

# Final Project: Part II

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In this part of the project, the task is to build and simulate a version of the Ross-MacDonald malaria model and examine the threshold for persistence of malaria.

Formulae:

$$\frac{dS_H}{dt} = \mu N_H - \frac{\beta_V I_V S_H}{N_H} + \sigma I_H - \mu S_H$$

$$\frac{dI_H}{dt} = \frac{\beta_V I_V S_H}{N_H} - \sigma I_H - \mu I_H$$

$$\frac{dS_V}{dt} = c N_V - \frac{\beta_H S_V I_H}{N_H} - c S_V$$

$$\frac{dI_V}{dt} = \frac{\beta_H S_V I_H}{N_H} - c I_V,$$

where  $\mu$  is the host mortality rate,  $\sigma$  is the host recovery rate,  $\beta_V = b p_{HV}$  (where  $b$  is the vector bite rate and  $p_{HV}$  is the probability of transmission from vector to host),  $c$  is the vector mortality rate, and  $\beta_H = b \frac{N_V}{N_H} p_{VH}$  (where  $N_V$  and  $N_H$  are the sizes of the vector and host populations and  $p_{VH}$  is the probability of transmission from host to vector).

```

# Load in R Library to do integration and other sources files
source("epi-helper.R")
source("epi-ode-SIS.R")

# set up initial population parameters
pop.size.host <- 1000
pop.size.vector <- 10000
initial.infecteds.host <- 1
initial.infecteds.vector <- 1
initial.susceptibles.host <- pop.size.host - initial.infecteds.host
initial.susceptibles.vector <-
  pop.size.vector - initial.infecteds.vector

# set host and vector Lifespans (L)
lifespan.host <- 50 * 52
lifespan.vector <- 1

# set host infectious period (D)
infectious.period <- 4

# set recovery rate (sigma)
sigma <- 1 / infectious.period

# set natural mortality rates for host (mu) and vector (c)
mu <- 1 / lifespan.host
c <- 1 / lifespan.vector

# set vector bite rate (b) and transmission probabilities from vector to
# host (pHV) and from host to vector (pVH)
bite.rate <- 0.5 * 7
pHV <- 0.5
pVH <- 0.8

# set vector and host transmission rates (beta)
beta.vector <- bite.rate * pHV
beta.host <- ((bite.rate * pop.size.vector) / pop.size.host) * pVH

# set simulation times
start.time <- 0
end.time <- 1
step <- 0.01

# set initial populations data frame
initial.populations <- data.frame(
  time = start.time,
  susceptibles.host = initial.susceptibles.host,
  infecteds.host = initial.infecteds.host,
  susceptibles.vector = initial.susceptibles.vector,
  infecteds.vector = initial.infecteds.vector
)

# integrate the differential equations

```

```

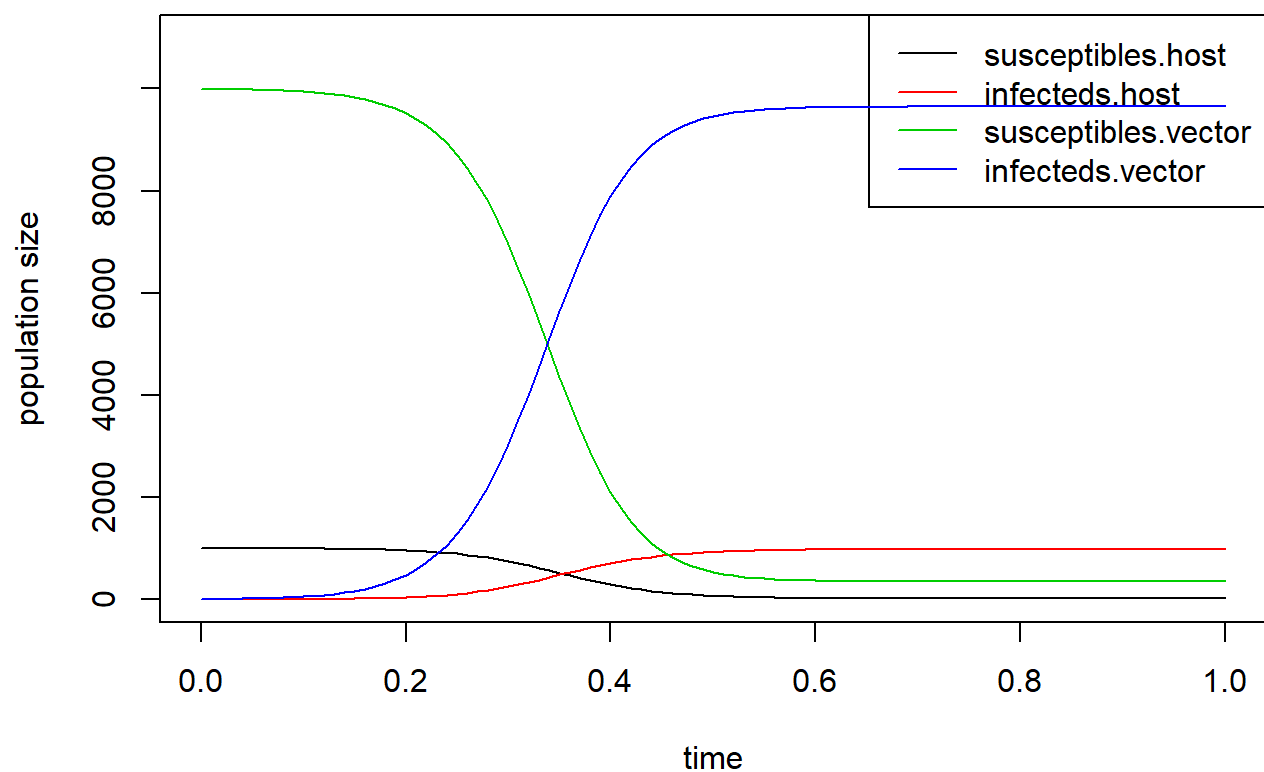
final.populations <- run.integration(
  ode.deterministic.SIS,
  initial.populations,
  end.time,
  timestep = step,
  beta.host = beta.host,
  beta.vector = beta.vector,
  mu = mu,
  c = c,
  sigma = sigma
)

```

```

# plot the results
plot.populations(final.populations)

```



Formula to calculate  $R_0$ :

$$R_0 = \sqrt{\frac{b^2 p_{HV} p_{VH}}{c(\mu + \sigma)} \frac{N_V}{N_H}}$$

```

R0 <-
  sqrt((bite.rate ^ 2 * pHV * pVH) / (c * (mu + sigma)) * (pop.size.vector /
pop.size.host))
R0

```

```
## [1] 13.98924
```

```
R0 <- 0.99
```

```
pop.size.host <- 1000
```

```
pop.size.vector <-
```

```
(((R0 ^ 2) * c * (mu + sigma)) / ((bite.rate ^ 2) * pHV * pVH)) * pop.size.host  
pop.size.vector
```

```
## [1] 50.08203
```

```
pop.size.vector <- 10 ^ 4
```

```
pop.size.host <-
```

```
((bite.rate ^ 2) * pHV * pVH) / ((R0 ^ 2) * c * (mu + sigma))) * pop.size.vector  
pop.size.host
```

```
## [1] 199672.4
```

The  $R_0$ , assuming the original parameters, is 14. To eliminate malaria, we would need to reduce mosquito density to around 50 mosquitos per square kilometer. At a mosquito density of 10,000 per square kilometer, the human population would need to increase to at least approximately 199,672 individuals per square kilometer to achieve an  $R_0$  of less than 1.

## Scenario 1: $R_0 < 1$ by Reducing the Mosquito

# Population Size

```
# set up initial population parameters
pop.size.host <- 1000
pop.size.vector <-
  (((R0 ^ 2) * c * (mu + sigma)) / ((bite.rate ^ 2) * pHV * pVH)) *
  pop.size.host
initial.infecteds.host <- 1
initial.infecteds.vector <- 1
initial.susceptibles.host <- pop.size.host - initial.infecteds.host
initial.susceptibles.vector <-
  pop.size.vector - initial.infecteds.vector

# set host and vector Lifespans (L)
lifespan.host <- 50 * 52
lifespan.vector <- 1

# set host infectious period (D)
infectious.period <- 4

# set recovery rate (sigma)
sigma <- 1 / infectious.period

# set natural mortality rates for host (mu) and vector (c)
mu <- 1 / lifespan.host
c <- 1 / lifespan.vector

# set vector bite rate (b) and transmission probabilities from vector to
# host (pHV) and from host to vector (pVH)
bite.rate <- 0.5 * 7
pHV <- 0.5
pVH <- 0.8

# set vector and host transmission rates (beta)
beta.vector <- bite.rate * pHV
beta.host <- ((bite.rate * pop.size.vector) / pop.size.host) * pVH

# set simulation times
start.time <- 0
end.time <- 1
step <- 0.01

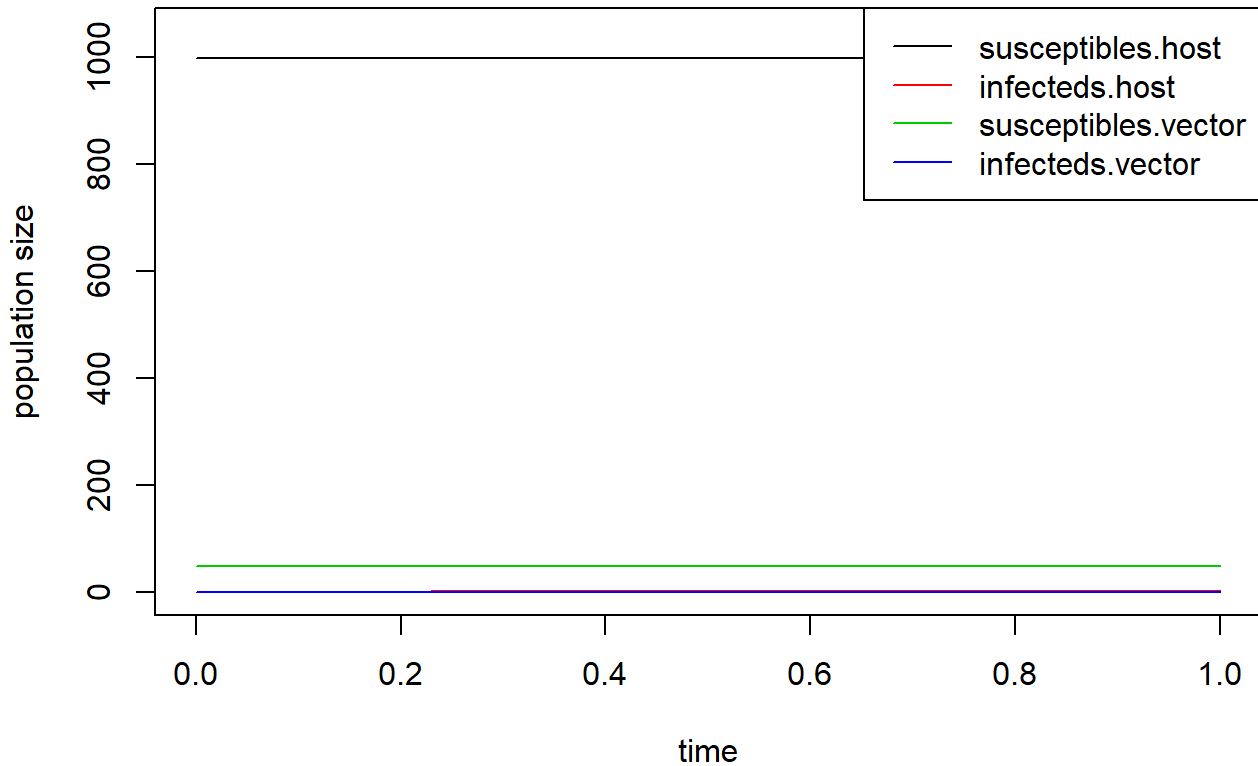
# set initial populations data frame
initial.populations <- data.frame(
  time = start.time,
  susceptibles.host = initial.susceptibles.host,
  infecteds.host = initial.infecteds.host,
  susceptibles.vector = initial.susceptibles.vector,
  infecteds.vector = initial.infecteds.vector
)
```

```

# integrate the differential equations
final.populations <- run.integration(
  ode.deterministic.SIS,
  initial.populations,
  end.time,
  timestep = step,
  beta.host = beta.host,
  beta.vector = beta.vector,
  mu = mu,
  c = c,
  sigma = sigma
)

# plot the results
plot.populations(final.populations)

```



When the mosquito population is brought down to below critical density (i.e., when  $R_0 < 1$ ), there are zero infected hosts or vectors by the end time.

## Scenario 2: $R_0 < 1$ by Reducing the Human

# Population Size

```
# set up initial population parameters
pop.size.vector <- 10000
pop.size.host <-
  (((bite.rate ^ 2) * pHV * pVH) / ((R0 ^ 2) * c * (mu + sigma))) *
  pop.size.vector
initial.infecteds.host <- 1
initial.infecteds.vector <- 1
initial.susceptibles.host <- pop.size.host - initial.infecteds.host
initial.susceptibles.vector <-
  pop.size.vector - initial.infecteds.vector

# set host and vector Lifespans (L)
lifespan.host <- 50 * 52
lifespan.vector <- 1

# set host infectious period (D)
infectious.period <- 4

# set recovery rate (sigma)
sigma <- 1 / infectious.period

# set natural mortality rates for host (mu) and vector (c)
mu <- 1 / lifespan.host
c <- 1 / lifespan.vector

# set vector bite rate (b) and transmission probabilities from vector to
# host (pHV) and from host to vector (pVH)
bite.rate <- 0.5 * 7
pHV <- 0.5
pVH <- 0.8

# set vector and host transmission rates (beta)
beta.vector <- bite.rate * pHV
beta.host <- ((bite.rate * pop.size.vector) / pop.size.host) * pVH

# set simulation times
start.time <- 0
end.time <- 1
step <- 0.01

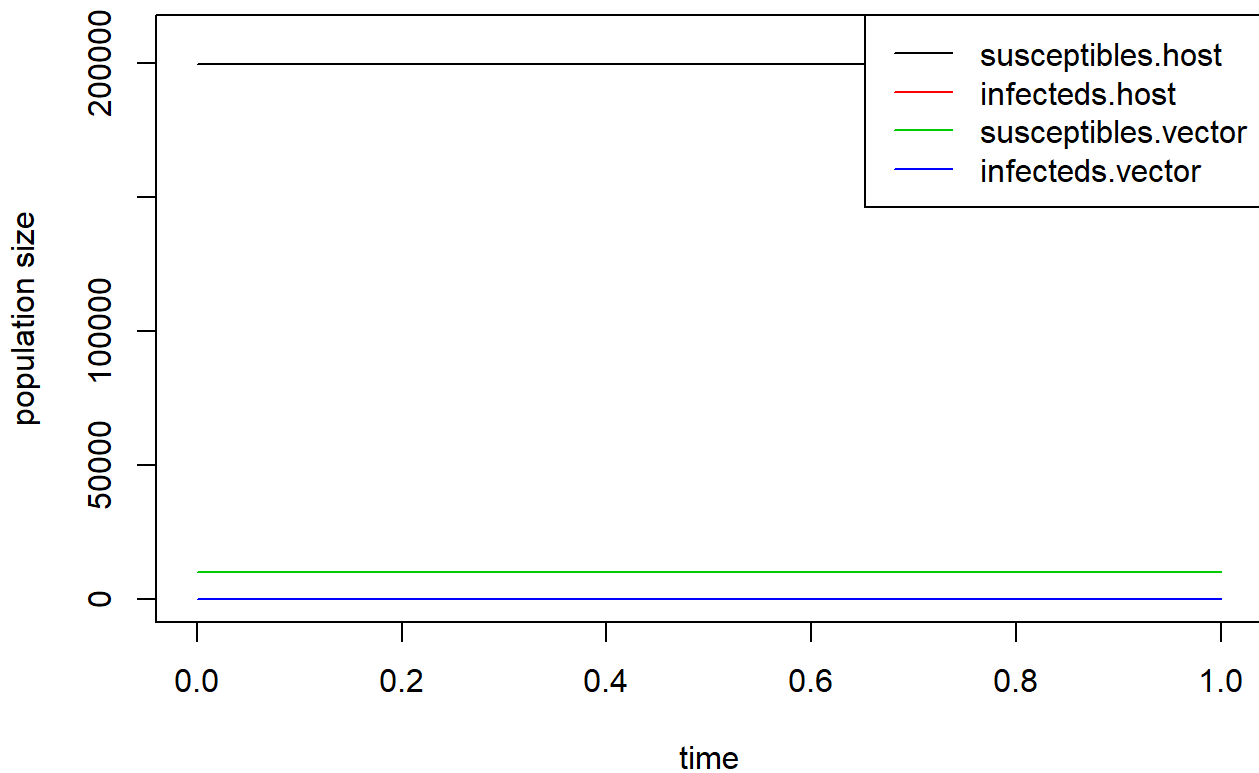
# set initial populations data frame
initial.populations <- data.frame(
  time = start.time,
  susceptibles.host = initial.susceptibles.host,
  infecteds.host = initial.infecteds.host,
  susceptibles.vector = initial.susceptibles.vector,
  infecteds.vector = initial.infecteds.vector
)
```

```

# integrate the differential equations
final.populations <- run.integration(
  ode.deterministic.SIS,
  initial.populations,
  end.time,
  timestep = step,
  beta.host = beta.host,
  beta.vector = beta.vector,
  mu = mu,
  c = c,
  sigma = sigma
)

# plot the results
plot.populations(final.populations)

```



Again, endemic equilibrium fails when  $R_0 < 1$ , this time due to bringing the host population size above the critical density threshold. Keeping the host population high and the vector population low is key to controlling vector-borne disease transmission.