BIOS13 - Question 2

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a Equilibrium protein concentration

Solving $\frac{dP}{dt} = 0$ to find the equilibrium:

$$a - bP = 0$$

$$\Leftrightarrow P = \frac{a}{b}$$

The equilibrium protein concentration in the cell is $P = \frac{a}{b}$ (b $\neq 0$)

b Stable equilibrium

Firstly to show this is a stable equilibirum, we need to find the derivative of $f(P) = a - bP$

$$f'(P) = -b$$

Since "leaking rate" could not be a negative number because it will mean that the protein instead of leaking out it goes inside the cell which is not the case here, we can assume that b is always a positive number, which make the derivative $f'(P)$ is always negative. Therefore this is an stable equilibrium.

c Calculate the equilibrium (P^*, Q^*)

$$\begin{cases} \frac{dP}{dt} = a - bP - cPQ & (1) \\ \frac{dQ}{dt} = rP - bQ & (2) \end{cases}$$

We need to find value of P and Q when both equation (1) and (2) are equal to 0 to find the equilibrium. From equation (1), we can present the value of P as Q:

$$a - bP - cPQ = 0$$

$$\Leftrightarrow P(b + cQ) = a$$

$$\Leftrightarrow P = \frac{a}{b + cQ} \quad (3)$$

Substitute the above value of P to equation (2), we get:

$$\frac{ra}{b+cQ} - bQ = 0$$

$$\Leftrightarrow bcQ^2 + b^2Q - ra = 0$$

Solve the above equation for Q, first calculate the Δ:

$$\Delta = b^4 + 4bcra$$

Assuming a,b,c,r are positive numbers, Δ is greater than 0, thus having two distinct real roots:

$$Q_1 = \frac{-b^2 - \sqrt{b^4 + 4bcra}}{2bc}$$

$$Q_2 = \frac{-b^2 + \sqrt{b^4 + 4bcra}}{2bc}$$

Since Q can not be a negative number (the value of concentration can not be smaller 0), and Q_1 will result in a negative number. Q_2 is always a positive number since b^2 is smaller than $\sqrt{b^4 + 4bcra}$. We reject Q_1 and accept Q_2 as the only answer. Substitute value of Q to (3), we have P:

$$P^* = \frac{a}{b + c\frac{-b^2+\sqrt{b^4+4bcra}}{2bc}}$$

$$\Leftrightarrow P^* = \frac{2ab}{b^2 + \sqrt{b^4 + 4bcra}}$$

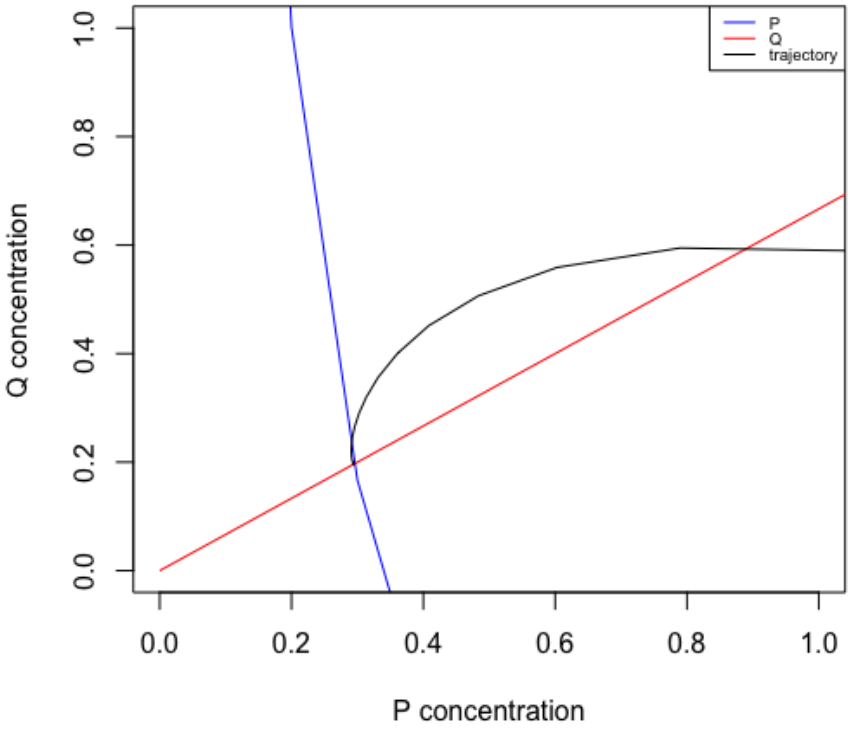
d Coordinate axes

The coordinate axes of this phase are P and Q.

e R script

```
rm(list=ls())
LV_isoclines <- function(r,a,b,c) {
  # Protein P isocline (dP/dt=0)
  fP = function(x) {
    a/(c*x)-b/c
  }
  p = seq(0,20,by=0.1)

  # Protein Q isocline (dQ/dt=0)
  fQ = function(x) {
    r*x/b
  }
```

```
  q = seq(0,20,by=0.1)

  # Plotting the isocline:
  plot(p,fP(p),type='l',col='blue', xlab="P concentration",
       ylab="Q concentration",xlim=c(0,1),ylim=c(0,1))
  lines(q,fQ(q),col='red')
}

LV_sys <- function(t, pq, P) {
  # extract vector content:
  p <- pq[1]
  q <- pq[2]

  # calculate the two growth rates:
  dpdt <- P$a - P$b*p - P$c*p*q
  dqdt <- P$r*p - P$b*q

  # the result as a vector in a list
  return(list(c(dpdt, dqdt )))
}

library(deSolve)

# set up a vector of time-points for the output:
timevec <- seq(0,20,by=0.1)

# list of parameters:
P <- list(r=2,a=1,b=3,c=2)
# initial protein concentration
pq0 <- c(p=1.5,q=0.5)

# call the ode function to solve the differential equation:
out <- ode( y = pq0, func = LV_sys, times = timevec, parms = P)
time <- out[,'time']
p <- out[,'p']
q <- out[,'q']

# next the phase plane, starting with the isoclines:
LV_isoclines(P$r,P$a,P$b,P$c)

# add the trajectory and legend:
lines(out[,'p'],out[,'q'])
legend("topright", legend = c("P", "Q","trajectory"),
       lwd = 1, col = c("blue", "red",'black'), cex=0.6)
```


P
Q
trajectory
Q concentration
P concentration
0.0
0.2
0.4
0.6
0.8
1.0