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BI 471

HW 1

1. $N(t) = N(0)e^{rt}$

   $\frac{ln[N\,(t)/N(0)]}{r} = t$

   r=0.1, N(0)=10, N(t)=100, 1000, 100,000,000, 100,000,000,000

   $\frac{ln[100/10]}{0.1} = t$ t =23.03 days

   $\frac{ln[1000/10]}{0.1} = t$ t =46.05 days

   $\frac{ln[100000000/10]}{0.1} = t$ t =161.18 days

   $\frac{ln[100000000000/10]}{0.1} = t$ t =230.26 days

2. The world's human population size is expected to double in size in approximately 50 years. Assuming continuous exponential population growth, calculate r for the human population. If the population size in 2009 was 6.9 billion, what is the projected population size for the year 2050?

   $N(t) = N(0)e^{rt}$
   $2 = 1e^{r(50)}$ $ln(2) = ln\left(e^{r(50)}\right)$ $0.69 = 50r$ $r = 0.0139\ per\ year$

   $N(41) = (6.9\ billion)e^{(0.0139)(41)}$ $N(41) = 12.2\ billion\ people$

3. A population of annual grasses increases by 12% every year. What is the approximate doubling time?

   $1.12 = 1.0e^{r(1)}$ $\ln(1.12) = r$ $r = 0.113\ per\ year$
   $2 = 1e^{(0.113)t}$ $\ln(2) = 0.113t$ $t = 6.134\ years$

4. Consider the town or city in which you live and the causes of human death there. Based on actual reasons people die there, explain why you think the human death rate is or is not significantly density-independent as assumed in Problem 2. Describe three mechanisms that do introduce density dependence, however trivial they may be compared with the total death rate, into human mortality.

According to the Oregon Public Health Division, the major causes of death in Oregon in 2013 were cancer, heart disease, chronic lower respiratory disease, unintentional injuries, and stroke. These causes of death are all density-independent, they are not affected by the size of the population and occur on a more random or person-by person basis. These causes are sicknesses that do not spread through the population. Based on this information, I would say that the human death rate is density-independent as we assumed in Problem 2. Three mechanisms of death that are density-dependent include spread of infectious diseases through a population like the flu, famine due to lack of resources for the entire population, and the accumulation of toxic waste in areas humans inhabit can lead to illnesses and death.

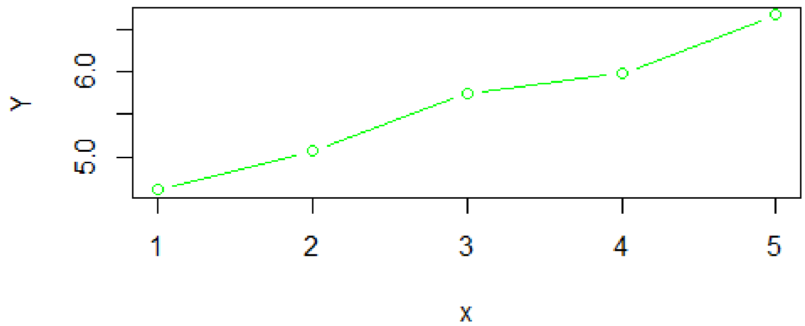
5. Upload into the [google slides] a photo of an organism that you will share with the class next week. Make sure to contribute a new species (one that a fellow student has not already uploaded). Explain in 3-4 sentences why you think the population dynamics of this organism should be modeled using a discrete versus continuous framework. Explain your reasoning in the HW you turn in and be prepared to discuss your findings with the class.

    Ring-tailed lemur:
    Female ring-tailed lemurs are sexually receptive during one breeding season in the year, usually for one to two days. The breeding season for the ring-tailed lemurs lasts between one to three weeks in May. All the adult female and male ring-tailed lemurs breed at the same time during this breeding season.

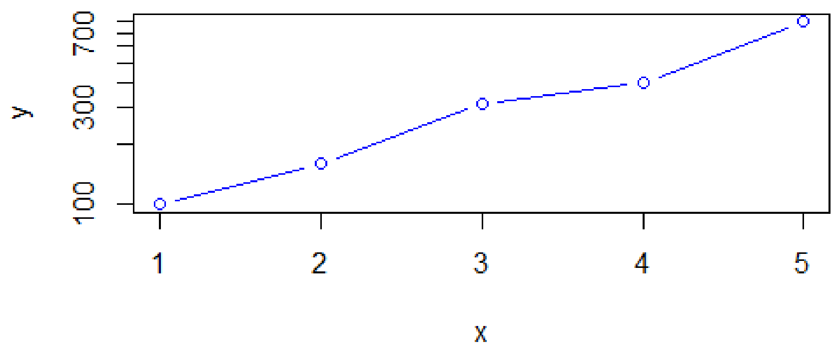
6. For five consecutive days, you measure the size of a growing population of nematodes as 100, 158, 315, 398, and 794 individuals. Plot the logarithm (base e) of population size vs. time to estimate *r*. Show and annotate your code; embed your figure. Hint: `?lm` might be helpful.

```
x<-c(1,2,3,4,5)
x
y<-c(100,158,315,398,794)
y

Y<-c(4.605,5.063,5.753,5.986,6.677)
Y

plot(x,Y,type='b',col='green')

plot(x,y,type='b',col='blue',log='y')
```

I began by creating an ‘x’ value that I could use for the x-axis of my chart which would be the length of time, or 5 days. Then I created the y value I would use for my figure. I did this two different ways to compare the two. For ‘y’ I used the population values as they were originally presented. For ‘Y’ I calculated the log value of these population sizes on my own and programmed them into R. Then, I plotted my figure in two different ways. The first was using the already logged values so I just did a basic plot. The second was using the original values so I did a basic chart with a log scale for the y-axis. These charts are shown below.



This chart shows the relationship between number of days on the x-axis and log values for population on the y-axis.



This chart shows the relationship between number of days on the x-axis and values for population on the y-axis which is on a log scale.

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`.

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

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

p<-c('r'=0.25)
y0<-c('N'=1)
t<-1:100

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

head(sim)
class(sim)

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

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

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

Above is the code I used to generate my first data set. I used the exponential growth equation as determined in class and programmed r to be 0.25, N(0) to be 1, and time to be 100 years. Following the procedure in class, I was able to produce a plot of my data which can be seen on the figure below.

```r
p2<-c('r'=0.5)

exp.growth2<-function(t,y,p2){
  N<-y[1]
  with(as.list(p2),{
    dN.dt<-r*N
    return(list(dN.dt))
  })
}

sim2<-ode(y=y0,times=t,func=exp.growth2,parms=p2,method='lsoda')

head(sim2)
class(sim2)
sim2.frame<-as.data.frame(sim2)

names(sim2.frame)
names(sim2.frame)<-c('t','abundance')
sim2.frame$t
sim2.frame$abundance

plot(abundance~t,data=sim2.frame,type='l',lwd=3,col='green',bty='l')
```

For the second data set I used the same method as before, but this time I labelled everything with a “2” so that I could maintain my original data values as well. For this data set, I used r=0.5. I again plotted my data, this time using green.

```
p3<-c('r'=1.5)

exp.growth3<-function(t,y,p3){
  N<-y[1]
  with(as.list(p3),{
    dN.dt<-r*N
    return(list(dN.dt))
  })
}

sim3<-ode(y=y0,times=t,func=exp.growth3,parms=p3,method='lsoda')

head(sim3)
class(sim3)
sim3.frame<-as.data.frame(sim3)

names(sim3.frame)
names(sim3.frame)<-c('t','abundance')
sim3.frame$t
sim3.frame$abundance

plot(abundance~t,data=sim3.frame,type='l',lwd=3,col='blue',bty='l')
```

For the third data set I used the same method again and labelled everything with a “3”. For this data set I used r=1.5. I also plotted this data, I used blue for the initial plot but then switched to red for the plot below in order to have more contrast.

```
plot(abundance~t,data=sim.frame,type='l',lwd=3,col='white',bty='l')

points(sim3.frame$t,sim3.frame$abundance,col='red')
points(sim2.frame$t,sim2.frame$abundance,col='green')
points(sim.frame$t,sim.frame$abundance,col='purple')

legend(60,6e+10, c("r=0.25", "r=0.5", "r=1.5"), col = c('purple', 'green', 'red'),
       text.col = "black", lty = c(-1, -1, -1), pch = c(1, 1, 1),
       merge = TRUE, bg = "white")
```

This was the code I used to generate the figure below. I began with the plot I generated from my first data set, but I set the line color to white so that the focus of the figure would be on the plot points. I then set the plot points to have x=time and y=abundance for my three data sets, each with a different color for the plot. I then created a legend to match the colors of my lines and to provide a key for the line meanings.