Series 2: SI model

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Classical models in biology (exercises) BL.6003

SI model

```
library(deSolve)
library(ggplot2)
library(tidyr)
#?ode
```

Phase space and vector field

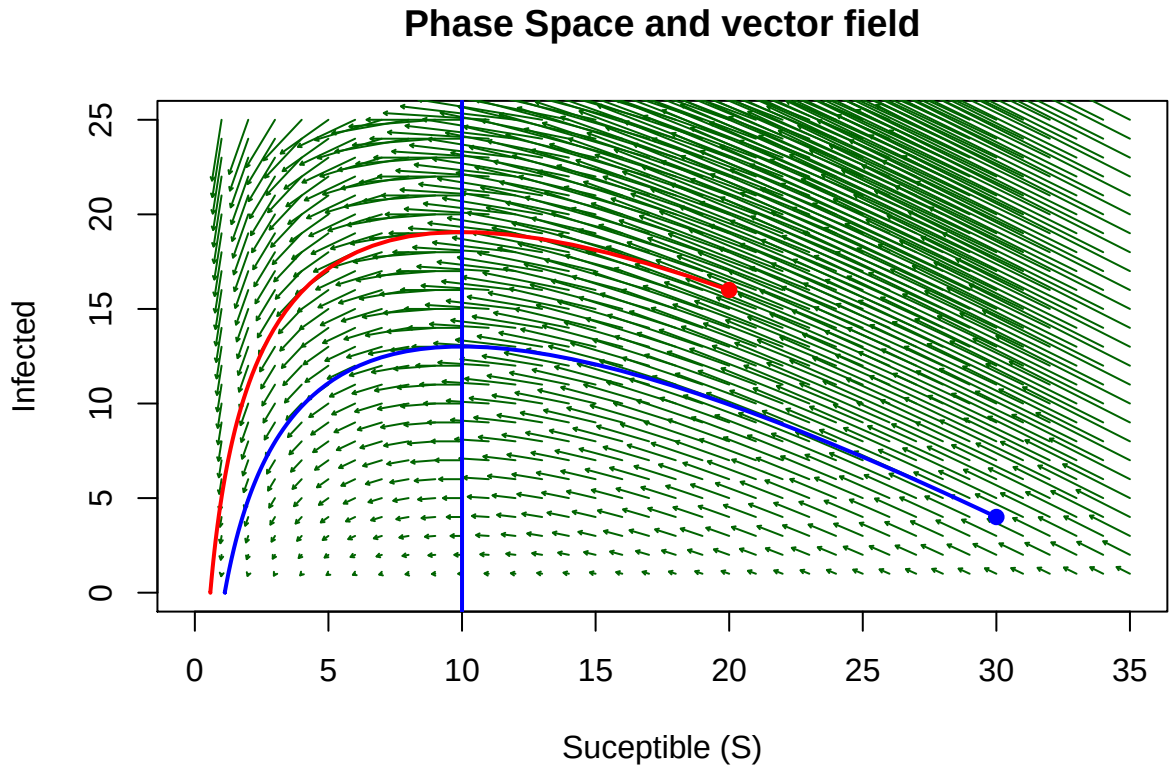
We aim at using the ode45 solver to integrate numerically the Kermack-McKendrick epidemic model. We will represent the vector field of the system in the phase space. Here the model's phase space is represented for the following parameters values:

- Infection rate: $\beta = 0.1$
- Recovery/death rate: $\alpha = 1$

Note: the notation used is from the slides (2020) and not from the exercises.

```
# Parameters
p <- list(beta = 0.1, alpha = 1)

# Derivative
f <- function(t,N,p){
  S <- N[1]
  I <- N[2]
  dS <- -p$beta * S * I
  dI <- p$beta * S * I - p$alpha * I
  return(list(c(dS,dI)))
}

time_steps <- seq(0,50,0.05)

# Initial states
N0 <- c(30,4)
N1 <- c(20,16)

# Model solutions
out0 <- ode(y = N0, times = time_steps, func = f, parms = p, method = c("ode45"))
out1 <- ode(y = N1, times = time_steps, func = f, parms = p, method = c("ode45"))


# Sequences for the vector field
N0.g <- seq(1,35,1)#S
N1.g <- seq(1,25,1)#I
```

```r
# Empty plot
plot(NA, xlab = "Suceptible (S)", ylab="Infected", xlim=c(0,35), ylim=c(0,25), main = "Phase Space and v

# Draw each arrow
for (i in 1:length(N0.g)){
  for (j in 1:length(N1.g)){
    S <- N0.g[i]
    I <- N1.g[j]
    dS <- -p$beta * S * I
    dI <- p$beta * S * I - p$alpha * I
    arrows(S, I, S+dS/7, I+dI/7, length = 0.02, col = "darkgreen")
  }
}

# Trajectories and start point
lines(x = out0[,2], y = out0[,3], col='blue', lwd = 2)
points(N0[1],N0[2],pch=19,cex=1,col='blue')

lines(x = out1[,2], y = out1[,3], col='red', lwd = 2)
points(N1[1],N1[2],pch=19,cex=1,col='red')

abline(v=p$alpha/p$beta, col = "blue", lwd = 2)
```



SI model without immunity and without death.

We consider a modification of the original Kermack-McKendrick model by assuming that the infected people, once the leave the infected class, become again susceptible (no death, but no immunity either).

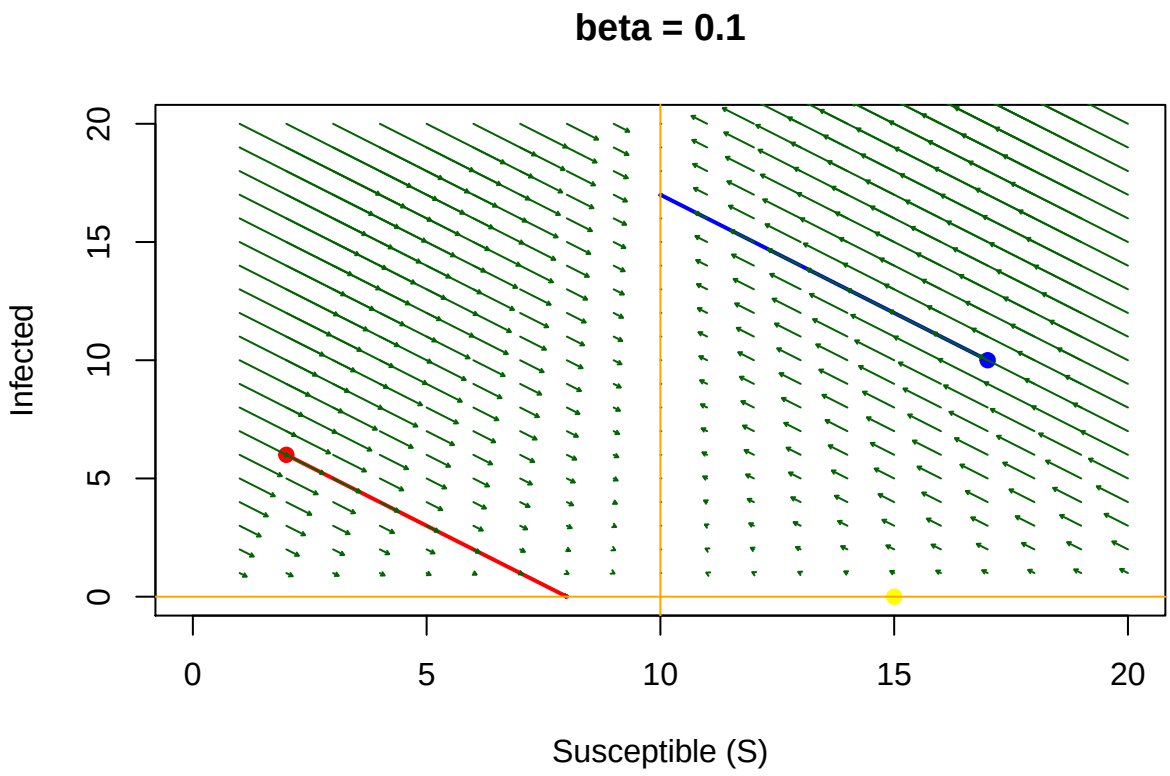
We have different starting points:

- Blue: 17 susceptibles and 10 infected
- Red: 2 susceptibles and 6 infected
- Yellow: 15 susceptible and 0 infected.

The new model is given by:

```
p <- list(beta = 0.1, alpha = 1)

f2 <- function(t,N,p){
  S <- N[1]
  I <- N[2]
  dS <- -p$beta * S * I + p$alpha * I
  dI <- p$beta * S * I - p$alpha * I
  return(list(c(dS,dI)))
}

time_steps <- seq(0,50,0.05)

# Initial states
# S - I
N0 <- c(17,10)
N1 <- c(2,6)
N2 <- c(15,0)

# Models solutions
out20 <- ode(y = N0, times = time_steps, func = f2, parms = p, method = c("ode45"))
out21 <- ode(y = N1, times = time_steps, func = f2, parms = p, method = c("ode45"))
out22 <- ode(y = N2, times = time_steps, func = f2, parms = p, method = c("ode45"))

# Ranges for the vector field
N1.g <- seq(1,20,1)#S
N2.g <- seq(1,20,1)#I


plot(NA, xlab = "Susceptible (S)", ylab="Infected", xlim=c(0,20), ylim=c(0,20), main = "beta = 0.1")

lines(x = out20[,2], y = out20[,3], col='blue', lwd = 2)
points(N0[1],N0[2],pch=19,cex=1,col='blue')

lines(x = out21[,2], y = out21[,3], col='red', lwd = 2)
points(N1[1],N1[2],pch=19,cex=1,col='red')

lines(x = out22[,2], y = out22[,3], col='yellow', lwd = 2)
points(N2[1],N2[2],pch=19,cex=1,col='yellow')

# Vector field
for (i in 1:length(N1.g)){
  for (j in 1:length(N2.g)){
    S <- N1.g[i]
```

```
    I <- N2.g[j]
    dS <- -p$beta * S * I + p$alpha * I
    dI <- p$beta * S * I - p$alpha * I

    arrows(S, I, S+dS/6, I+dI/6, length = 0.02, col = "darkgreen")

  }
}
abline(v=p$alpha/p$beta, col = "orange")
abline(a=0, b=0, col = "orange")
```



Find a theoretical explanation of what you can observe numerically.

We always reach a steady state. Depending on how many people were in the two categories (Infected or Susceptible) at the beginning, the steady state will have either 0 infected or the number of infected will be located on the α/β vertical line. In other words, the system will end on either on the x axis or on the epidemic threshold's vertical line.

The location of the vertical line depends on the infection and recovery rates. We can (maybe) draw a paralell with the annual flu. If we consider that the flu has a constant infection rate, and that nobody dies of it, it means that every year, depending on how many people are susceptible, we would reach an equilibrium point.

To take a present-day example, the hospitals capacities are based on this equilibrium point. If suddenly a flue with a higher infection rate appears, the steady state of infected people will be much higher as the threshold will move to the left (see the graph bellow).

Note, here we still consider a recovery rate of 100% at every step but changing it will just move the epidemic

threshold's vertical line left (more infectious and harder to recover) or right (less infectious). Also note that the part left of the α/β line makes less sense as we would more often start with a few infected people for a bigger number of suceptible (right side).