The SIR model

A model developed based on a template markdown file

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Introduction

This document describes a simple SIR model, as specified in the COVID exercise:

```
require(RTM)
RTMexercise("COVID")
```

Model definition

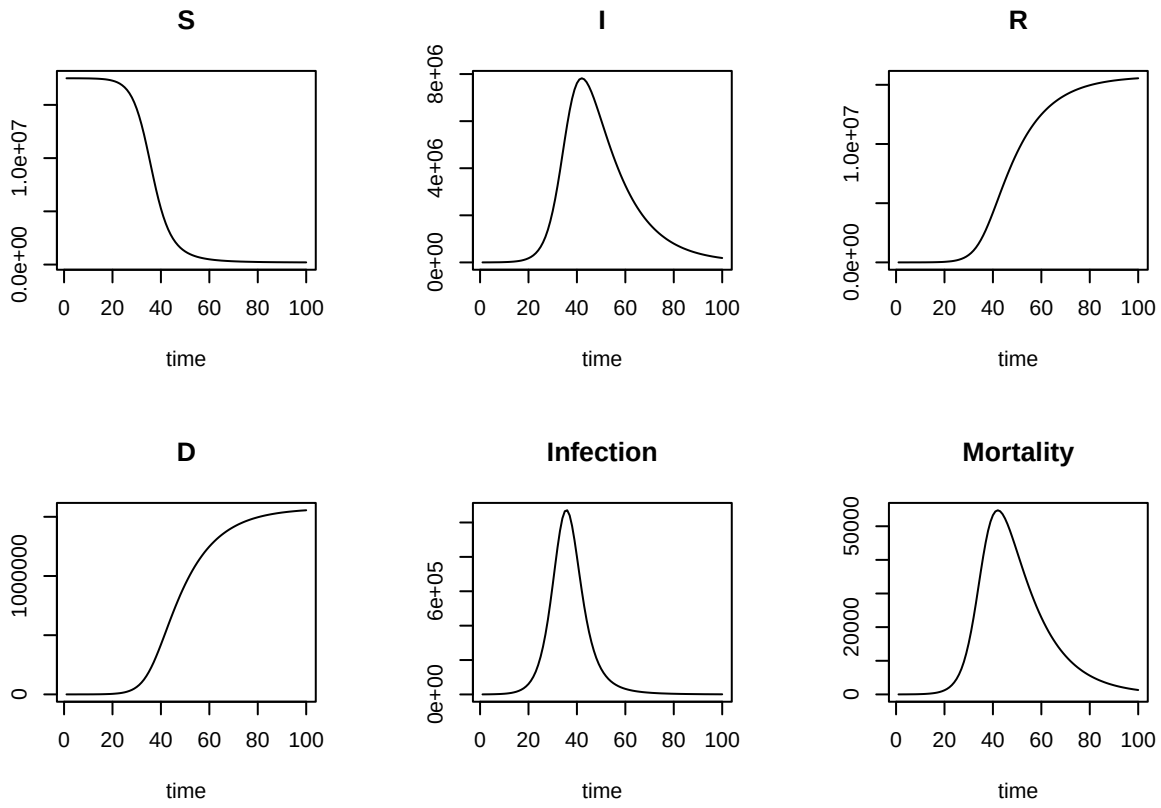
```
# Initial conditions of the state variables (D=deceased)
yini <- c(S = 17.5e6, I = 1e3, R = 0, D = 0) # number of people

# Model parameters
pars <- c(
  b   = 0.00000002, # [/ind/d]  infection rate constant
  g   = 0.07,       # [/d]      recovery  rate constant
  m   = 0.007       # [/d]      mortality rate constant
)

# Model function: calculates time-derivatives and other output
SIRmodel <-function(t, state, pars) {
  # t: time, state: state variables, pars: model parameters
  with (as.list(c(state, pars)),{

  # rate expressions [ind/d]
    Infection <- b * I * S # infection rate
    Recovery  <- g * I     # recovery rate
    Mortality <- m * I     # mortality rate

  # Time-derivatives: dC/dt = production - consumption [ind/d]
    dSdt      <- -Infection
    dIdt      <-  Infection - Recovery - Mortality
    dRdt      <-  Recovery
    dDdt      <-  Mortality

  # return time-derivatives and ordinary variables as a list
    list(c(dSdt, dIdt, dRdt, dDdt), # vector with derivatives
                            # (the same order as state variables!)
      Infection  = Infection,  # other output
      Mortality  = Mortality)
  })
}
```

Model solution

Dynamic solution

We run the model dynamically over 100 days, using two different values of the reaeration rate constant:

```
require(deSolve)  # package with integration methods
# vector of output times
outtimes <- seq(from = 1, to = 100, length.out = 100)
# ode integrates the model
out <- ode(y=yini, parms=pars, func=SIRmodel, times=outtimes)
# plot the model output
plot(out)
```

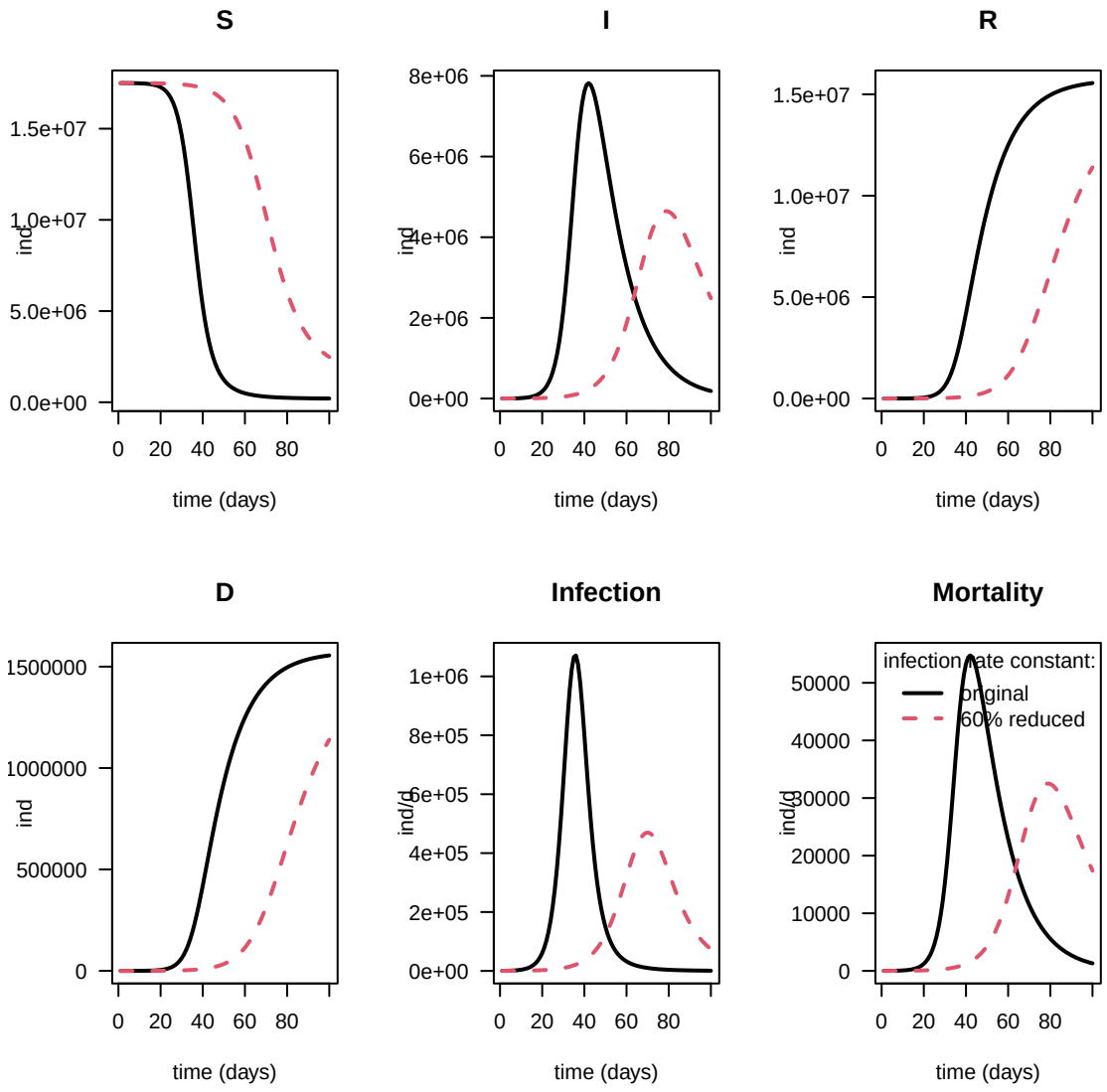



```
# change the value of the infection rate constant
pars2      <- pars           # copy the original parameter vector
pars2["b"] <- pars["b"]*0.6  # 60% of original

# integrate the model with the new parameters
out2 <- ode(y = yini, parms = pars2, func = SIRmodel,
            times = outtimes)
```

```
# print summary of the solution
summary(out)
```

We plot both solutions in one graph:

```
plot(out, out2, xlab="time (days)", las=1, lwd=2,
     ylab=list("ind","ind","ind", "ind", "ind/d","ind/d"))
legend("topright", legend = c("original", "60% reduced"),
       title="infection rate constant:",
       col=1:2, lwd=2, lty=1:2, bty="n")
```



Steady-state solution

We find the steady-state solution:

```
require(rootSolve) # package with solution methods
std <- steady(y = yini, parms = pars, func = SIRmodel,
              positive = TRUE) # to ensure that the solution is positive
```

```
## Warning in stode(y, times, func, parms = parms, ...): error during factorisation
## of matrix (dgefa); singular matrix
```

```
## diagonal element is zero
## [1] 4
```

```
## Warning in stode(y, times, func, parms = parms, ...): steady-state not reached
```

```
std$y
```

```
##        S        I        R        D
## 17500000     1000        0        0
```

Model definition with a forcing function

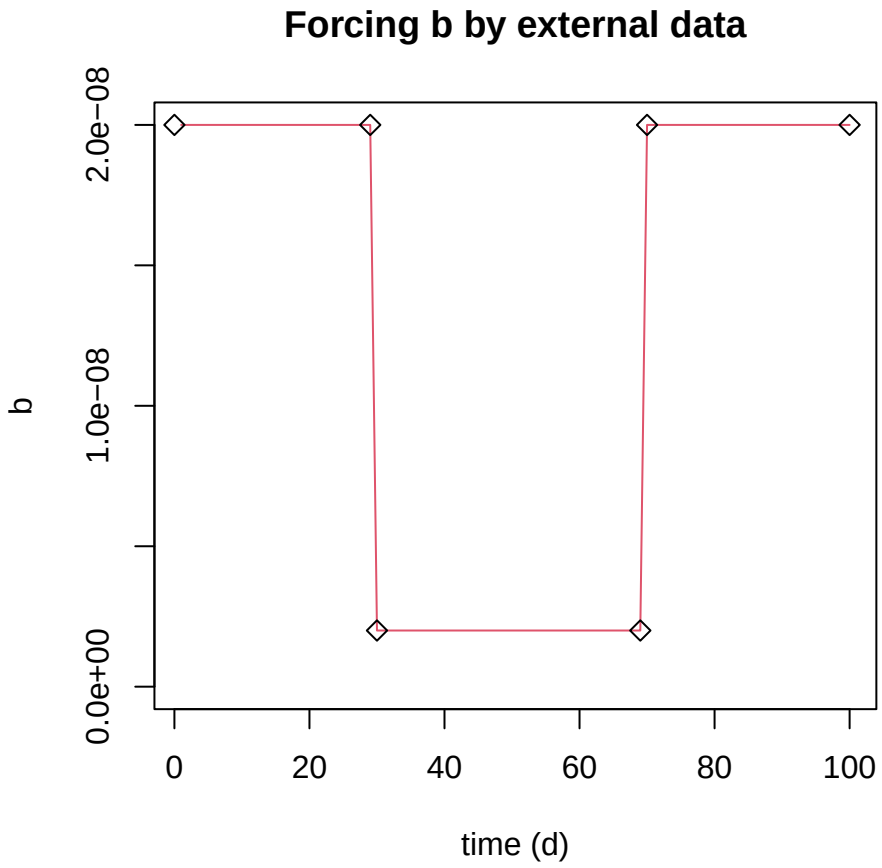
```
# Initial conditions of the state variables (D=deceased)
yini <- c(S = 17.5e6, I = 1e3, R = 0, D = 0) # number of people

# Model parameters
pars <- c(
  b   = 0.00000002, # [/ind/d]  infection rate constant
  g   = 0.07,       # [/d]      recovery  rate constant
  m   = 0.007       # [/d]      mortality rate constant
)

# Model function: calculates time-derivatives and other output
SIRmodel2 <-function(t, state, pars, bDyn) {
  # t: time, state: state variables, pars: model parameters
  with (as.list(c(state, pars)),{

  # parameter b is determined by an external forcing function
    b <- bDyn(t)

  # rate expressions [ind/d]
    Infection <- b * I * S # infection rate
    Recovery  <- g * I     # recovery rate
    Mortality <- m * I     # mortality rate

  # Time-derivatives: dC/dt = production - consumption [ind/d]
    dSdt      <- -Infection
    dIdt      <-  Infection - Recovery - Mortality
    dRdt      <-  Recovery
    dDdt      <-  Mortality

  # return time-derivatives and ordinary variables as a list
    list(c(dSdt, dIdt, dRdt, dDdt), # vector with derivatives
                            # (the same order as state variables!)
      Infection  = Infection,  # other output
      Mortality  = Mortality)
  })
}
```

Now we define the forcing function:

```
# define forcing function based on data
bDATA <- data.frame(time = c(0, 29,  30,  69, 70, 100),
                    b    = c(2,  2, 0.2, 0.2,  2,   2)*1e-8)
fbDATA <- approxfun(x=bDATA)
```

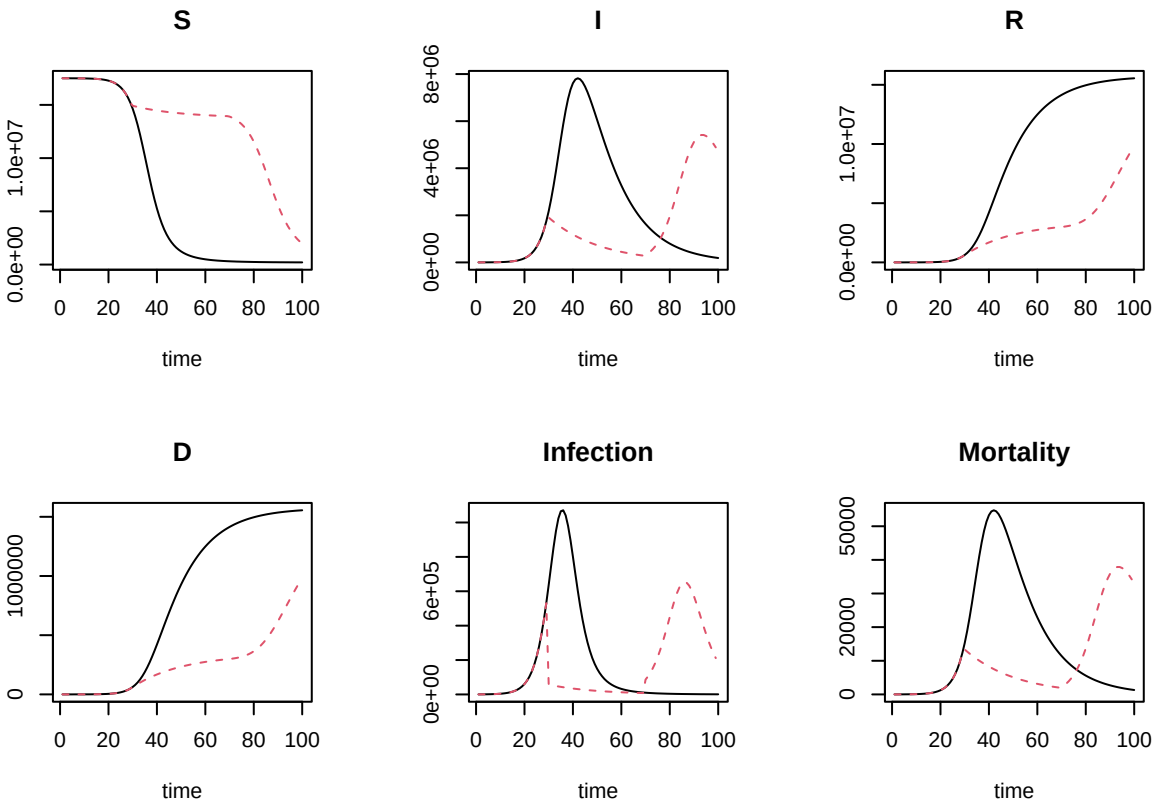
Plot the forcing function:

```
plot(outtimes, fbDATA(outtimes), main="Forcing b by external data",
     type = "l", col=2, xlab="time (d)", ylab="b", ylim=c(0, 2e-8))
points(bDATA, col=1, pch=5)
```



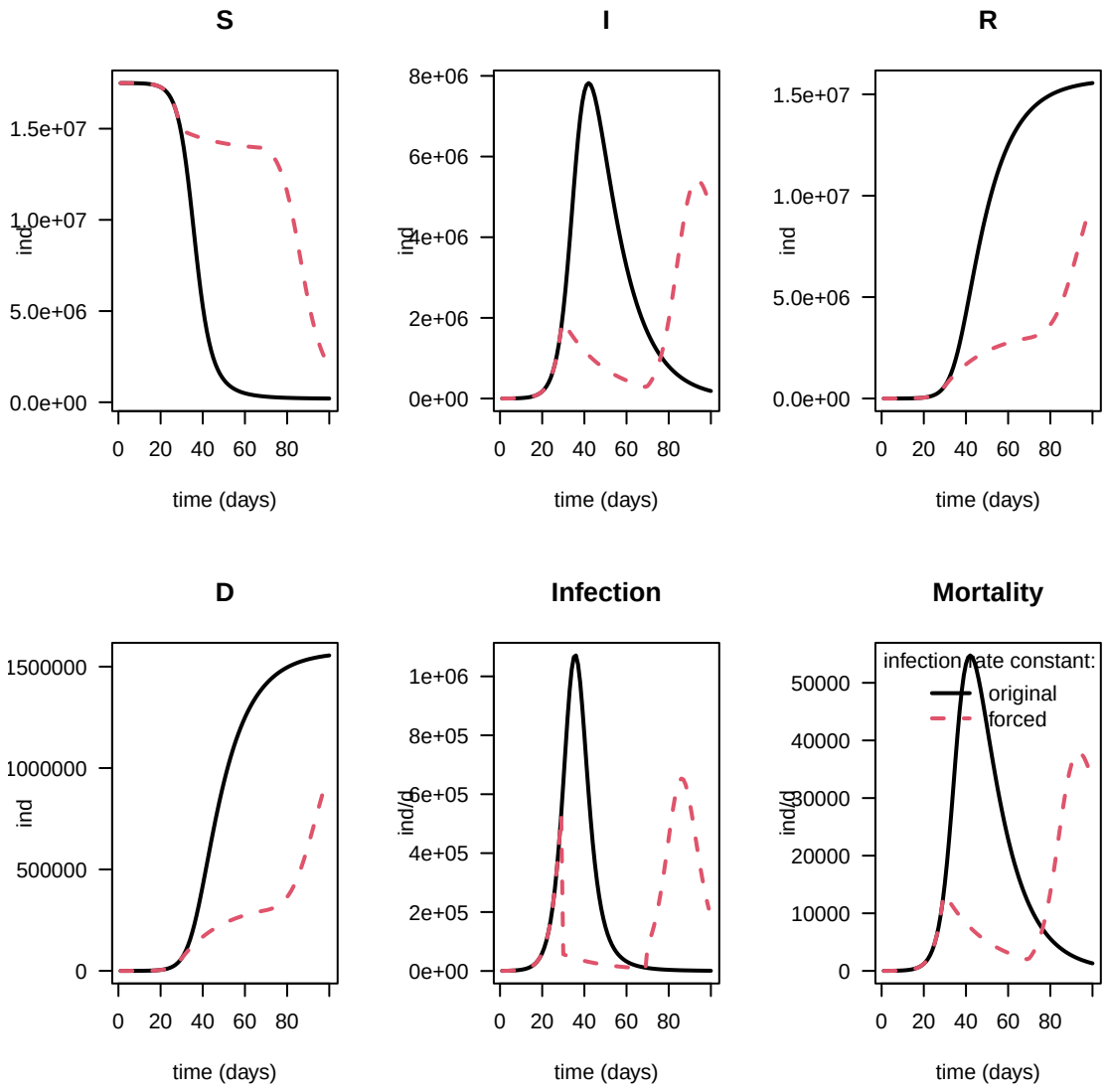
Model solution with a forcing function

```
require(deSolve)
# ode integrates the model
out2 <- ode(y=yini, parms=pars, func=SIRmodel2, times=outtimes,
            bDyn=fbDATA) # forcing function included
# plot the model output
plot(out, out2)
```



We plot both solutions in one graph:

```
plot(out, out2, xlab="time (days)", las=1, lwd=2,
     ylab=list("ind","ind","ind", "ind", "ind/d","ind/d"))
legend("topright", legend = c("original", "forced"),
       title="infection rate constant:",
       col=1:2, lwd=2, lty=1:2, bty="n")
```



References

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

Soetaert Karline (2009). rootSolve: Nonlinear root finding, equilibrium and steady-state analysis of ordinary differential equations. R-package version 1.6

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