

Package: spleenrbc (via r-universe)

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Title The role of the spleen in red blood cell loss due to malaria

Version 0.0.1

Description A mathematical model of red blood cell (RBC) dynamics in a malaria infection, which includes the spleen as a separate model compartment that can retain large amounts of infected and uninfected RBCs.

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BugReports <https://gitlab.unimelb.edu.au/rgmoss/malaria-spleen-rbc-loss/issues>

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alpha_c	<i>Age-structured parasite multiplication rates (the number of released merozoites that successfully invade uRBCS of age a) in the circulation.</i>
---------	---

Description

Age-structured parasite multiplication rates (the number of released merozoites that successfully invade uRBCS of age a) in the circulation.

Usage

```
alpha_c(u_rbc, pmf, beta)
```

Arguments

u_rbc	The RBC count.
pmf	The parasite multiplication factor.
beta	The (age-dependent) merozoite preference for uninfected RBCs.

alpha_r	<i>Age-structured parasite multiplication rates (the number of released merozoites that successfully invade uRBCS of age a) in the spleen.</i>
---------	--

Description

Age-structured parasite multiplication rates (the number of released merozoites that successfully invade uRBCS of age a) in the spleen.

Usage

```
alpha_r(u_rbc, pmf, beta)
```

Arguments

u_rbc	The RBC count.
pmf	The parasite multiplication factor.
beta	The (age-dependent) merozoite preference for uninfected RBCs.

baseline_parameters	<i>Return the baseline parameter values, including all derived parameters.</i>
---------------------	--

Description

Return the baseline parameter values, including all derived parameters.

Usage

```
baseline_parameters(species = c("Pf", "Pv"), nospleen = FALSE, derived = TRUE)
```

Arguments

species	The malaria species: 'Pf' or 'Pv'.
nospleen	Whether the spleen has been removed.
derived	Whether to define parameters whose values are derived from other parameters.

beta	<i>Age-dependent merozoite preference for uninfected RBCs.</i>
------	--

Description

Age-dependent merozoite preference for uninfected RBCs.

Usage

```
beta(p, age)
```

Arguments

p	The parameter values for the scenario.
age	The RBC age.

calculate_irbc_ratio	<i>Calculate the ratio of (a) the fraction of RBCs in the spleen that are infected; to (b) the fraction of RBCs in the circulation that are infected.</i>
----------------------	---

Description

Calculate the ratio of (a) the fraction of RBCs in the spleen that are infected; to (b) the fraction of RBCs in the circulation that are infected.

Usage

```
calculate_irbc_ratio(results)
```

Arguments

results	A dataframe of simulation results.
---------	------------------------------------

Value

A dataframe that includes the following columns, in addition those in results:

iRBC_Ratio The ratio of infected cell fractions in the spleen and circulation.

calculate_steady_state_outputs	<i>Calculate steady-state values for high-level model outputs.</i>
--------------------------------	--

Description

Calculate steady-state values for high-level model outputs.

Usage

```
calculate_steady_state_outputs(results, average_over_days = 10)
```

Arguments

results	A dataframe of simulation results.
average_over_days	The window at the end of each simulation over which to calculate steady-state values.

Value

A dataframe that contains the following columns:

U_t The circulating uRBC population.

Ur_t The splenic uRBC population.

I_t The circulating iRBC population.

Ir_t The splenic iRBC population.

M_t The splenic macrophage population.

iRBC_Ratio The ratio of infected cell fractions in the spleen and circulation.

iRBC_Count_Ratio The ratio of iRBC counts in the spleen and circulation.

uRBC_Loss_Ratio The ratio of uRBC loss (from the circulation) due to splenic retention and due to parasitisation.

uRBC_Retention_Ratio The ratio of uRBC retention, relative to homeostasis.

calculate_urbc_loss_ratio

Calculate the ratio of (a) the unparasitised RBC loss due to malaria (additional uRBC retention in the spleen); to (b) the parasitised RBC loss due to RBC infection.

Description

Calculate the ratio of (a) the unparasitised RBC loss due to malaria (additional uRBC retention in the spleen); to (b) the parasitised RBC loss due to RBC infection.

Usage

```
calculate_urbc_loss_ratio(results)
```

Arguments

results A dataframe of simulation results.

Value

A dataframe that includes the following column, in addition to those in results:

uRBC_Loss_Ratio The ratio of uRBC loss (from the circulation) due to splenic retention and due to parasitisation.

delta_i	<i>Rate of infected RBC removal from the circulation into the spleen.</i>
---------	---

Description

Rate of infected RBC removal from the circulation into the spleen.

Usage

```
delta_i(p, age)
```

Arguments

p	The parameter values for the scenario.
age	The RBC age.

delta_i_fold	<i>Increase in infected RBC removal into the spleen due to RBC congestion.</i>
--------------	--

Description

Increase in infected RBC removal into the spleen due to RBC congestion.

Usage

```
delta_i_fold(p, net_u_rbc, net_i_rbc)
```

Arguments

p	The parameter values for the scenario.
net_u_rbc	The total number of uninfected RBCs in the circulation.
net_i_rbc	The total number of infected RBCs in the circulation.

delta_i_prime	<i>Rate of infected RBC reentry into the circulation from the spleen.</i>
---------------	---

Description

Rate of infected RBC reentry into the circulation from the spleen.

Usage

```
delta_i_prime(p, age)
```

Arguments

p	The parameter values for the scenario.
age	The infected RBC age(s).

delta_u	<i>Rate of uninfected RBC removal from the circulation into the spleen.</i>
---------	---

Description

Rate of uninfected RBC removal from the circulation into the spleen.

Usage

```
delta_u(p, age)
```

Arguments

p	The parameter values for the scenario.
age	The RBC age.

delta_u_fold	<i>Increase in uninfected RBC removal into the spleen due to RBC congestion.</i>
--------------	--

Description

Increase in uninfected RBC removal into the spleen due to RBC congestion.

Usage

delta_u_fold(p, net_u_rbc, net_i_rbc)

Arguments

- p The parameter values for the scenario.
- net_u_rbc The total number of uninfected RBCs in the circulation.
- net_i_rbc The total number of infected RBCs in the circulation.

delta_u_prime	<i>Rate of uninfected RBC reentry into the circulation from the spleen.</i>
---------------	---

Description

Rate of uninfected RBC reentry into the circulation from the spleen.

Usage

delta_u_prime(p, age)

Arguments

- p The parameter values for the scenario.
- age The RBC age.

erythropoiesis	<i>Rate of RBC production.</i>
----------------	--------------------------------

Description

Rate of RBC production.

Usage

```
erythropoiesis(p, u_rbc)
```

Arguments

p	The parameter values for the scenario.
u_rbc	The RBC count.

hhs_asymp	<i>Red blood cell counts collected from asymptomatic Papuans who reported no fever within the preceding 24 hours (708 uninfected, 50 Pf infections, 45 Pv infections) in a cross-sectional household survey conducted in southern Papua, Indonesia.</i>
-----------	---

Description

See [Pava et al., 2016](#) for details.

Usage

```
hhs_asymp
```

Format

hhs_asymp:

A data frame with 803 rows and the following columns:

species One of "Pf", "Pv", or "neg"

total_rbc The red blood cell count

individual_results	<i>Record key outputs for a single scenario.</i>
--------------------	--

Description

Record key outputs for a single scenario.

Usage

```
individual_results(p, keep)
```

Arguments

p	The scenario parameters.
keep	The model state at each of the relevant time-steps.

Value

A data frame that includes the following columns:

scenario	The scenario number
time	The simulation time (hours)
U_t	The number of uRBCs in the circulation
Ur_t	The number of uRBCs in the spleen
Retic_c_t	The number of reticulocytes in the circulation
Retic_r_t	The number of reticulocytes in the spleen
I_t	The number of iRBCs in the circulation
Ir_t	The number of iRBCs in the spleen
Iq_t	The number of iRBCs in the microvasculature
M_t	The number of macrophages in the spleen
E_t	The erythropoiesis rate
r_t	The number of normoblasts and reticulocytes in the bone marrow
pmr_c_t_1	The number of merozoites released in the circulation
pmr_r_t_1	The number of merozoites released in the spleen
flow_r_to_c	The number of reticulocytes released from the bone marrow
flow_uc_to_r	The number of uRBCs removed from the circulation into the spleen
flow_uc_to_r_no_inf	The number of uRBCs that would have been removed from the circulation into the spleen, in the absence of a malaria infection
flow_ur_to_c	The number of uRBCs released from the spleen into the circulation
flow_ur_out	The number of uRBCs phagocytised in the spleen
flow_ic_to_r	The number of iRBCs removed from the circulation into the spleen

flow_ic_to_q The number of iRBCs sequestered into the microvasculature
flow_ir_to_c The number of iRBCs released from the spleen into the circulation
flow_ir_out The number of iRBCs phagocytised in the spleen
flow_uc_to_ic The number of uRBCs in the circulation that became infected
flow_ur_to_ir The number of uRBCs in the spleen that became infected
inf_from_ic The number of RBCs infected from iRBCs in the circulation
inf_from_iq The number of RBCs infected from iRBCs in the microvasculature
inf_from_ir The number of RBCs infected from iRBCs in the spleen
rho_t The release rate of the youngest reticulocytes
deltaUfold The fold increase in uRBC removal from the circulation
deltaIfold The fold increase in iRBC removal from the circulation
Ur_frac_inf The fraction of RBCs in the spleen that become infected

infection_flows_and_loss

Calculate quantities related to uRBC infection and retention in the spleen due to malaria infection.

Description

Calculate quantities related to uRBC infection and retention in the spleen due to malaria infection.

Usage

```
infection_flows_and_loss(results)
```

Arguments

results A dataframe of simulation results.

Value

A dataframe that includes the following columns, in addition those in **results**:

U_and_I_t The value of $U_c(t) + I_c(t)$
Ur_frac_U the fraction of uRBCs that are retained in the spleen
flow_uc_to_r_inf The retention of uRBCs due to malaria infection
flow_uc_to_r_ratio The rate of uRBC retention that is due to malaria infection, relative to baseline uRBC retention
Uc_loss_ratio_c The ratio of uRBC retention due to malaria loss, relative to the infection of uRBCs in the circulation
Uc_loss_ratio_cr The ratio of uRBC retention due to malaria loss, relative to the infection of uRBCs in the circulation and the spleen

inf_total The number of uRBC infections in the circulation and spleen

inf_from_icq The number of uRBC infection in the circulation due to merozoites released in the circulation and microvasculature

initial_spleenrbc_state	<i>Construct the initial model state.</i>
-------------------------	---

Description

Construct the initial model state.

Usage

initial_spleenrbc_state(p)

Arguments

p The parameter values for the scenario.

lambda_i	<i>Phagocytosis rate of infected RBCs in the spleen.</i>
----------	--

Description

Phagocytosis rate of infected RBCs in the spleen.

Usage

lambda_i(p, macrophages)

Arguments

p The parameter values for the scenario.

macrophages The macrophage count.

lambda_u	<i>Phagocytosis rate of uninfected RBCs in the spleen.</i>
----------	--

Description

Phagocytosis rate of uninfected RBCs in the spleen.

Usage

```
lambda_u(p, macrophages, age)
```

Arguments

p	The parameter values for the scenario.
macrophages	The macrophage count.
age	The RBC age.

parameters_pf	<i>Pf parameter values for each scenario.</i>
---------------	---

Description

Pf parameter values for each scenario.

Usage

```
parameters_pf
```

Format

```
parameters_pf:
A data frame with 34 rows and 3 columns:
name Parameter name
baseline Baseline value
```

parameters_pv	<i>Pv parameter values for each scenario.</i>
---------------	---

Description

Pv parameter values for each scenario.

Usage

parameters_pv

Format

parameters_pv:
A data frame with 34 rows and 3 columns:
name Parameter name
baseline Baseline value

prepare_spleenrbc_snapshot	<i>Construct a list that will record the model state over time.</i>
----------------------------	---

Description

Construct a list that will record the model state over time.

Usage

prepare_spleenrbc_snapshot(p, time_steps)

Arguments

p The parameter values for the scenario.
time_steps The number of time-steps (hours).

qlunif	<i>Quantile function for the log-uniform distribution.</i>
--------	--

Description

Quantile function for the log-uniform distribution.

Usage

```
qlunif(p, min, max)
```

Arguments

p	A vector of probabilities.
min	The lower limit of the distribution.
max	The upper limit of the distribution.

rbc_counts_to_haemoglobin	<i>Convert red blood cell counts into haemoglobin (g/dL).</i>
---------------------------	---

Description

For this conversion, we assume that the steady-state RBC count corresponds to 12.8 g/dL of haemoglobin (the mean haemoglobin of Papuans with no malaria infection, as reported by [Pava et al., 2016](#)).

Usage

```
rbc_counts_to_haemoglobin(rbc_counts)
```

Arguments

rbc_counts	One or more RBC counts.
------------	-------------------------

Value

Haemoglobin levels (g/dL).

See Also

[hhs_asymp](#) RBC counts from asymptomatic Papuans.

Examples

```
rbc_counts_to_haemoglobin(1e15 * c(2.3, 2.4, 2.5, 2.6, 2.7))
```

rbc_steady_state	<i>The red blood cell count at homeostasis.</i>
------------------	---

Description

Defined as the median red blood cell count for uninfected Papuans in the [hhs_asymp](#) data set.

Usage

rbc_steady_state

Format

rbc_steady_state:
A scalar value.

resolve_negative_rbc	<i>Subtract negative U values from other (positive) U values.</i>
----------------------	---

Description

Subtract negative U values from other (positive) U values.

Usage

resolve_negative_rbc(u, t_urbc, pmf, beta_a, alpha_fun)

Arguments

- | | |
|-----------|---|
| u | A population of red blood cells. |
| t_urbc | The RBC lifetime. |
| pmf | The parasite multiplication factor. |
| beta_a | The (age-dependent) merozoite preference for uninfected RBCs. |
| alpha_fun | The function that calculates RBC infections. |

retic_steady_state	<i>The reticulocyte production rate at homeostasis.</i>
--------------------	---

Description

Returns the steady-state values for:

- normoblast production rate (γ);
- normoblast and reticulocyte population in the bone marrow (r_a);
- reticulocyte population in the circulation (R_a);
- normocyte population in the circulation (N_a);
- RBC population in the spleen (U_r_a); and
- circulating RBC imbalance wrt homeostasis (difference).

Usage

```
retic_steady_state(p)
```

Arguments

p	The parameter values for the scenario.
---	--

reticulocyte_prod	<i>The reticulocyte production rate for the given normoblast population.</i>
-------------------	--

Description

The reticulocyte production rate for the given normoblast population.

Usage

```
reticulocyte_prod(p, rho_ss, lambdaU, deltaU_a, gamma, z = 0)
```

Arguments

p	The parameter values for the scenario.
rho_ss	The release rate of reticulocytes from the bone marrow into the circulation at homeostasis.
lambdaU	The phagocytosis rate of uninfected RBCs in the spleen.
deltaU_a	The rate of uninfected RBC removal from the circulation into the spleen.
gamma	The normoblast population in the bone marrow.
z	The initial number of circulating reticulocytes (age of 1 hour).

rho	<i>Age-structured release rate of reticulocytes from the bone marrow into the circulation.</i>
-----	--

Description

Age-structured release rate of reticulocytes from the bone marrow into the circulation.

Usage

rho(p, age, u_rbc)

Arguments

- | | |
|-------|--|
| p | The parameter values for the scenario. |
| age | The reticulocyte age. |
| u_rbc | The RBC count (must be a scalar). |

rho_release_age	<i>The minimum age at which reticulocytes are released from the bone marrow into the circulation.</i>
-----------------	---

Description

The minimum age at which reticulocytes are released from the bone marrow into the circulation.

Usage

rho_release_age(p, u_rbc)

Arguments

- | | |
|-------|--|
| p | The parameter values for the scenario. |
| u_rbc | The RBC count (must be a scalar). |

run_spleenrbc	<i>Run model scenarios.</i>
---------------	-----------------------------

Description

Run model scenarios.

Usage

```
run_spleenrbc(  
  scenarios = NULL,  
  days = 50,  
  time_steps = days * 24,  
  verbose = FALSE  
)
```

Arguments

scenarios	A dataframe of parameter combinations for each scenario.
days	The number of days to simulate.
time_steps	The number of time-steps (hours).
verbose	Whether to print a message when starting each scenario.

Value

A data frame whose columns capture model state variables at each time-step.

See Also

[individual_results\(\)](#) for a description of the returned data frame.

run_spleenrbc_model	<i>Run a single scenario and return the model state history.</i>
---------------------	--

Description

Run a single scenario and return the model state history.

Usage

```
run_spleenrbc_model(p, time_steps, debug = FALSE)
```

Arguments

p	The parameter values for the scenario.
time_steps	The number of time-steps (hours).
debug	Whether to check invariant properties after each time-step.

Value

A data frame whose columns capture model state variables at each time-step.

See Also

[individual_results\(\)](#) for a description of the returned data frame.

sample_parameters	<i>Create parameter samples for each scenario.</i>
-------------------	--

Description

Create parameter samples for each scenario.

Usage

```
sample_parameters(
  species = c("Pf", "Pv"),
  nospleen = FALSE,
  dists = NULL,
  rbc_ss = NULL,
  n_samples = 1000,
  seed = 1691987
)
```

Arguments

species	The malaria species: 'Pf' or 'Pv'.
nospleen	Whether the spleen has been removed.
dists	The parameter distributions from which to draw samples. This should be a named list that maps each parameter name to a quantile function (qnorm, qunif, etc). See the examples below, which use purrr-style lambda formulae. If no distributions are defined, the default uncertainty_distributions will be used.
rbc_ss	The red blood cell count at homeostasis.
n_samples	The number of scenarios.
seed	The seed for the random number generator.

Examples

```
dists <- list(
  x = ~ qnorm(.x, mean = 5, sd = 1),
  y = ~ qexp(.x, rate = 0.2)
)
samples <- sample_parameters(species = "Pf", dists = dists, n_samples = 10)
mean(samples$x)
#> 5.033116
sd(samples$x)
#> 0.8708642
mean(samples$y)
#> 4.587215
sd(samples$y)
#> 3.996536
```

splenectomised	<i>Uninfected and infected RBC counts in the circulation and spleen of 15 asymptomatic adults in Papua, Indonesia (9 Pf infections, 6 Pv infections) who underwent splenectomy, mostly due to trauma.</i>
----------------	---

Description

See [Kho et al., 2021](#) for details.

Usage

```
splenectomised
```

Format

splenectomised:

A data frame with 17 rows and the following columns:

patient Patient identifier

infection One of "Pf", "Pv", or "neg"

irbc_peri Infected RBC count in the peripheral circulation

irbc_spleen Infected RBC count in the spleen

urbc_peri Uninfected RBC count in the peripheral circulation

urbc_spleen Uninfected RBC count in the spleen

`step_spleenrbc_model` *Update the model state by simulating forward one time-step.*

Description

Update the model state by simulating forward one time-step.

Usage

```
step_spleenrbc_model(p, s, t)
```

Arguments

<code>p</code>	The parameter values for the scenario.
<code>s</code>	The current model state.
<code>t</code>	The time for which to calculate the model state.

`uncertainty_distributions`
Define uncertainty distributions for each parameter.

Description

Define uncertainty distributions for each parameter.

Usage

```
uncertainty_distributions(species, check_names = TRUE)
```

Arguments

<code>species</code>	The malaria species: 'Pf' or 'Pv'.
<code>check_names</code>	Check whether each parameter has a distribution.

uncertainty_intervals	<i>Calculate uncertainty intervals for each column, except for "time" and "scenario".</i>
-----------------------	---

Description

Calculate uncertainty intervals for each column, except for "time" and "scenario".

Usage

```
uncertainty_intervals(results, pcnt = c(50, 60, 70, 80, 90, 95))
```

Arguments

- results A dataframe of simulation results.
- pcnt The uncertainty intervals to calculate, expressed as percentages.

Value

A dataframe with the following columns:

- name** The statistic name (character)
- time** The time (numeric, hours)
- interval** The interval (ordered factor, widest to narrowest)
- ci_min** The interval lower bound (numeric)
- ci_max** The interval upper bound (numeric)

zeta	<i>Age-structured rate of RBC sequestration into the microvasculature.</i>
------	--

Description

Age-structured rate of RBC sequestration into the microvasculature.

Usage

```
zeta(p, age)
```

Arguments

- p The parameter values for the scenario.
- age The RBC age.

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