

Predator-prey model with two interactions

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Tips for working in Rmarkdown:

- If you haven't worked with RMarkdown before you may need to *install the package* by typing this code `install.packages("rmarkdown")`
- To close all chunks on windows: `Alt+o`
- To open all chunks on windows: `Alt+shift+o`
- To compile the script into an HTML-file, press `knit`

This is the *model of two interactions*

1. Can you understand what the different parts of the differential equations mean biologically?

```
predpreyLV <- function(t, y, params) {  
  R <- y[1]  
  C <- y[2]  
  with(as.list(params), {  
    dR.dt <- r * R * (1 - R / k) - a * R * C  
    dC.dt <- e * a * R * C - d * C  
    return(list(c(dR.dt, dC.dt)))  
  })  
}
```

These are the *parameters specified*

2. Discuss and *understand* what role they play in the equation

```
r <- 2 #Intrinsic growth rate of resource (logistic)  
a <- 0.2 #Attack rate of predator on resource  
e <- 0.2 #Efficacy of take-up from resource to predator  
d <- 0.4 #Death rate of predator  
k <- 50 #Carrying capacity of resource  
  
R0 <- 2 #Initial resource population  
C0 <- 6 #Initial predator population  
params1 <- c(r = r, a = a, e = e, d = d, k = k) # specify parameters
```

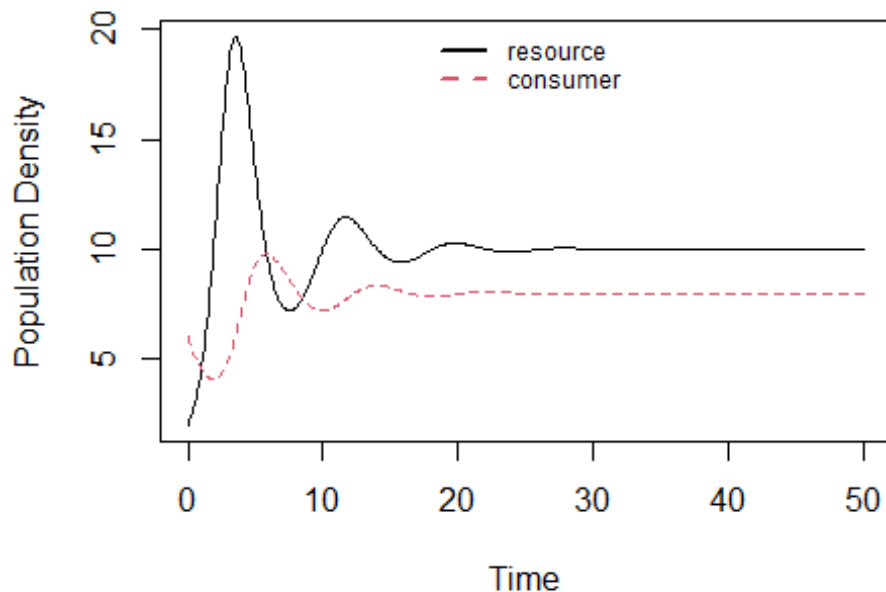
Run the model

```
MaxTime <- 50 # length of the time series
Time <- seq(0, MaxTime, by = 0.1) # here we produce a sequence of time points
at which we will determine the population densities
LV.out1 <- ode(c(R0, C0), Time, predpreyLV, params1) # here we call the
function "ode" that does the hard work of numerical integration and which is
part of the package "deSolve"
```

Plot the model...

- ...using *matplot*

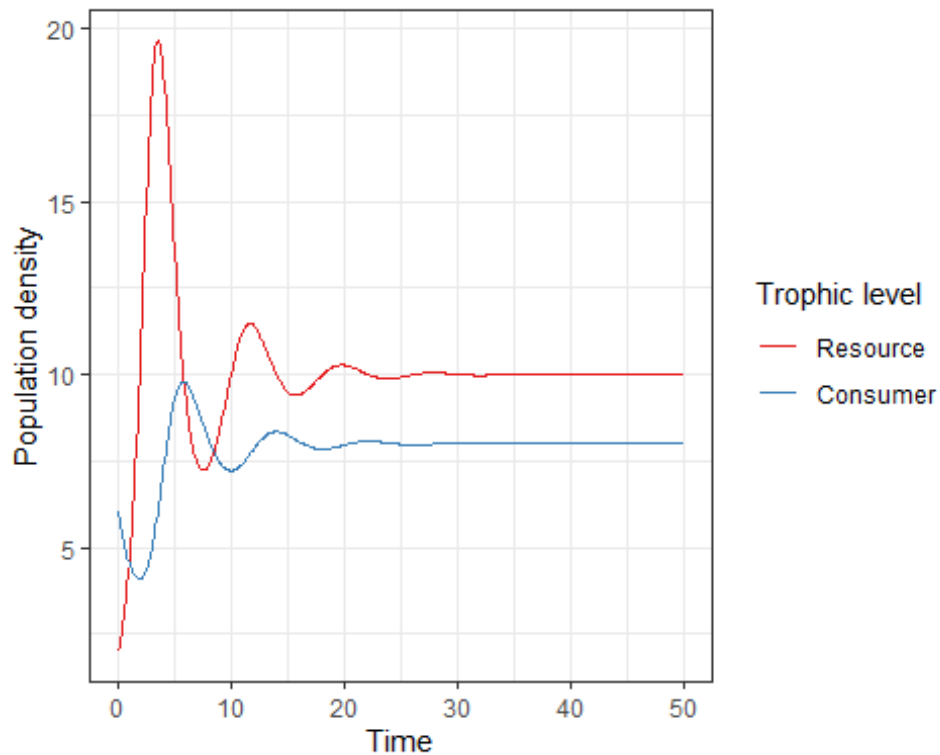
```
matplot(Time, (LV.out1[, 2:3]), type = "l", lty = 1:5, col=1:5, ylab = "Popul
ation Density", xlab="Time")
legend("top", c(expression("resource"), expression("consumer")), lty = 1:5, c
ol = 1:5, lwd = 2, bty = "n", cex = 0.75)
```



- ...using *ggplot*

```
#Reshape to Long format
LV.out <- as.data.frame(LV.out1)
LV.out$time <- as.numeric(LV.out$time)
LV.out <- gather(LV.out, key = "Trophic level", value = "Population_size", -t
ime)
#Plot
ggplot(data = LV.out, aes(x = time, y = Population_size, col = `Trophic level
`)) + geom_line() +
  theme_bw() +
```

```
labs(x = "Time", y = "Population density") + scale_color_brewer(palette="Set1", labels=c('Resource', 'Consumer'))
```



Your task

3. Discuss and interpret how the species interact in the different models and compare them. All the tasks and questions are specified in the document
4. Hand in one HTML Rmarkdown file with the **results** and **conclusions** of all the models you have built during this exercise according to the document