EEMB 279 Project

Time Series

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A time series simulation of the model by Oliveira NM & Hilker FM (2010), Modelling disease introduction as biological control of invasive predators to preserve endangered prey, **Bulletin of Mathematical Biology**, 72:444-468.

In the case of this model, the authors introduced dimensionless parameters to simply the model and thus avoid making incorrect assumptions about unknown variables such as

$$\mu$$

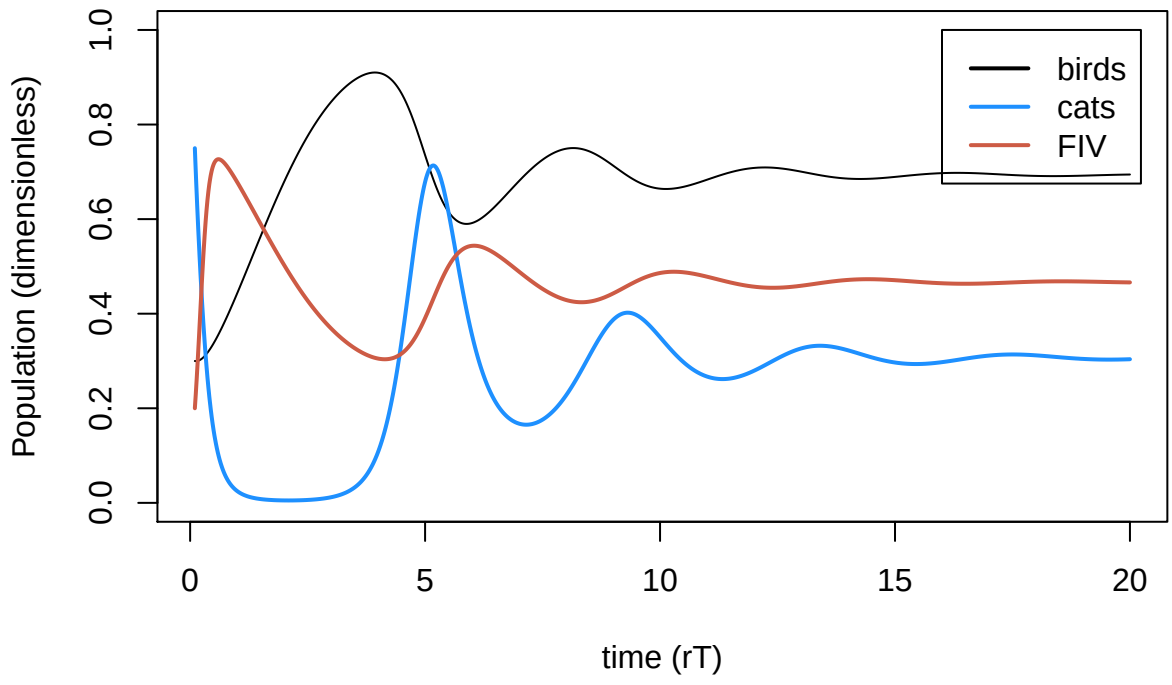
, the predation rate, and **K**, the bird population carrying capacity, as well as initial population sizes for birds, cats, and FIV.

Thus, a lot of our values below are classified as `NaN` as they are not applied in the model, but do exist.

```
##Variables
#N.v <- NaN    ## population size for victims (birds)
#N.p <- NaN    ## population size for predators (cats)
t.time.set <- seq(1, 200, length.out= 2000) ## time

##Parameter values##
#K <- NaN            # carrying capacity              (will be estimated from dimensionless parameters
#u <- NaN            # predation rate                 (will be estimated from dimensionless parameters
#beta.ma <- NaN      # contact rate for mass action   (will be estimated from dimensionless parameters

r.v <- 0.1          # per capita growth rate of birds in the model
a <- 0.03           # trophic conversion efficiency of cats
d.p <- 0.6          # natural per capita death rate of cats
beta.pm <- 1.5      # contact rate for proportionate mixing
delta <- 0.2        # virulence

#core equations
#B <- N.v/K
B.set <-seq(0, 1, length.out=20000)
#C <- N.p*u/r.v
t.set <- r.v*t.time.set

#dimensionless parameters
sigma.pm <- beta.pm/r.v
#sigma.pm.set <- seq(0,25, length.out = 20000)
#sigma.ma <- beta.ma * C/u
#sigma.ma.set<- seq(0, 250, length.out = 20000)

#e <- alpha*u*K/r.v
e <- 10
#e.set <- seq(0, 25, length.out = 20000)
m <- d.p/r.v
alpha <- delta/r.v
```

In this time series we selected a biologically relevant, yet random value for e (10 in this case), from the range provided by the authors of the study. We can produce a time series with different values of e. In this simulation, the disease is present at the beginning.

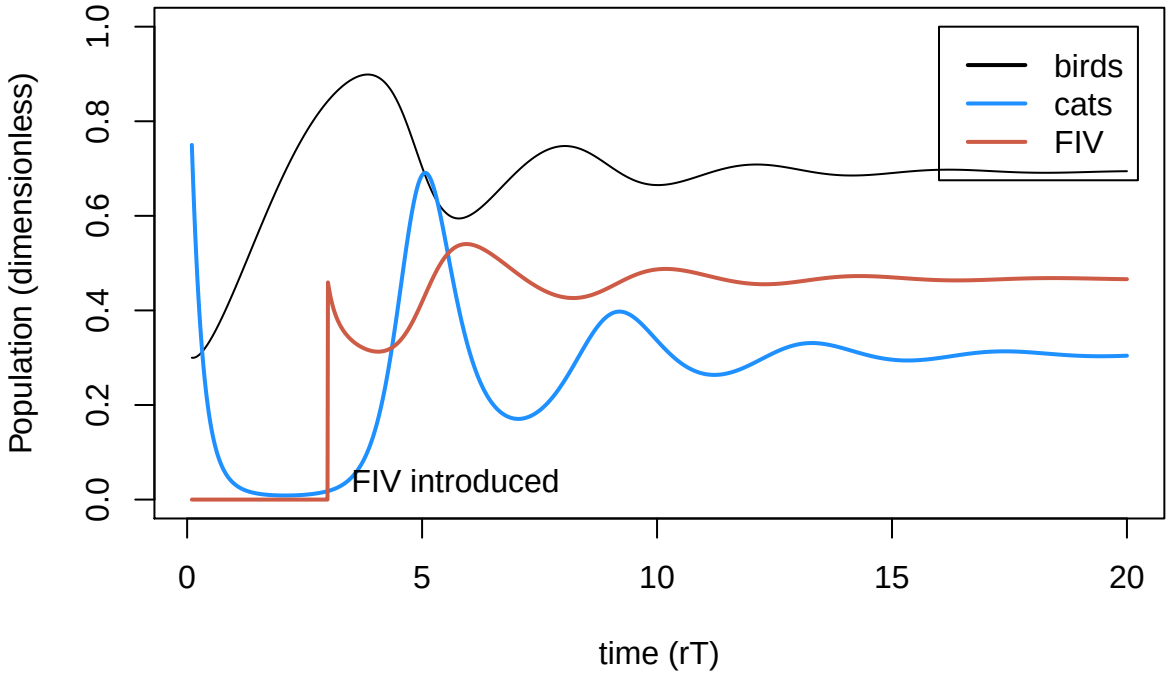
```
B.simu1 <- NaN*t.set
  B.simu1[1] <- .3
C.simu1 <- NaN*t.set
  C.simu1[1] <- .75
I.simu1 <- NaN*t.set
 I.simu1[1] <- 0.2

#for PM
for(i in 2:length(t.set)){

  dt <- t.set[i]-t.set[i-1]
  B <- B.simu1[i-1]
  C <- C.simu1[i-1]
  I <- I.simu1[i-1]

  dB <- (B*(1-B) -B*C) *dt
  dC <- (e*B*C - m*C - alpha*C*I)*dt
  dI <- (((sigma.pm - alpha)* (1-I) - e*B)*I) *dt

  B.simu1[i] <- B + dB
  C.simu1[i] <- C + dC
  I.simu1[i] <- I + dI
}


plot(t.set, B.simu1, type= "l", ylim= c(0, 1), ylab="Population (dimensionless)", xlab="time (rT)")
lines(t.set,C.simu1,lwd=2,col='dodgerblue')
lines(t.set, I.simu1, lwd = 2, col= "coral3")
legend(x=16,y=1, col = c("black","dodgerblue","coral3"), lty=1,lwd=2,legend = c("birds", "cats", "FIV"))
```



As was done in a time series in the study, there was a lag in the introduction of FIV to the cat population. In this case we introduced FIV at time step 3.

```
B.simu2 <- NaN*t.set
  B.simu2[1] <- .3
C.simu2 <- NaN*t.set
  C.simu2[1] <- .75
I.simu2 <- NaN*t.set
# I.simu2[1] <- 0
```

```
#for PM
for(i in 2:length(t.set)){

    if(t.set[i] < 3){I.simu2[i-1] <- 0 } else {
      if(t.set[i] == 3) {I.simu2[i-1] <- 0.2} else { I<- I.simu2[i-1]}}

  dt <- t.set[i]-t.set[i-1]
  B <- B.simu2[i-1]
  C <- C.simu2[i-1]
  #I.simu2[i-1]

  dB <- (B*(1-B) -B*C) *dt
  dC <- (e*B*C - m*C - alpha*C*I)*dt
  dI <- (((sigma.pm - alpha)* (1-I) - e*B)*I) *dt

  B.simu2[i] <- B + dB
  C.simu2[i] <- C + dC
  I.simu2[i] <- I + dI
}

plot(t.set, B.simu2, type= "l", ylim= c(0, 1), ylab="Population (dimensionless)", xlab="time (rT)")
lines(t.set,C.simu2,lwd=2,col='dodgerblue')
lines(t.set, I.simu2, lwd = 2, col= "coral3")
legend(x=16,y=1, col = c("black","dodgerblue","coral3"), lty=1,lwd=2,legend = c("birds", "cats", "FIV"))
text(x=3.5, y=0.04, adj=0, label="FIV introduced")
```


Population (dimensionless)
0.0
0.2
0.4
0.6
0.8
1.0
0
5
10
15
20
time (rT)
birds
cats
FIV
FIV introduced