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BI471: Population Ecology
HW#1

1.

$$\frac{\ln{(N_t/N_0)}}{r} = t$$

If $N_0 = 10$, r = .1, and $N_t = 100$ then:

$$\frac{\ln{(\frac{100}{10})}}{.1} = t = \mathbf{23.03\ days}$$

$N_t = 1000$

$$\frac{\ln{(\frac{1000}{10})}}{.1} = t = \mathbf{46.05\ days}$$

$N_t = 1\times10^8$

$$\frac{\ln{(\frac{1\times10^8}{10})}}{.1} = t = \mathbf{161.2\ days}$$

$N_t = 1\times10^{11}$

$$\frac{\ln{(\frac{1\times10^{11}}{10})}}{.1} = t = \mathbf{230.3\ days}$$

2.

$$N_t = 2N_0 \quad t = 50yrs$$

$$\frac{\ln{(2N_0/N_0)}}{t} = r$$

$$\frac{\ln{(2)}}{50} = r$$

$$\boldsymbol{r} = \textbf{.01386 people/day}$$

$$N_0 = 6.9\times10^9 \quad N_t = ? \quad t = 2050 - 2009 = 41yrs$$

$$N_t = N_0e^{rt}$$

$$N_t = (6.9\times10^9)e^{(\mathbf{.01386})(41)}$$

$$\boldsymbol{N_t} = \mathbf{12.18} \times\mathbf{10^9}\ \textbf{people}$$

3.

$$b - d = .12$$
$$\lambda = 1 + .12 = 1.12$$
$$N_T = N_0\lambda^T$$
$$2N_0 = N_0 1.12^T$$
$$\ln(2) + \ln(N_0) = \ln(N_0) + T\ln(1.12)$$
$$\ln(2) = \mathrm{T}\ln(1.12)$$
$$T = \frac{\ln(2)}{\ln(2.12)}$$

$$\boldsymbol{T = 6.12yrs}$$

4. Given certain standards of food and medical care in Eugene, most deaths are probably related to old-age, or diseases associated with aging. Another major cause of death might be diet related, such as heart disease. However, none of these causes of death are density-dependent. The death rate of elderly individuals in a high density population is not likely to be higher than that of elderly individuals in low density populations.

One mechanism that might introduce density dependence could be disease. If a specific pathogen is transmitted by close human-human contact a population with greater density might experience greater infection rates and as a result, greater death rates. Another similar mechanism could be competition for resources. High density human populations could exceed the carrying capacity of agricultural land and run into food shortages. A third mechanism could be the lack of space for a high density population to grow into. There could simply be not enough space for new dwellings in a very high-density human population.

5. My organism was the brown kiwi (*Apteryx mantelli).* I think the population dynamics of the brown kiwi should be measured with a continuous framework, due to the fact that it often reproduces two to three times a year. In addition, the kiwi can be variable in the amount it reproduces per year, varying from one clutch in a season to three clutches. Given this information, a discrete model would not fit the population growth of this kiwi species.

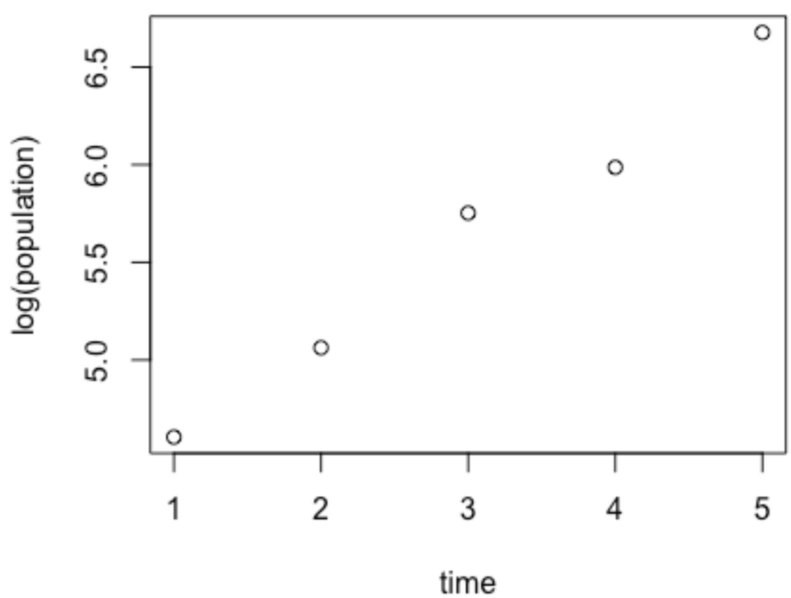
6. For five consecutive days, you measure the size of a growing population of

nematodes as 100, 158, 315, 398, and 794 individuals. Plot the logarithm (base e) of population size vs. time to estimate *r*. Show and annotate your code; embed your figure. Hint: ***?lm*** might be helpful.

```
# assigned population values to "population" vector
population <- c(100,158,315,398,794)

# assigned time values to "time" vector
time <- c(1:5)

# plotted nematode population vs. time
plot(time, log(population))
```




7. Simulate a population growing exponentially in continuous time for 100 time steps; *r* = 0.25 and *N0* = 1. Store the results of this simulation in a data frame. Repeat this for two additional values of *r*, of your choosing. Visualize the results of all three simulations on a single plot, coloring each line a different color. Add a legend so it's clear which runs correspond to which values of *r*. Show and annotate your code; embed your figure. Hint: check ***?points*** and ***?legend***.

```
#installs deSolve
install.packages('deSolve')
library(deSolve)
```

```
#codes for exponential growth equation
exp.growth <- function(t, y, p) {
  N <- y[1]
  with(as.list(p),{
    dN.dt <- r*N
    return(list(dN.dt))
  })
}

#specifies parameters for the above function
p <- c('r'=.25)
y0 <- c('N'= 1 )
t <- 1:100

#inputs information into ODE
sim <- ode( y = y0, times = t, func = exp.growth, parms = p, method= 'lsoda')

#puts ODE output into dataframe
head(sim)
class(sim)
sim.frame <- as.data.frame(sim)

# manipulates datafram, names sim.frame
names(sim.frame) <- c('t', 'abundance')
sim.frame$t
sim.frame$abundance

# plots data for r=.25
plot(abundance ~ t, data = sim.frame, type = 'l', col='green', bty = '1')
```