutation_rate = rep(1e-07, num_loci),
  mutation_flag = FALSE,
  mutation_treated_modifier = 1,
  full_save = FALSE,
  full_update_save = FALSE,
  human_only_full_save = FALSE,
  update_save = FALSE,
  update_save_func = NULL,
  human_update_save = FALSE,
  genetics_df_without_summarising = FALSE,
  summary_saves_only = FALSE,
  set_up_only = FALSE,
  mean_only = TRUE,
  save_lineages = FALSE,
  saved_state_path = NULL,
  seed = as.integer(runif(1, 1, 1e+09)),
  sample_size = Inf,
  sample_states = 0:5,
  age_breaks = c(-0.001, 5, 15, 100.1),
  sample_reps = 1,
  housekeeping_list = housekeeping_list_create(),
  drug_list = drug_list_create(),
  vector_adaptation_list = vector_adaptation_list_create(num_loci),
  only_allele_freqs = TRUE,
  nmf_list = nmf_list_create(),
  ...
)
```

Arguments

EIR	Numeric for desired annual EIR. Default = 120
ft	Vector of treatment frequency. Default = 0.4
itn_cov	Vector for ITN coverages that change at update_length intervals. Default = 0

irs_cov Vector for IRS coverages that change at update_length intervals. Default = 0

use_historic_interventions
Boolean as to whether to use interventions on file for the admin and country specified. If TRUE then provide the years as a year range, e.g. 2000:2015. WARNING - Best to have this as FALSE and manually specify the itn_cov, irs_cov and ft.

survival_percentage
Mumeric for Default = 0.2

oocyst_mean Mean for number of oocysts formed from a bite. Default=2.5

oocyst_shape Shape parameter for oocysts formed. Default=1

Spatial

N Population Size. Default = 100000

years Lenth of simulation. Default = 20

update_length How long each update is run for in days. Default = 365

country Character for country within which admin2 is in. Default = NULL

admin Character for admin region. Some fuzzy logic will be used to match. If not provided then no seasonality is introduced. Default = NULL

spatial_type Default = NULL. If spatial is wanted then provide a character describing the type of spatial simulation, which must be one of "island" or "metapop".

spatial_incidence_matrix
Spatial incidence for humans, i.e. importation vector

spatial_mosquitoFOI_matrix
Spatial mosquio FOI, i.e. importation to mosquitoes vector

Genetic Params

island_imports_plaf_linked_flag
Boolean. Whether imported barcodes for island model are drawn dependent on other sites. Currently, if TRUE, imported barcodes will either be all 0 or will be 1 at all loci where plaf > 0, if `rbinom(1, 1, plaf[plaf>0][1])` is TRUE. I.e. the first loci greater than 0 is used to determine if the incoming barcode is 1 at all sites where plaf is greater than 0.

num_loci Number of loci. Default = 24

ibd_length If we are simulating IBD dynamics, each loci is now represented by a bitset of ibd_length. Thus ibd_length needs to be long enough to ensure that as new identity relationships occur, i.e. an importation barcode will be a new identity. e.g. If are population is 1000, we may expect at 80 2400 different identities, i.e. 2^ibd_length > 2400. However, keep in mind importations as these need to be continually new, i.e. if we are simulating for 30 years, with 3 importations a day, then we will need at least length to ensure that 2^ibd_length > 2400 + (30*365*3). This will probably be automatically calculated in the future. If we are not ding IBD, then this should be 1, which is the defalt.

plaf Vector of population level allele frequencies for the barcode. Default = rep(0.5, num_loci)

prob_crossover Vector of probabilities for crossover events for the barcode. Default = rep(0.5, num_loci)

`starting_ibd` Starting IBD. Default = 0, which means that each infected individual at initialisation is given a unique ID for their parasites.

`mutation_rate` Probability of mutation occuring and fixing

`mutation_flag` Boolean for simulating mutations

Saving Params

`mutation_treated_modifier`
Multiplier for how much more likely mutations are to occur in treated individuals with respect to resistance. Default = 1, i.e no difference

`full_save` Boolean detailing whether the entire simulation is saved. Default = FALSE

`full_update_save`
Boolean to save entire simualation at each update save. Default = FALSE

`human_only_full_save`
Boolean detailing whether just the human component of the simulation is saved within full_save. Default = FALSE

`update_save` Boolean detailing whether the logging output is saved each update_length up to years. Default = FALSE

`update_save_func`
As opposed to having to provide arguments for the update behaviour, you can pass in a function. See `update_saves` for the default one.

`human_update_save`
Boolean detailing if the human state is also saved during each update_length. Default = FALSE

`genetics_df_without_summarising`
Boolean for returning just the genetics data frame without summarising with `COI_df_create`. Default = FALSE

`summary_saves_only`
Boolean if summary tables about COI are saved within human yearly save only. Dataframes of age, clinical status binned COI.

`set_up_only` Boolean for whether to return just the initialised simulation. Default = FALSE

`mean_only` Boolean for returning only the mean when summarising the population COI, COU etc. Default = TRUE

`save_lineages` Boolean for whether we save the frequency of each strain when summarising with `genetics_df_without_summarising`=TRUE. Default = FALSE

`saved_state_path`
Full file path to a saved model state to be loaded and continued. Default = NULL, which will trigger initialisation

`seed` Random seed. Default is Random

`sample_size` Numeric for number of individuals to be sampled at the end of each update. Default = Inf, which samples everyone. If you provide a vector of sample sizes it will sample at each specified sample size.

`sample_states` Numeric for which sample infection states are to be included in sampling. Default = 0:5 (i.e. all states). 1:4 for example would ensure only infected individuals are included.

age_breaks	What age breaks are used when summarising the population. Default is 'c(-0.001, 5, 15, 100.1)'
sample_reps	Numeric for how many sample reps are done. Default = 1.
	# Parameter Lists
housekeeping_list	
	List created by housekeeping_list_create
drug_list	List created by drug_list_create
vector_adaptation_list	
	List created by vector_adaptation_list_create
only_allele_freqs	
	Boolean for returning the summarised genetics (allele frequencies and maybe strain frequencies) or the whole data frame produced by pop_strains_df. Default = TRUE
nmf_list	List created by nmf_list_create
...	Other parameters to model_param_list_create
	pipeline

Details

Main Params

`population_get_genetics_df_n` *Returns the population's parasite genetics summarised by coi for given sample size and state*

Description

Returns the population's parasite genetics summarised by coi for given sample size and state

Usage

```
population_get_genetics_df_n(param_list)
```

Arguments

param_list	param_list containing statePtr, sample_size, and sample_states

Value

list of population information

`population_get_genetics_ibd_df_n`

Returns the population's parasite genetics for ibd style summarised by pibd for given sample size and state

Description

Returns the population's parasite genetics for ibd style summarised by pibd for given sample size and state

Usage

```
population_get_genetics_ibd_df_n(param_list)
```

Arguments

`param_list`	param_list containing statePtr, sample_size, and sample_states

Value

list of population information

`Simulation_Finalizer_cpp`

Returns whole model to R in series of nested lists

Description

Returns whole model to R in series of nested lists

Usage

```
Simulation_Finalizer_cpp(param_list)
```

Arguments

`param_list`	parameter list generated with `param_list_simulation_finalizer_create`

Value

list of 1 confirming finalizer has finished

Simulation_Get_cpp *Returns whole model to R in series of nested lists*

Description

Returns whole model to R in series of nested lists

Usage

```
Simulation_Get_cpp(param_list)
```

Arguments

param_list	parameter list generated with Param_List_Simulation_Get_Create

Value

list of 4 lists with the entire model state

Simulation_Init_cpp *Creates initial model simulation using paramter list provided*

Description

Creates initial model simulation using paramter list provided

Usage

```
Simulation_Init_cpp(param_list)
```

Arguments

param_list	parameter list generated with Param_List_Simulation_Init_Create

Value

list with ptr to model state and loggers describing the current model state

`simulation_R` *simulation_R function*

Description

This function triggers the main magenta simulation from the R side

Usage

```
simulation_R(param_list, seed)
```

Arguments

`param_list`	paramlist passed from `param_list_simulation_init_create` or from `param_list_simulation_upda`
`seed`	Seed for the simulation

`Simulation_Saved_Init_cpp` *Creates initial model simulation using a saved model state*

Description

Creates initial model simulation using a saved model state

Usage

```
Simulation_Saved_Init_cpp(param_list)
```

Arguments

`param_list`	parameter list generated with `Param_List_Simulation_Get_Create`

Value

list with ptr to model state and loggers describing the current model state

Simulation_Update_cpp *Continues simulation forward for as long as specified in param_list*

Description

Continues simulation forward for as long as specified in param_list

Usage

```
Simulation_Update_cpp(param_list)
```

Arguments

param_list	parameter list generated with Param_List_Simulation_Update_Create

Value

list with ptr to model state and loggers describing the current model state

spl_grab *Spatial matrix grab*

Description

Grabs spatial incidence and mosquitoFOI matrix from database

Usage

```
spl_grab(country, admin, year_range)
```

Arguments

country	Country string
admin	Admin string
year_range	Year range

`vector_adaptation_list_create` *Create vector adaptation list*

Description

List for vector adaptations relating to oocyst success

Usage

```
vector_adaptation_list_create(
  vector_adaptation_loci,
  vector_adaptation_flag = FALSE,
  local_oocyst_advantage = 0.5,
  gametocyte_sterilisation_flag = FALSE,
  gametocyte_sterilisation = 0.5,
  oocyst_reduction_by_artemisinin = 0.2
)
```

Arguments

`vector_adaptation_loci`
: Vector of integers detailing which loci in the barcode correspond to the vector adaptation phenotype

`vector_adaptation_flag`
: Boolean are we doing vector adaptation.

`local_oocyst_advantage`
: Numeric for probability that non adapated parasites will get through. Default = 0.5

`gametocyte_sterilisation_flag`
: Boolean for whether we are doing gametocye sterilisation as a result from artemisinin. Default = FALSE

`gametocyte_sterilisation`
: Numeric for theimpact of artemisinin on male gametocytes. Default = 0.5, which causes the probability that a wild type male gametocyte will be chosen to be in oocysts is halved.

`oocyst_reduction_by_artemisinin`
: Numeric for reduction in oocyst under artemisinin drug pressure. default = 0.2

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