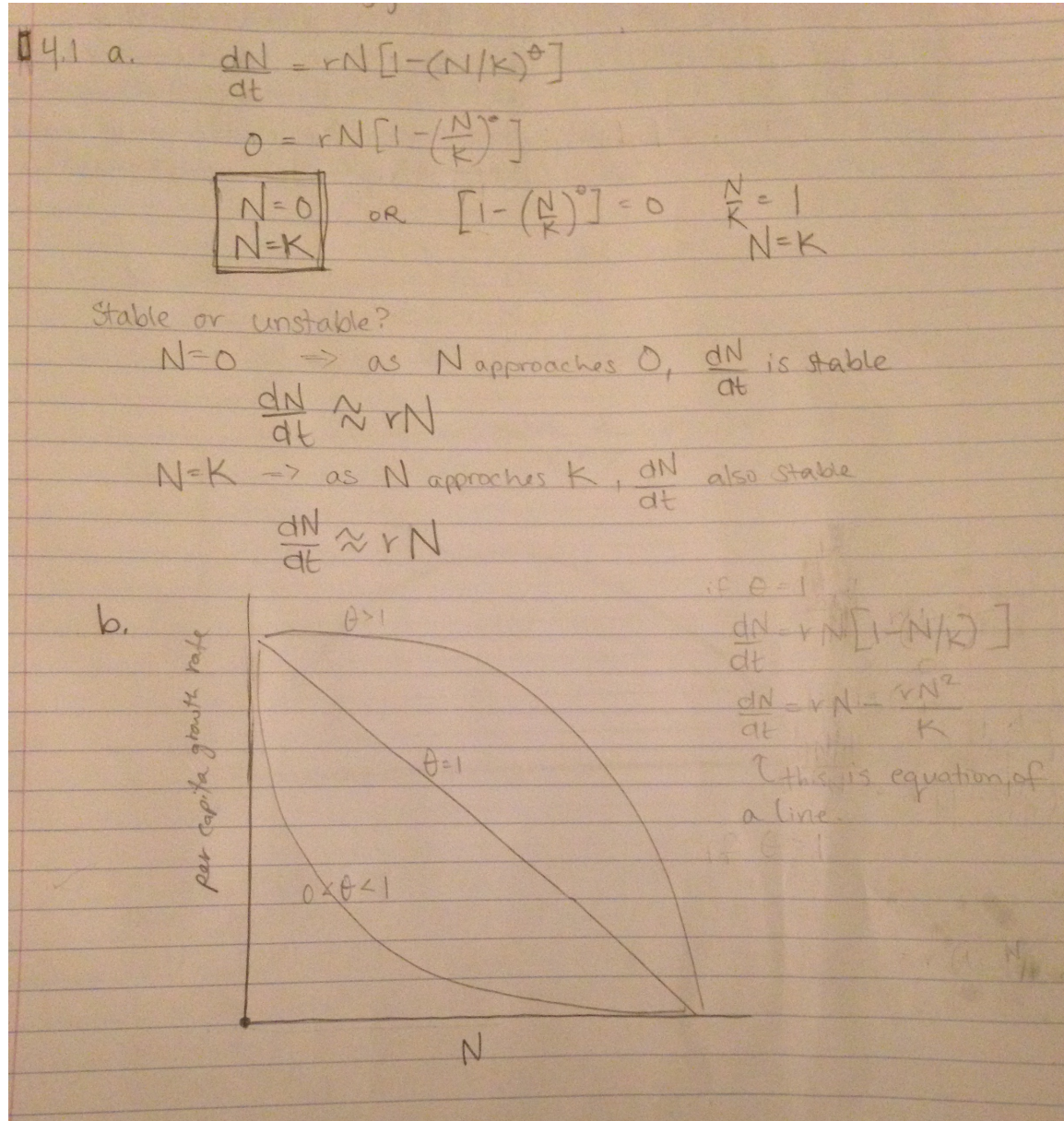


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 BI471 HW 2

4.1:

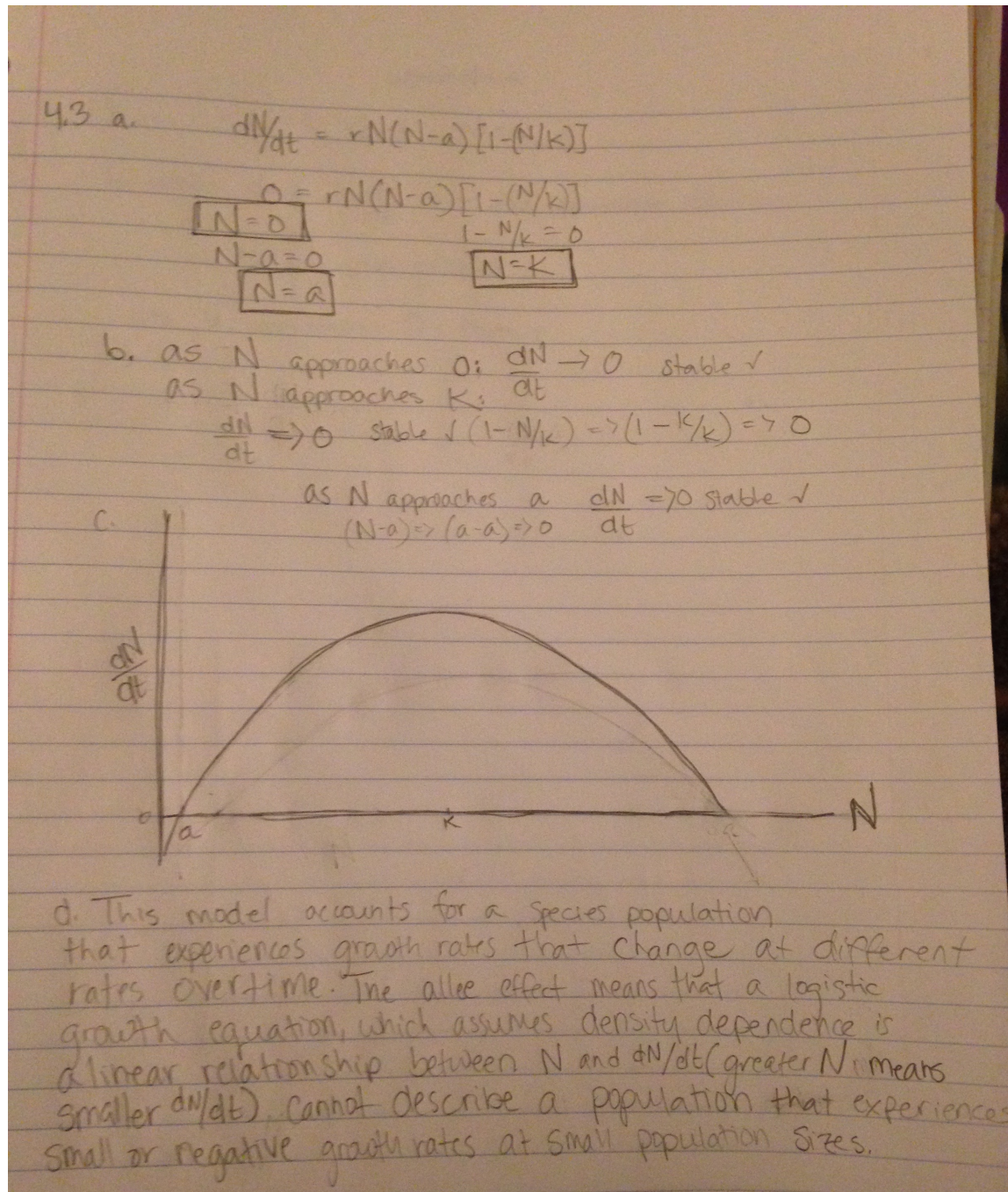


c. This model takes into account the degree to which a species population growth rate is dependent on population density. While the logistic growth equation assumes that at any  $N$  the growth rate is equally dependent on the population size. For instance, for organisms with a  $\theta$  between 0 and 1, the growth rate of small populations is greatly changed by small changes in  $N$ . For a larger population of this same species, a small increase in  $N$  results in a small decrease in growth rate. For species with a  $\theta$  greater than 1, the reverse relationship is true. Small populations experience little change in growth rate as



they grow, while large populations experience a sharp decline in their growth rate as  $N$  increases. The theta model introduces more complexity to the logistic model in that it can model a species population whose growth rate is changing at multiple different rates over time.

4.3:



**2a.**

```
## write logistic growth equation by editing exp.growth with  $*(1 - (N/K))$ 
```

```
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))
  })
}
```

```
## set up parameters, run if selects number at random. runif wants # of # you want, min
and max
```

```
p <- c('r'= 0.25, 'K'= 100, 'theta' = 1)
y0 <- c('N'= runif(1, min= .01, max = .1))
t <- 1:100
```

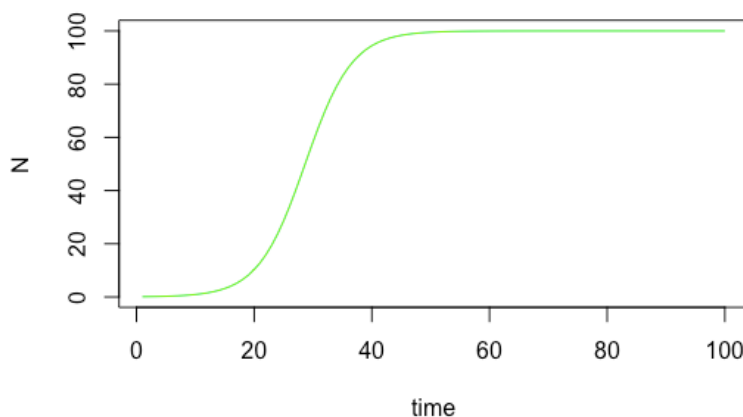
```
sim <- ode(y=y0, times=t, func = log.growth, parms = p, method = 'lsoda')
```

```
## Then I enter simulated function into data frame
```

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

```
## plot simulation
```

```
plot(N~ time, data = sim, type = 'l', col = 'green')
```

**2b.**

```
## Here I simulate the model with K = 25
```

```
p.2 <- c('r'=.25, 'K'= 25)
```

```
sim.2 <- ode(y=y0, times = t, func= log.growth, parms = p.2, method = 'lsoda')
```

```
sim.2 <- as.data.frame(sim.2)
```

```
## next I simulate the model with K = 50
```

```
p.3 <- c('r'=.25, 'K'= 50)
```

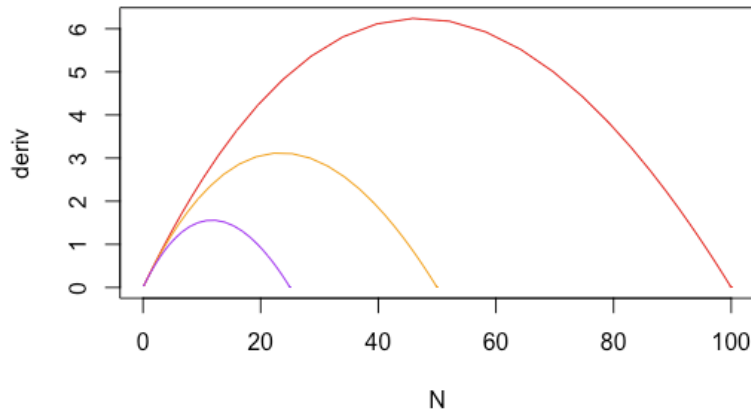
```
sim.3 <- ode(y=y0, times = t, func = log.growth, parms = p.3, method = 'lsoda')
sim.3 <- as.data.frame(sim.3)
```

## Next I will compute the population growth rates (derivatives) for model simulations 1, 2, and 3, and then add these values to my sim data frame.

```
sim$deriv <- c(diff(sim$N), NA)
sim.2$deriv <- c(diff(sim.2$N), NA)
sim.3$deriv <- c(diff(sim.3$N), NA)
```

## Here I graph the population growth rates calculated above vs. population abundance (N) on the same plot

```
plot(deriv~N, data = sim, type = 'l', col= 'red')
points(deriv~N, data = sim.3, type = 'l', col= 'orange')
points(deriv~N, data = sim.2, type = 'l', col= 'purple')
```



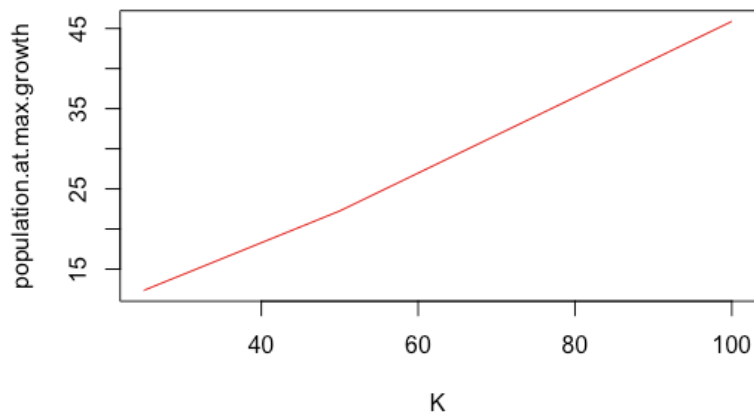
## 2c.

```
Nmax <- sim$N [which(sim$deriv == max(sim$deriv, na.rm =TRUE))]
Nmax.2 <- sim.2$N [which(sim.2$deriv == max(sim.2$deriv, na.rm =TRUE))]
Nmax.3 <- sim.3$N [which(sim.3$deriv == max(sim.3$deriv, na.rm =TRUE))]
```

#I then assign the values for population abundance at max growth to a vector named Nmax, and assign the 25, 50, and 100 values to a vector named K, and then plot Nmax values vs. the corresponding K values.

```
population.at.max.growth <- c(Nmax, Nmax.3, Nmax.2)
K <- c(100,50,25)
```

```
plot(population.at.max.growth~K, type = 'l', col= 'red')
```



3.

```
## write logistic growth equation
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))
  })
}
```

# using log.growth I simulate this model for a defined parameter set.

```
p.A <- c('r' = .25, 'K' = 100, 'theta' = .5)
y0 <- c('N' = .05)
t <- 1:100
```

```
sim.A <- ode(y = y0, times = t, func = log.growth, parms = p.A, method = 'lsoda')
sim.A <- as.data.frame(sim.A)
```

#then I run a simulation for fish population B with new parameters (just a different theta value)

```
p.B <- c('r' = .25, 'K' = 100, 'theta' = 1)
```

```
sim.B <- ode(y = y0, times = t, func = log.growth, parms = p.B, method = 'lsoda')
sim.B <- as.data.frame(sim.B)
```

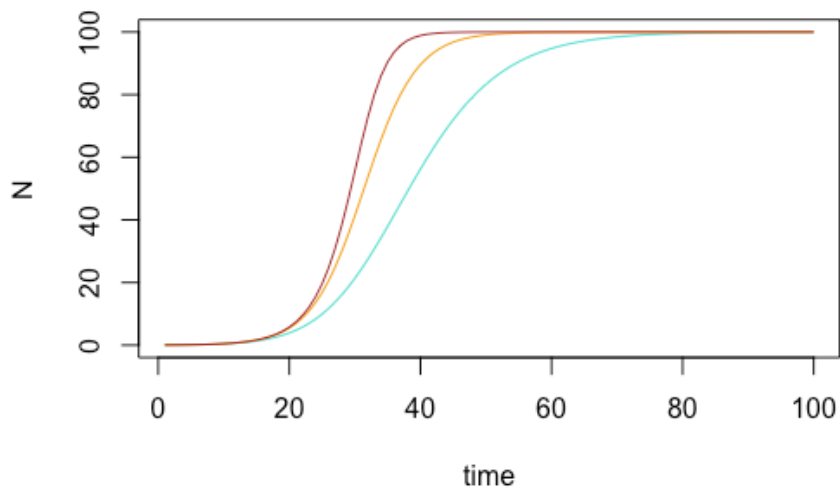
# and then do the same for population C

```
p.C <- c('r' = .25, 'K' = 100, 'theta' = 1.8)
```

```
sim.C <- ode(y = y0, times = t, func = log.growth, parms = p.C, method = 'lsoda')
sim.C <- as.data.frame(sim.C)
```

```
max(sim.A$N, na.rm=TRUE)
max(sim.B$N, na.rm=TRUE)
max(sim.C$N, na.rm=TRUE)
```

```
plot(N~time, data = sim.A, type = 'l', col = 'turquoise')
points(N~time, data = sim.B, type = 'l', col = 'orange')
points(N~time, data = sim.C, type = 'l', col = 'brown')
```



Species B and C are both maintained at 100 individuals, however species C reaches its maximum abundance faster than either A or B.