

**Collin McElroy**

**4/14/16**

**HW #2**

## HW #2

4.1  $\frac{dN}{dt} = rN \left[ 1 - \left( \frac{N}{K} \right)^\theta \right]$

a)  $0 = r \cdot N \left[ 1 - \left( \frac{N}{K} \right)^\theta \right]$   
 $0 = 1 - \left( \frac{N}{K} \right)^\theta$   
 $0 = 1 - \frac{N^\theta}{K^\theta}$   
 $1 = \frac{N^\theta}{K^\theta}$   
 $K^\theta = N^\theta$

$K = N$

b) Arbitrary Designations  $r = 0.1$   $N = 10$   $K = 100$  Changes [plot with continuous population values]

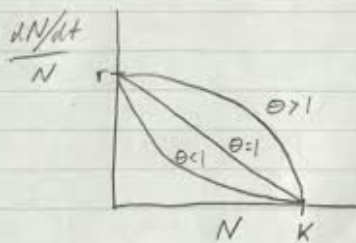
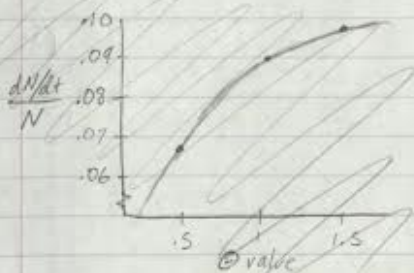
$\frac{dN/dt}{N} = r \left[ 1 - \left( \frac{N}{K} \right)^\theta \right] = (0.1) \left[ 1 - \left( \frac{10}{100} \right)^\theta \right]$

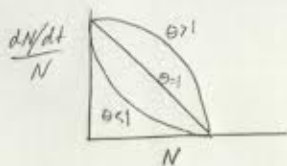
when  $\theta = 1.5$   $(0.1) \left[ 1 - (0.1)^{1.5} \right] = \frac{dN/dt}{N} = 0.097$

when  $\theta = 1$   $(0.1) \left[ 1 - (0.1)^1 \right] = \frac{dN/dt}{N} = 0.090$

when  $\theta = 0.5$   $(0.1) \left[ 1 - (0.1)^{0.5} \right] = \frac{dN/dt}{N} = 0.068$

The per-capita growth rate is positively correlated with a greater  $\theta$  value when the population is below the carrying capacity.





c) This model is superior to the logistic model because it takes into account the change in growth rate due to population abundance. When theta is greater than one, the growth rate only becomes density dependent at high population abundance. When theta is less than one, the growth rate becomes density dependent at much lower population abundance. When theta equals one, the equation directly follows the normal logistic model. One example of a species that falls under  $\theta > 1$ , (any 'K' selected species) would be the Blue Whale. One example of a species that falls under  $\theta < 1$ , (any 'r' selected species) would be any ant species. One example of a species that would fall under  $\theta = 1$  would be any song bird, such as the Tit Mouse.

4.3 Allee effect  $\frac{dN}{dt} = r \cdot N(N-a) \left[ 1 - \left( \frac{N}{K} \right) \right]$   $a = \text{Threshold Population}$

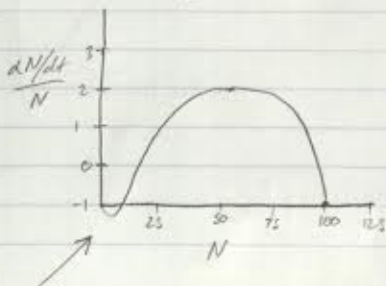
a)  $0 = r \cdot N(N-a) \left[ 1 - \left( \frac{N}{K} \right) \right]$   
 $0 = (N-a) \left[ 1 - \left( \frac{N}{K} \right) \right]$

$N = a$   
 $N = K$

b) Stability?

c) Graph  $\frac{dN/dt}{N}$  vs  $N$   $r = 0.1$   $K = 100$   $a = 10$

$\frac{dN/dt}{N} = r(N-a) \left[ 1 - \left( \frac{N}{K} \right) \right]$   $N \text{ from } 0 \text{ to } 120$



D) The allee effect growth model is different from the logistic growth model because it takes into account the negative effect of small population size. This model would be useful when looking at species that either have small population sizes or species with low genetic diversity (problems with inbreeding). One example species that could fall under the allee effect model is the Florida Panther.

```
log.growth <- function(t, y, p) {
  N <- y[1]
  with(as.list(p), {
    dN.dt <- r * N * (1 - (N / K)^theta)
    return(list(dN.dt))
  })
}
```

```
N<-runif(1,min=0.01,max=0.1)
```

```
p<-c('r'=0.25,'K'=100,'theta'=1)
```

```
t<-1:100
```

```
y<-c('N'=N)
```

```
sim <- ode(y = y, times = t, func = log.growth, parms = p, method = 'lsoda')
```

```
sim <- as.data.frame(sim)
```

```
plot(N ~ t, data = sim, type = 'l', lwd = 3, bty = 'l', col = 'purple')
```

```
p2<-c('r'=0.25,'K'=50,'theta'=1)
```

```
sim2 <- ode(y = y, times = t, func = log.growth, parms = p2, method = 'lsoda')
```

```
sim2<-as.data.frame(sim2)
```

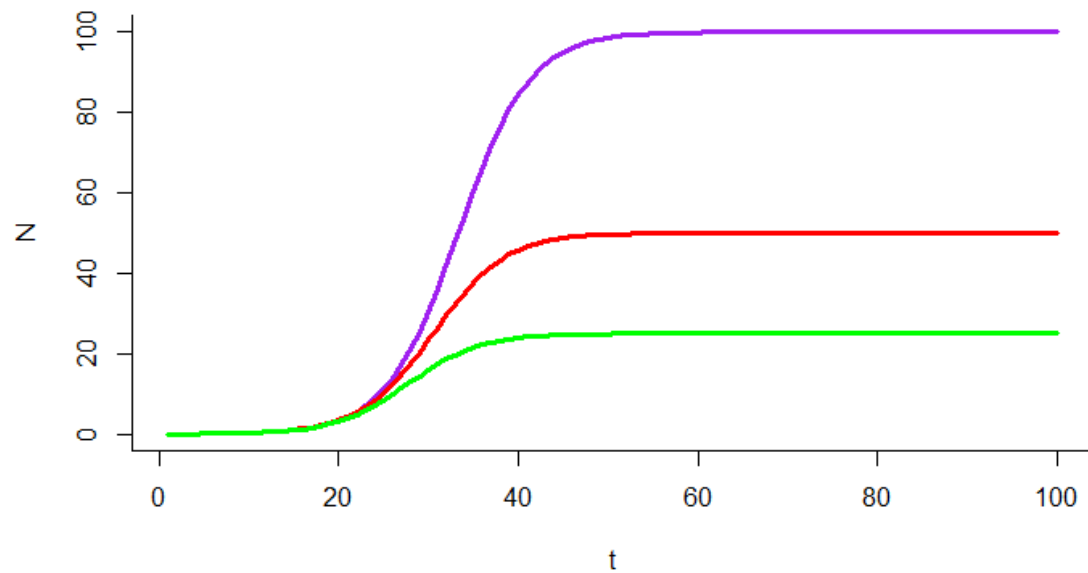
```
lines(N ~ t, data = sim2, type = 'l', lwd = 3, bty = 'l', col = 'red')
```

```
p3<-c('r'=0.25,'K'=25,'theta'=1)
```

```
sim3<-ode(y = y, times = t, func = log.growth, parms = p3, method = 'lsoda')
```

```
sim3<-as.data.frame(sim3)
```

```
lines(N ~ t, data = sim3, type = 'l', lwd = 3, bty = 'l', col = 'green')
```



**2.b)**

```
sim$deriv<-c(diff(sim$N),NA)
```

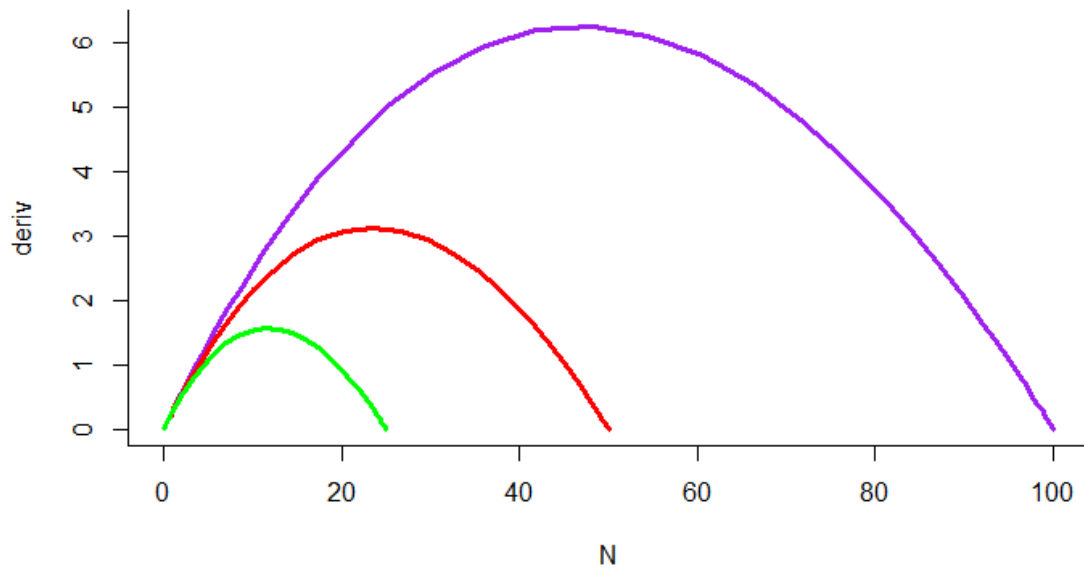
```
plot(deriv ~ N, data = sim, type = 'l', lwd = 3, col = 'purple', bty = 'l')
```

```
sim2$deriv<-c(diff(sim2$N),NA)
```

```
lines(deriv ~ N, data = sim2, type = 'l', lwd = 3, col = 'red', bty = 'l')
```

```
sim3$deriv<-c(diff(sim3$N),NA)
```

```
lines(deriv ~ N, data = sim3, type = 'l', lwd = 3 , col = 'green', bty = 'l')
```



**2.c)**

```
Max.rate.1<-max(sim$deriv, na.rm = TRUE)
```

```
Max.rate.2<-max(sim2$deriv, na.rm = TRUE)
```

```
Max.rate.3<-max(sim3$deriv, na.rm = TRUE)
```

```
which(sim$deriv == max(sim$deriv, na.rm = TRUE))
```

```
which(sim2$deriv == max(sim2$deriv, na.rm = TRUE))
```

```
which(sim3$deriv == max(sim3$deriv, na.rm = TRUE))
```

```
install.packages('deSolve')
```

```
library(deSolve)
```

```
K/2
```

```
N.max.rate.1<-50
```

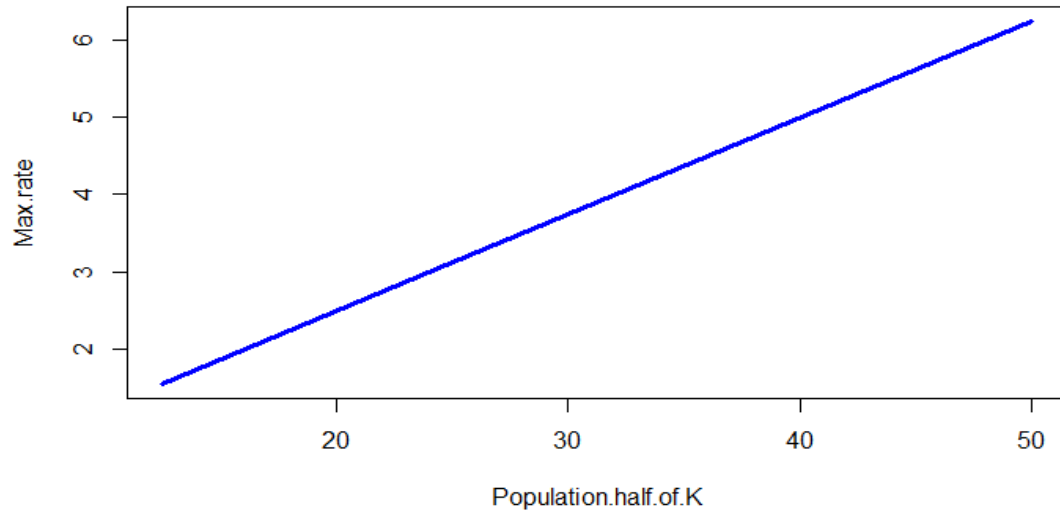
```
N.max.rate.2<-25
```

```
N.max.rate.3<-12.5
```

```
Population.half.of.K<-c(50,25,12.5)
```

```
Max.rate<-c(Max.rate.1,Max.rate.2,Max.rate.3)
```

```
plot(Population.half.of.K,Max.rate, col="blue",lwd=3,type='l')
```



**3)**

```
log.growth.N <- function(t, y, p) {
```

```
  N <- y[1]
```



```

with(as.list(p), {
  dN.dt <- r * (1 - (N / K)^theta)
  return(list(dN.dt))
})
}

r<-0.1
K<-100
N<-50
theta.A<-0.5
theta.B<-1.0
theta.C<-1.8

Rate.A<-(r*(1-(N/K)^(theta.A)))
Rate.B<-(r*(1-(N/K)^(theta.B)))
Rate.C<-(r*(1-(N/K)^(theta.C)))

Per.Capita.Growth.Rate<-c(Rate.A,Rate.B,Rate.C)
Theta.Value<-c(theta.A,theta.B,theta.C)

plot(Per.Capita.Growth.Rate~Theta.Value,col="purple",type='l',lwd=3)

```

Species 'C' will have the highest population abundance because  
it has the highest growth rate.

