

ODE modelling in Life Sciences

INSA - 3BS 2020/2021

Practical session 2: epidemiological models

Introduction

This second practical session is dedicated to the study of epidemiological models, especially the *SIRS* models, under the R software. For this purpose, we will use the R package `phaseR` as already introduced with population dynamics in dimension 1 during the first practical session.

This package should already be installed on your computer. You just need to load it into your current R session:

```
library("phaseR")
```

The *SIRS* model

As previously introduced, the *SIRS* model with a **density-dependent** infection strength (Figure 1) can be written in dimension 2 as follows, given that $S(t) + I(t) + R(t) = \text{constant}$:

$$\begin{cases} \frac{dS(t)}{dt} = -\beta I(t) S(t) + \gamma(N - S(t) - I(t)) \\ \frac{dI(t)}{dt} = \beta I(t) S(t) - \nu I(t) \end{cases}$$

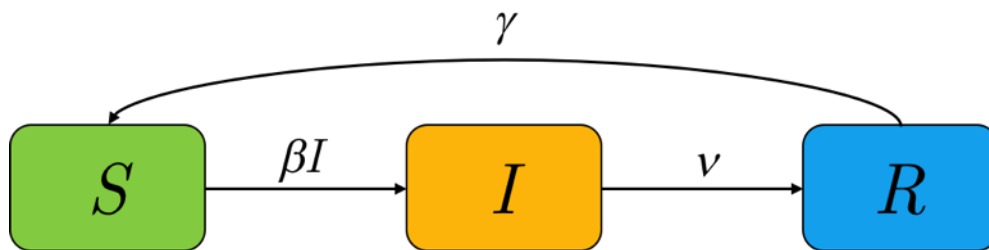


Figure 1: Schematic diagram of the *SIRS* model

The aim of this first section is to simulate this model with the day as time unit.

1. Use the function below to define the model according to its variables and parameters.

```
SIRSmod <- function(time, y, parameters){  
  dy1 <- - parameters[1] * y[1] * y[2] + parameters[2] * (parameters[3] - y[1] - y[2])  
  dy2 <- parameters[1] * y[1] * y[2] - parameters[4] * y[2]  
  list(c(dy1, dy2))  
}
```

2. To which variables do objects `y[i]`, $i = 1, 2$ correspond?
3. To which parameters do objects `parameters[i]`, $i = 1, \dots, 4$ correspond? Recall their respective biological interpretation.
4. Given that $\gamma = 0.5$, and based on the slides introducing you with epidemiological models, assign the correct numerical values to the other parameters.
5. Assign the correct initial condition to an object `Init` based on the flu epidemic in the English boarding school for boys as reported by the *British Medical Journal* in 1978.

We will first draw the phase portrait in the phase plane (S, I) with the flow field, the nullclines and some appropriately chosen trajectories.

6. Use function `flowField()` of package `phaseR` to first draw the flow field of the SIRS model.
7. Add the horizontal and the vertical nullclines. It may be needed to change x- and y-limits in order to fully draw the nullclines. Remove the legend that is automatically added.
8. Add some trajectories keeping in mind that $S(t) + I(t) + R(t)$ is constant. You may add a straight line symbolizing this condition.
9. Add black dots to denote equilibrium points on the phase portrait. For that purpose, you will need function `findEquilibrium()` of package `phaseR` as well as to give a starting point for the search of the coordinates of the equilibrium points (option `y0`). Assign outputs of function `findEquilibrium()` to objects `eq1` and `eq2` for both equilibrium points, respectively. Explore option `plot.it` in function `findEquilibrium()`; what is the meaning of the point character used to draw the equilibrium points?
10. To what does object `eq1$ystar` correspond? What type of object is it?

The partial R code below may help you to perform the previous steps.

```
# Flow field drawing
flowField(deriv = ..., xlim = c(0, N), ylim = c(0, N),
          parameters = ..., add = FALSE, las = 1,
          xlab="...", ylab="...")
# Nullclines
nullclines(deriv = ..., xlim = ..., ylim = ...,
            parameters = ..., add = TRUE, ...)
# Trajectories
trajectory(deriv = ..., y0 = ..., tlim = c(0, 50),
            parameters = ..., add = TRUE)
# Equilibrium points
eq1 <- findEquilibrium(deriv = ..., y0 = ...,
                      parameters = ...)
```

11. Exploring the sub-objects in `eq1` and `eq2`, give the Jacobian matrix at both equilibrium points.
12. Exploring the sub-objects in `eq1` and `eq2`, find the stability and the nature of both equilibrium points.

Remark: function `stability()` could also have been used to answer question 12.

13. Try to use function `phasePlaneAnalysis()`. What can you do with it?
14. Use function `numericalSolution()` in order to plot chronicles corresponding to one of the trajectories of your previous phase portrait. It could be interesting to first try with the initial condition defined above in object `Init`. Try option `typeof` of function `numericalSolution()`. Try to reproduce a similar figure as the one provided on slide 41 of the general introduction on epidemiological models.
15. Based on the formula given at slide 31 of the general presentation on epidemiological models, calculate the basic reproduction rate, namely R_0 . What do you think regarding its numerical value?

16. Try to find new parameter values for β and ν allowing to eradicate the epidemic; what does this mean in terms of the R_0 value. Of course, several pairs of parameters (β, ν) may be possible, among which one is leading to $R_0 \simeq 0.858$. For such a particular pair, draw the corresponding chronicles.
17. For the previous pair of (β, ν) parameter values you found, plot again chronicles and discuss the output on a biological point of view.

About vaccination

In this section, we will attempt to assess the impact of a vaccination campaign on the spread of an epidemic, under the hypothesis that this epidemic follows a time course as described by the SIRS model. The fraction of the population to be vaccinated to eradicate a disease is usually called p . We should therefore choose p such as:

$$(1 - p)R_0 < 1 \Leftrightarrow p > 1 - \frac{1}{R_0}$$

18. Plot the minimal immunization coverage p_{min} as a function of R_0 . Add a vertical line corresponding to the R_0 value you found under the maintenance of the epidemic (namely, $R_0 > 1$). What should be the approximate minimal immunization coverage to ensure the eradication of the epidemic, without any change in the other parameters. What other comment is this figure inspiring to you?
19. In 1983, Robert May published estimates of R_0 value for a collection of human infectious diseases¹. This data frame is provided within file `data-may-1983.txt` (see the R code below to get the data). Add data on the previous curve (function `points()`); be careful to the unit.

```
dfmay83 <- read.table("http://bmm.univ-lyon1.fr/bmm/fascicules/data-may.txt", header = TRUE)
```

20. To which kind of disease could we assimilate the current COVID-19 that affected all the world in 2020 when the sanitary crisis was at its paroxysm in spring?

¹May RM. 1983. Parasitic infections as regulators of animal populations. *The American Scientist*. 71:36–45.