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BI 472  
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## 7.1

Beginning with the Lotka-Volterra model equations:

$$\frac{dN_1}{dt} = r_1 N_1 (1 - N_1 - \alpha_{12} N_2)$$

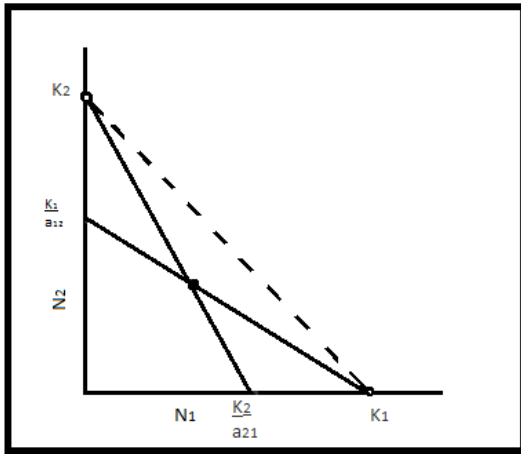
$$\frac{dN_2}{dt} = r_2 N_2 (1 - N_2 - \alpha_{21} N_1)$$

We add the effect of the experimenter on the populations as “ $-mN_i$ ”:

$$\frac{dN_1}{dt} = r_1 N_1 (1 - N_1 - \alpha_{12} N_2) - mN_1$$

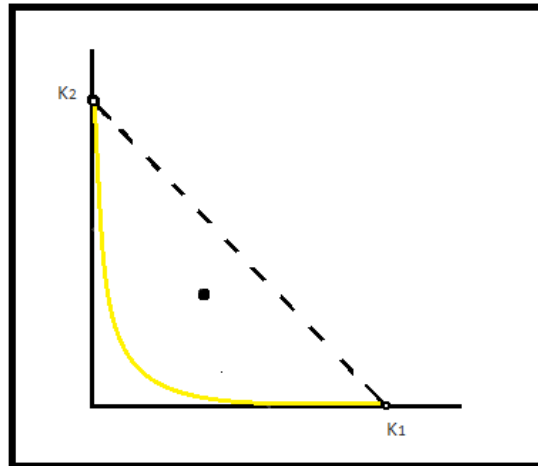
$$\frac{dN_2}{dt} = r_2 N_2 (1 - N_2 - \alpha_{21} N_1) - mN_2$$

In the experiment the  $-mN_i$  represents the removal of a portion of the total population and is effectively a simulated culling or extinction (possibly like a forest/wild fire).



This is the original organization of the two species where one species will always outcompete the other. Which one wins depends on where you start (equilibrium is unstable). This represents a competitive relationship where coexistence is never possible.

For the Lotka-Volterra model the point of equilibrium exists under the connector line (shown as ---) and so any real meta population with such organization must be explained with a curved isocline (in yellow) if the species are actually able to coexist.



That is, unless you add a culling element like “ $-mN_i$ ”, you can maintain the point of equilibrium by artificially subtracting those individuals from the population that would otherwise outcompete or cause a disturbance to the equilibrium. ‘ $m$ ’ seems to represent an entire function in and of itself where ‘ $m$ ’ is based off of the concurrent values of  $N_1$  and  $N_2$ . There would likely have to be an  $m_1$  and  $m_2$  as the  $m_1$  would increase as  $N_1$  increases and  $N_2$  decreases and  $m_2$  would increase as  $N_2$  increases and  $N_1$  decreases. As such this would mean the closer you get to equilibrium the closer  $m_i$  would get to 0.

7.2

a)

$$\begin{aligned}
 \frac{dp_1}{dt} &= m_1 p_1 (1 - p_1) - e p_1 \\
 0 &= m_1 p_1 (1 - p_1) - e p_1 \\
 0 &= p_1 (m_1 (1 - p_1) - e) \\
 p_1 = 0 \text{ and } 0 &= m_1 (1 - p_1) - e \\
 e &= m_1 (1 - p_1) \\
 \frac{e}{m_1} &= (1 - p_1) \\
 p_1 &= 1 - \frac{e}{m_1}
 \end{aligned}$$

Since in this model  $m_1$  is the colonization rate and  $e$  is the extinction rate it makes a lot of sense that in order for the  $p_1$  to stay positive that the colonization rate must be larger than the extinction rate.

b)

$$\begin{aligned}
 \frac{dp_2}{dt} &= m_2 p_2 (1 - p_1 - p_2) - m_1 p_1 p_2 - e p_2 \\
 \frac{dp_2}{dt} &= m_2 p_2 \left( 1 - 1 - \frac{e}{m_1} - p_2 \right) - m_1 p_2 \left( 1 - \frac{e}{m_1} \right) - e p_2 \\
 0 &= m_2 p_2 \left( 1 - 1 - \frac{e}{m_1} - p_2 \right) - m_1 p_2 \left( 1 - \frac{e}{m_1} \right) - e p_2 \\
 0 &= m_2 p_2 \left( -\frac{e}{m_1} - p_2 \right) - m_1 p_2 - e p_2 - e p_2 \\
 0 &= p_2 \left( m_2 \left( -\frac{e}{m_1} - p_2 \right) - m_1 - e - e \right) \\
 p_2 = 0 \text{ or } 0 &= m_2 \left( -\frac{e}{m_1} - p_2 \right) - m_1 - 2e \\
 0 &= \left( -\frac{em_2}{m_1} - p_2 m_2 \right) - m_1 - 2e \\
 p_2 m_2 &= -\frac{em_2}{m_1} - m_1 - 2e \\
 p_2 &= -\frac{e}{m_1} - \frac{m_1}{m_2} - \frac{2e}{m_2}
 \end{aligned}$$

Based off of this model and the way that I solved for the equilibrium, it seems that  $p_2$  will never survive as it will always be negative. At equilibrium,  $p_1$  requires the colonization rate to be greater than the rate of extinction and  $p_2$  would require a negative value for migration or extinction which I'm not sure is entirely possible. The way I initially solved for it, the model seems to require that  $m_1$  be much greater than  $m_2$  and  $e$  in order for  $p_2$  to remain positive. It might be possible that in order for both to be positive that  $m_1$  must be negative and the absolute value would have to be much smaller than that of  $m_2$ .

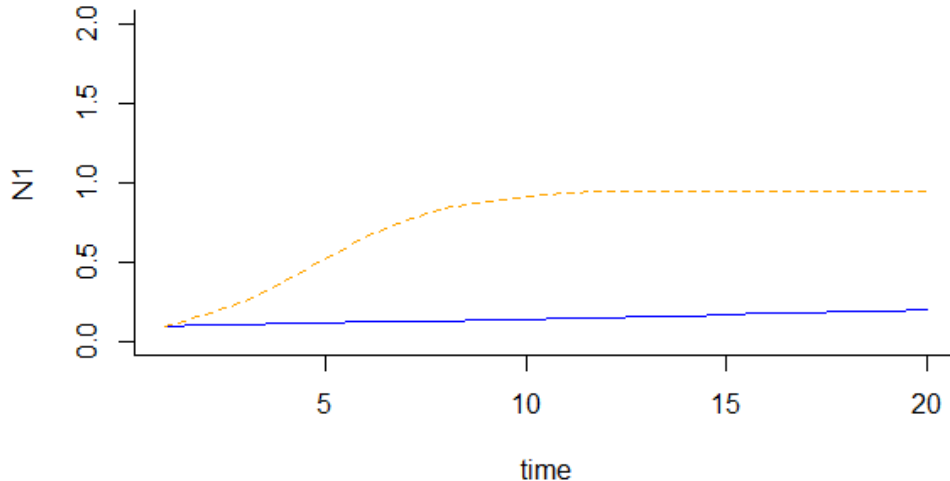
#### 7.4

I think its most interesting to approach the Lotka-Volterra model with an open mind. It is not a rigid or specific equation like that of a physical law or conversion. It is a mathematical representation of species interactions and conveys the dynamics of a system. It is a building block that can be used to explain the dynamics of real data, and can be used to fit to a model. One specific idea I had as an alteration to the model is to assume that the  $\alpha_{ii}$  of an organism is not just 1. I believe this is applicable in an experiment where the next generation has varying adaptations that cause their  $\alpha_{ii}$  to be greater than or less than 1. If the  $\alpha_{ii}$  of the newest generation is greater than 1 they are better adapted to a subset of conditions and if  $\alpha_{ii}$  is less than 1 it is less adapted. This model could include another species but would be different as the new generation could use all the same resources as the previous and the competitive species would only use one or a few.

$\alpha_{ii}$  in and of itself could be a function derived from changes in resources as well as possible mutualistic effects that occur even between two species that otherwise compete. Or, in the same vein, increase or decrease  $\alpha_{ii}$  based on density dependent effect of a species.

2.

```
comp <- function(t, y, p) {  
  N1 <- y[1]  
  N2 <- y[2]  
  with(as.list(p), {  
    dN1.dt <- (r1 * N1 / K1) * (1 - N1 - a12 * N2)  
    dN2.dt <- (r2 * N2 / K2) * (1 - N2 - a21 * N1)  
    return(list(c(dN1.dt, dN2.dt)))  
  })  
}  
  
#Initial experiment with time frame of 20 days  
  
p <- c('r1' = 0.1, 'K1' = 2, 'r2' = 0.6, 'K2' = 1,  
      'a12' = 0.15,  
      'a21' = 0.3)  
y0 <- c('N1' = 0.1, 'N2' = 0.1)  
t <- 1:20  
  
sim.20 <- ode(y = y0, times = t, func = comp, parms = p, method = 'lsoda')  
sim.20 <- as.data.frame(sim.20)  
  
plot(N1 ~ time, data = sim.20, type = 'l', col = 'blue', ylim = c(0, 2), bty = 'l')  
points(N2 ~ time, data = sim.20, type = 'l', col = 'orange', lty = 2)
```



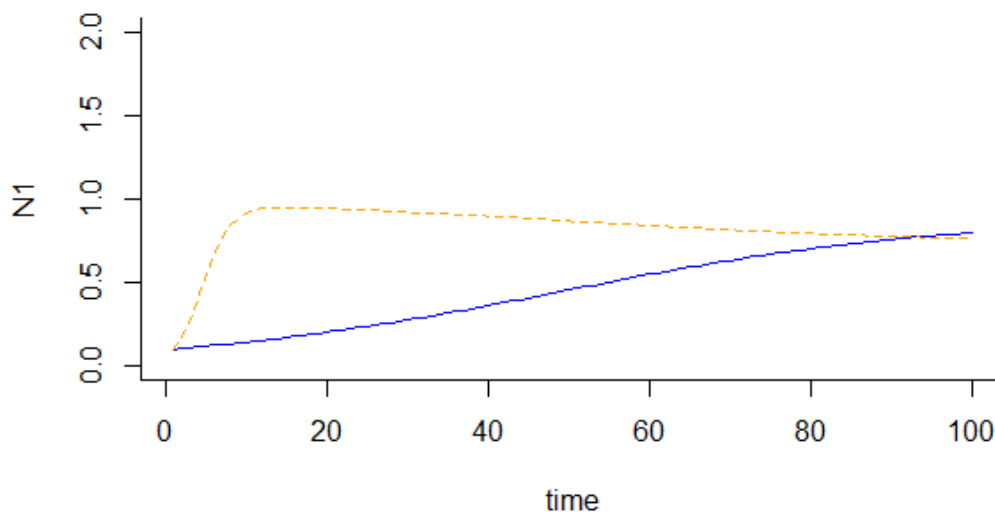
According to the initial experiment of 20 days it appears that the species 2 outcompeted species 1 by growing much more quickly over the first 8 or so days. At the end of the 20 days there were at least 4 times as many of species 2!

```
##If we have 100 days

t.100 <- 1:100

sim.100 <- ode(y = y0, times = t.100, func = comp, parms = p, method =
'lsoda')
sim.100 <- as.data.frame(sim.100)

plot(N1 ~ time, data = sim.100, type = 'l', col = 'blue', ylim = c(0, 2), bty
= 'l')
points(N2 ~ time, data = sim.100, type = 'l', col = 'orange', lty = 2)
```



From this second experiment where the time course was 100 days we got drastically different results. It appears that the two species took around 95+ days to reach equilibrium/coexistence. An interesting aspect of these models that we haven't really looked at yet is time scale and how to calculate the amount of time it takes for a species/system to reach equilibrium. Time, so far, has been stuck under the derivative of the equations and models we've been looking at. Time scale is a huge part of experimentation as for the most part we must be patient. Results, especially in microbiology do not come instantly.

### 3. Microbiome response to global change.