

# Viruses in the aquatic environment

## Exercises Accompanying the Course Environmental Modelling

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### Questions

#### Problem formulation

In this exercise your task will be to interpret model equations.

The model is devised to study the impact of viruses in the aquatic environment. Viral infection is of considerable interest in aquatic sciences, because viruses play an important role in biogeochemical cycles by causing death in a variety of organisms, including algae.

Equations in this exercise are adapted from a model that describes the dynamics of the *HIV* virus, which is responsible for the acquired immune-deficiency syndrome (AIDS). The model has three components, including the number of uninfected (i.e., healthy) cells,  $H$ , the number of infected cells,  $I$ , and the number of free virions,  $V$  (Figure 1).

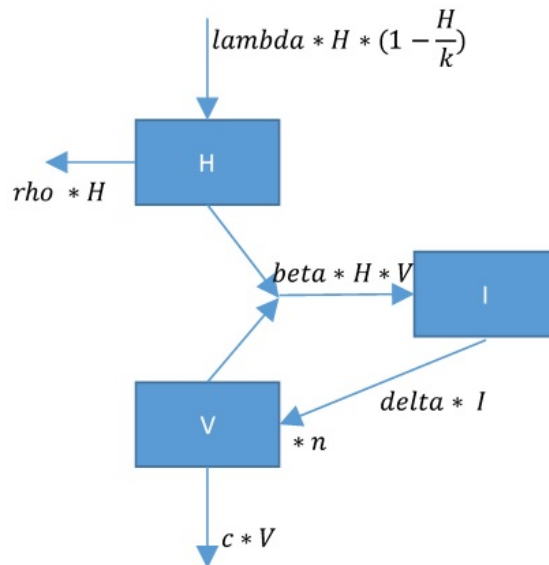


Figure 1: Schematic diagram of the algae+virus model.

## Tasks

Based on the flow chart:

- What are suitable units of the state variables?
- Give a name to each flow (arrow). Try to understand the mechanistic expression for each flow. That is, which expression has been chosen and why?
- What are the units of the parameters?
- Create mass balance equations, using the flow names you just assigned.
- Replace each flow by its mechanistic expression as represented in the flowchart.

Implement the model in *R*. You can start with the R-markdown template file *RTM\_0D.Rmd*.<sup>1</sup> Adapt the R-code from the template file to represent the viral infection model.

Use the following values for initial conditions and for the model parameters:

state variable	Value
H	100
I	150
V	50000

parameter	Value
lambda	1
delta	0.55
beta	0.00002
c	5.5
k	1e5
n	100
e	1

Run the model for one year.

## Answers

### Units

Reasonable units for the state variables are

- algal cells:  $cells\ ml^{-1}$
- viruses:  $virions\ ml^{-1}$

### Mass balances and rate expressions

- Healthy (uninfected) algal cells ( $H$ ) are created by cell division, and die due to natural causes (i.e., independent of the presence of viruses). The net growth of the algal cells is described by the logistic growth model characterized by the rate constant  $\lambda$  (units of  $d^{-1}$ ) and the carrying capacity  $k$  (units of  $cells\ ml^{-1}$ ).

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<sup>1</sup>You can obtain this file from Rstudio: File → new File → Rmarkdown → from template → RTM\_0D. Save this file under a different name, and do not forget to change the heading of this file.

- Viral infection of algal cells depends on a random encounter between free virions and algae. Thus, the process is proportional to the product of the concentration of healthy cells,  $H$ , and the concentration of free virions,  $V$ . The corresponding rate constant,  $\beta$ , has units of  $(\text{virions ml}^{-1})^{-1} d^{-1}$ .
- Death of infected cells (by bursting) is a first-order process characterized by a rate constant  $\delta$  (units of  $d^{-1}$ ).
- When an infected algal cell bursts, it releases  $n$  free virions. Conversely, it takes *one* virion to infect a healthy algal cell. Thus, the infection efficiency parameter is  $e = 1 \text{ virions cell}^{-1}$ .
- Free virions are not immortal but decay at a first-order rate characterized by the rate constant  $c$  (units of  $d^{-1}$ ).

Based on these considerations, the mass balance equation for the uninfected ( $H$ ) and infected ( $I$ ) algal cells and for the free virions are:

$$\begin{aligned}\frac{dH}{dt} &= \text{NetAlgalGrowth} - \text{Infection} \\ \frac{dI}{dt} &= \text{Infection} - \text{Bursting} \\ \frac{dV}{dt} &= n \cdot \text{Bursting} - \text{VirusDeath} - e \cdot \text{Infection}\end{aligned}$$

where

$$\begin{aligned}\text{NetAlgalGrowth} &= \lambda \cdot H \cdot \left(1 - \frac{H}{k}\right) \\ \text{Infection} &= \beta \cdot H \cdot V \\ \text{Bursting} &= \delta \cdot I \\ \text{VirusDeath} &= c \cdot V\end{aligned}$$

## Parameters

The parameter values are in the following table:

parameter	Value	Units	Description
lambda	1	$d^{-1}$	Net growth rate constant of healthy cells
delta	0.55	$d^{-1}$	Burst rate constant of infected cells
beta	0.00002	$(\text{virions ml}^{-1})^{-1} d^{-1}$	Infection rate constant
c	5.5	$d^{-1}$	Death rate constant of viruses
k	1e5	$\text{cells ml}^{-1}$	Algal carrying capacity
n	100	$\text{virions cell}^{-1}$	Burst size
e	1	$\text{virions cell}^{-1}$	Infection efficiency

## R-implementation

Here is the code specifying the model:

```
require(deSolve) # package with solution methods

# state variables, units = cells/ml (H, I) or virions/ml (V)
```

```

state <- c(H = 100, I = 150, V = 50000)

# parameters
parms <- c(
  lambda = 1,      # [/d] net growth rate constant of healthy algal cells
  delta = 0.55,    # [/d] burst rate constant of infected cells
  beta = 0.00002,  # [(virions/ml)^-1 d-1] infection rate constant
  c = 5.5,         # [/d] death rate constant of virus
  k = 1e5,         # [cells/ml] carrying capacity for algal cells
  n = 100,         # [virus/cell] burst size
  e = 1           # [virus/cell] number of viruses required to infect an algal cell
)

# Model function
VirusDynamics <- function(t, state, params) {
  with(as.list(c(state, params)), {

    # Rate expressions
    NetAlgalGrowth <- lambda*H*(1-H/k) # [cells/ml/d]
    Infection      <- beta * H * V     # [cells/ml/d]
    Bursting       <- delta*I          # [cells/ml/d]
    VirusDeath     <- c*V              # [virions/ml/d]

    # Mass balances [cells/ml/d]
    dH <- NetAlgalGrowth - Infection
    dI <- Infection - Bursting
    dV <- n*Bursting - VirusDeath - e*Infection

    list(c(dH, dI, dV), Cells = H + I, Bursting = Bursting,
         Infection = Infection, logV = log10(V), logC = log10(H+I))
  })
}

```

Here are plots of the model solution:

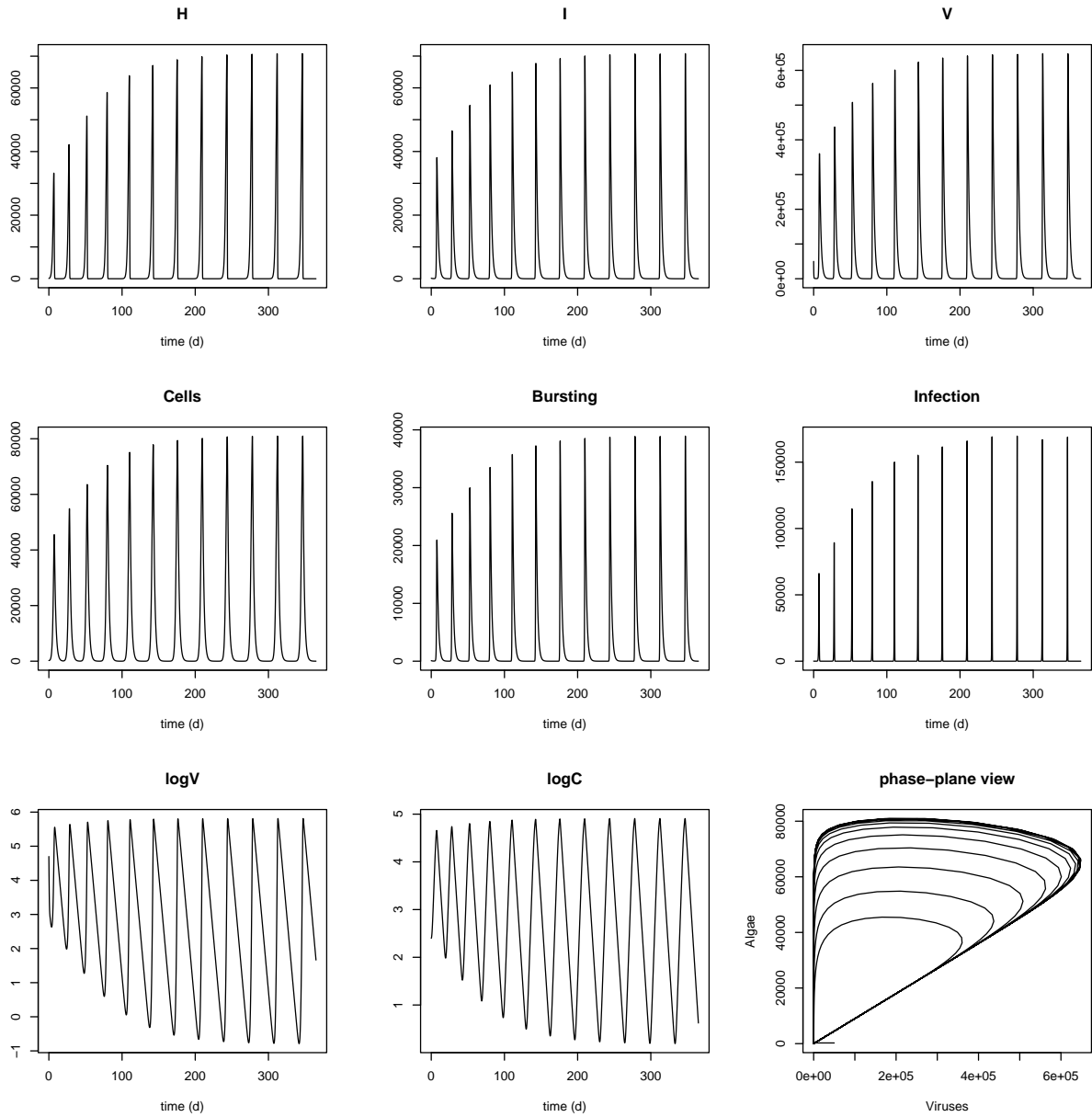
```

# output time
outtimes <- seq(from = 0, to = 365, length.out = 365*10) # run for 365 days

# solve this model, using the ode function from deSolve
out <- ode(y = state, parms = parms, func = VirusDynamics, times = outtimes)

plot(out, mfrow = c(3, 3), xlab="time (d)")
plot(out[,c(4,5)], type = "l", main = "phase-plane view",
     xlab = "Viruses", ylab = "Algae")

```



## References

R Core Team (2020). R: A language and environment for statistical computing. R Foundation for Statistical Computing, Vienna, Austria. URL <https://www.R-project.org/>.

Karline Soetaert, Thomas Petzoldt, R. Woodrow Setzer (2010). Solving Differential Equations in R: Package deSolve. Journal of Statistical Software, 33(9), 1–25. URL <http://www.jstatsoft.org/v33/i09/> DOI 10.18637/jss.v033.i09