Contents

Chapter 1

Thurs Sept 10: Syllabus

1.1 Instructor Information

Instructor: Dr. Amy Hurford
Office: Teaching remotely
Email: ahurford@mun.ca
I will try to reply to emails within 24 hours (excluding evenings, weekends and holidays). I am always available during the lecture times. Please email to request a meeting for a different time. Please check my schedule and suggest a time I am free that works for you.

1.2 Course Information

TR 12.00-12.50pm
F 1-1.50pm
WebEx links for lecture times are on the course Brightspace under Announcements.

Course description:
Population and Evolutionary Ecology is an introduction to the theory and principles of evolutionary ecology and population dynamics. Pre-requisites: BIOL 2600; at least one of BIOL 2010, 2122 or 2210.

Course format:
The course has been re-designed for online delivery. Specifically, no exams that require invigilation are part of the grading scheme because these are challenging to deliver remotely. Pre-recorded lectures limit my ability to interact with

students. Therefore, I have elected to dedicate all lecture time to interacting with students. For each class there is a list of questions you are required to answer and hand-in. Prior to some classes there may be a *Required Reading*, that if completed will allow you to answer the day's assignment questions. Prior to the day of class you should complete the *Required Reading*. In addition, I can most effectively help you if you have read over the questions ahead of time.

Course expectations:
Any students that are disruptive, violating university policies, or acting in a potentially unsafe way will be warned and asked to leave.

Learning goals:
I consider your completed assignments to be a portfolio of your knowledge in population and evolutionary ecology. You will also get some exposure to coding in R. It takes time to become proficient in a programming language, but the time you will spend coding in this class will help you towards becoming more proficient. The course content emphasizes a deeper understanding of fewer concepts. You have the opportunity to further explore a topic of interest to you for the final project.

Required Text and Resources:
The course materials are online at https://ahurford.github.io/BIOL-3295-Fall-2020/. In addition you will need a computer to install R and RStudio. This will be covered on Thursday Sept 17 (see Chapter 4). Class announcements and WebEx links will be provided on the course BrightSpace and your assignments are to be submitted to BrightSpace.

1.3   Method of Evaluation

- 27 assignments (equal weighting) - 50%
- Midterm (due Fri Nov 6 at 5pm) - 15%
- Final Project (due Monday Dec 14 at 9am) - 35%

You should aim to complete each assignment before the next class, but assignments will be accepted, without penalty, up to a week later.

Late assignments, labs, and missed midterms, and final exams will be accommodated as described by University Regulation 6.7.3 and 6.7.5 (see https://www.mun.ca/regoff/calendar/sectionNo=REGS-0474 for Regulations).

1.4 Additional Policies

1.4.1 Accommodation of students with disabilities

Memorial University of Newfoundland is committed to supporting inclusive education based on the principles of equity, accessibility and collaboration. Accommodations are provided within the scope of the University Policies for the Accommodations for Students with Disabilities see www.mun.ca/policy/site/ policy.php?id=239. Students who may need an academic accommodation are asked to initiate the request with the Glenn Roy Blundon Centre at the earliest opportunity (see www.mun.ca/blundon for more information).

1.4.2 Academic misconduct

Students are expected to adhere to those principles, which constitute proper academic conduct. A student has the responsibility to know which actions, as described under Academic Offences in the University Regulations, could be construed as dishonest or improper. Students found guilty of an academic offence may be subject to a number of penalties commensurate with the offence including reprimand, reduction of grade, probation, suspension or expulsion from the University. For more information regarding this policy, students should refer to University Regulation 6.12.

1.4.3 Equity and Diversity

A safe learning environment will be provided for all students regardless of race, colour, nationality, ethnic origin, social origin, religious creed, religion, age, disability, disfigurement, sex (including pregnancy), sexual orientation, gender identity, gender expression, marital status, family status, source of income or political opinion.

You should not photograph or record myself, teaching assistants, or other students in the class without first obtaining permission. Accommodation will be made for students with special needs.

The sound should be turned off on phones and computers during class.

1.5 Additional Supports

Resources for additional support can be found at:

- www.mun.ca/currentstudents/student/
- https://munsu.ca/resource-centres/

1.6   Tentative course schedule

The course schedule is found in the toolbar of the class materials, see https: //ahurford.github.io/BIOL-3295-Fall-2020/.

The last day to drop the course without academic prejudice is Wednesday Nov. 4.

1.7   Handing in your work

1.7.1   Making figures to hand-in

The graphs you hand in need to have descriptive axeses and a figure caption. You may put these elements together using a word processing software such as *Microsoft Word*. Elements of a good figure caption:

- Has a label, i.e., "Figure 1",

- The first sentences provides a summary of what the figure shows, i.e., "The price of oranges has increased steadily since 1964",

- Provide all necessary information to understand everything in the figure, i.e., if the figure has no legend, but multiple line types/symbols, be sure to indicate what is represented by the different symbols. If the axes labels are overly brief due to space constraints in the graph, provide a more thorough description in the figure caption. If any assumptions have been made in making the figure, disclose these, i.e., a point that was excluded from the analysis due to being considered an outlier.

1.7.2   Writing R scripts to hand-in

To write your own R scripts follow the guidelines described in Chapter 7 Best Practices of *Quantitative training in Biology*. If you are asked to hand in your R script this means you need to submit an `.R` file on Brightspace.

Chapter 2

Friday Sept 11: What is a population?

For the questions below, submit your answers to Brightspace ideally before the next class. The deadline to submit your answers is Friday Sept 18.

The *Resources* below are sufficient to answer all the questions, however, you are encouraged to find your own textbooks or peer-reviewed articles to answer the questions if you feel comfortable. You can search for textbooks using and the library catalogue and peer-reviewed articles using Web of Science.

2.1 Questions

1. Give a definition of a population from a textbook or peer-reviewed publication. Provide the citation. [2 marks]

2. Find a peer-reviewed paper where a population is studied. Write 1 paragraph discussing how a population is defined for the study and how this compares to your definition of a population given in Question 1. [5 marks]

2.2 Resources

Vandermeer, J.H., Goldberg, D.E., 2013. Population Ecology: First Principles (Second Edition). Princeton University Press, Princeton, United States. Link

The Princeton Guide to Ecology, edited by Simon A. Levin, et al., Princeton University Press, 2009. ProQuest Ebook Central, Link

Sacchi, R., Gentilli, A., Razzetti, E., Barbieri, F., 2002. Effects of building features on density and flock distribution of feral pigeons Columba livia var. domestica in an urban environment. Can. J. Zool. 80, 48-54. Link

Chapter 3

Tues Sept 15: Exponential growth - discrete time

Please submit your answers before the next class. You have until Tues Sept 22 to submit your answers.

3.1 Required reading

Vandermeer, J.H., Goldberg, D.E., 2013. Population Ecology: First Principles (Second Edition). Princeton University Press, Princeton, United States. p1-3. Link

3.2 Questions

1. Suppose $\lambda = 5$ in equation (3) (see the required reading). Explain in 1-2 sentences the meaning of $\lambda = 5$. [1 mark]

2. Suppose the number of lilypads during week 7 is 78,125. Let $\lambda = 5$, and assume that the units of t are weeks. Use equation (3) to calculate the number of lilypads in week 8. Show your calculations. [2 marks]

3. Use your answer to question 2. to calculate the number of lilypads in week 9. Show your calculations. [2 marks]

4. Equation (4) for the required reading assumes that $N_0 = 1$, however, this formula can be generalized such that

$$N_t = N_0 \lambda^t$$

where N_t is the population size at time, t. Define time such that $t = 0$ is week 7 and t is then the number of weeks since week 7. Use the equation above to answer question 3 and confirm that the answer is the same (i.e., find the population size for week 9, when $\lambda = 5$ and the population size for week 7 is 78,125). Show your calculations. [2 marks]

5. Use the formula from question 4 to find the population size for week 15, where $N_0 = 1$ and $\lambda = 5$. Define time as the number of weeks since week 0. Show your calculations [2 marks]

6. It is important to note that all mathematical formulas should have the same units on both sides of the equals sign, and for each term that is added or subtracted. The units of the population size, N_t, at time, t, are number. The geometric growth rate, λ is unitless. Choose an equation from the required reading and give the units for each of the terms to show that both sides of the equals have the same units. For example, for the equation that appears in question 4, we have:

$$
\begin{aligned}
N_t &= N_0\lambda^t \\
\text{(number)} &= \text{(number)}\text{(unitless)}^{weeks} \\
\text{(number)} &= \text{(number)}
\end{aligned}
$$

Note that:

$$
\begin{aligned}
\text{(unitless)} \times \text{(quantity with units)} &= \text{(quantity with units)} \\
\text{(unitless)}^{\text{(quantity)}} &= \text{(unitless)}
\end{aligned}
$$

[2 marks]

7. Although not stated in the reading, $\lambda = 1 + b - d$ where b is the per capita birth rate over one time step (i.e. one week for this example), and d is the fraction of the lilypad population that dies over one time step. The number 1 is considered unitless, what must the units of b and d be? [1 mark]

8. In the reading, $\lambda = 2$. Given that $\lambda = 1 + b - d$, what are some possible values of b and d. Note that d is a fraction and must be $1 \geq d \geq 0$ and $b > 0$. [1 mark]

9. [True or False] For discrete time exponential growth (as per the reading), the change in population size from one week to the next depends not so much on the per capita birth rate, but on the difference between the per capita birth rate and the per capita death rate. [1 mark]

Chapter 4

Thurs Sept 17: Getting started with R

You need to have the `R` and `RStudio` softwares installed before you can proceed with the next class. Your answer to the question is due Thursday Sept 24.

4.1 Required reading

You are required to read and complete all the exercises in Chapters 1 *Introduction*, 3 *R and RStudio*, and 4 *Finding your way around RStudio* of:

Quantitative skills for biology https://ahurford.github.io/quant-guide-all-courses/

When you are finished you should have `R` and `RStudio` installed on your computer, or you should be familar with running `RStudio Cloud`.

4.2 Questions

1. Write 1 paragraph describing your experience completing the the exercises. [5 marks. You will receive full marks for attempting the question and submitting an answer.]

4.3 Just for fun

Type into the R Console:

```r
install.packages("praise")
require("praise")
praise()
```

Chapter 5

Fri Sept 18: Protection Island 1

Today's exercise will be challenging. You should aim to complete this exercise before the next class. This exercise is due by Fri Sept 25. There will be a lot of carryover to the next exercise.

The information below is taken from the following source: Newcomb, HR. 1940. Ring-necked pheasant studies on Protection Island in the Strait of Juan de Fuca, Washington. MS thesis. Oregon State University.

a. Pheasant chicks are born during the summer.
b. In May 1937, 10 pheasants were introduced to the island. Before the next breeding season there were 35 pheasants.
c. November 10, 1938 a census estimated 110 pheasants.
d. October 13, 1939 a census estimated 400 pheasants.

5.1   Questions

1. Read and complete all the exercises in Chapters 6.3 *Variables and assignment* to 6.10 *R packages* and 11 *Making graphs in R* of *Quantitative skills for biology*

- Answer all questions marked HAND IN in the reading [5 marks]

2. To make a graph of the data listed in b.-d., we need to learn how to work with dates. We will consider two possible approaches:

i. Use a built-in `R` function to convert dates to a format that can be plotted (todays class); and

ii. Convert the dates to number of days since a reference date. Now the dates are numbers and these values can be plotted on the x-axis of a graph (next class).

In this question, we will proceed with option i. The function we will use is `as.Date()`. You can learn how to use this function using an internet search or by typing the following into your `Console`:

```
?as.Date
```

These files can be difficult to understand (see R Help files. A good way to proceed is to experiment with the function in the `Console`. Try these:

```
as.Date(2012-01-31, format = %Y-%m-%d)
as.Date("2012-01-31", format = "%Y-%m-%d")
```

Note that only the second command is error-free. The first command fails because the date argument for the `as.Date()` function must be a character string, i.e., must be enclosed in `""` (see `?character`).

It is also possible to omit the format argument and just code: `as.Date("2012-01-31")`. The help file notes that when the format argument is not specified, that formats will be tried one by one and an error will be returned if none work. It is advisable to specify the format, as allowing the function to infer the format could introduce errors.

Chapter 6.9 Data structures describes how to make a vector (note a vector is a list of numbers rather than just a single number). We need to make a vector of the dates so that we can make our plot. For example,

```
x <- as.Date(c("2012-01-31", "2012-03-05", "2013-01-11"), format = "%Y-%m-%d")
```

Having completed Chapter 11 Making graphs in R, and having learned how to work with dates, you should now be able to write an R script to make plot using the information in b.-d. above.

HAND IN

- A graph and figure caption. The graph should have dates on the x-axis and the pheasant population size on the y-axis drawing from the information provided in b.-d. You will need to guess the date of 'before the breeding season' as stated in b. and you should disclose the value of this guess in the figure caption. See 1.7.1 for more information. The solutions to this problem have figure caption that is 2 sentences long. *[Note that the graph will likely have years, not months on the x-axis - changing this is a quite fiddle-y and not worth it at this stage of your R journey]* [10 marks]

- An R Script that produces the figure described above. See 1.7.2 for more information. [5 marks]

Chapter 6

Tues Sept 22: Protection Island 2

Continuing from last week, today we will try approach ii. to make the graph of the number of pheasants on Protection Island as it changes with time. Under approach ii. we will work with the dates by converting them to the number of days since a reference date. To do this we will use the `julian()` function, which is part of the `chron` package.

Today's questions are due by Tues Sept 29, however, ideally you will have them completed for the next class.

Read Section 4.4 of Quantitative skills for biology regarding installing packages. Install the package `chron` using either the `Install` button on the `Packages` tab, or by using the command `install.packages("chron")` in the `Console` window. Note that the package is only available for use once you check the box on the `Packages` tab or by running the following command in the `Console`:

```
require("chron")
```

After the `chron` package is loaded, we can then query the `julian` function,

```
?julian
```

or use an internet search to better understand how to use it. As the help files can be difficult to understand, another approach to is to try out the function. Try the following:

```
julian(1,1,1970)
julian(1,2,1970)
julian(2,1,1970)
julian(1,1,1971)
julian(1,1,1969)
```

Which argument position of the `julian()` function corresponds to the month? Note also that by default the origin (the origin is when the returned value is 0) is set to January 1, 1970. Experiment by running the following lines of code:

```
julian(1,1,2000)
julian(1,1,2000, origin = c(1,1,1970))
julian(1,1,2000, origin = c(1,1,2000))
```

Finally, we need to make our figure. Recall that the plot function requires vectors of equal length for the x- and y-axes. Make a vector of the days since a reference date as follows:

```
ref.day = c(1,1,2000)
x = c(julian(1,1,2000, origin = ref.day), julian(1,1,2002, origin = ref.day))
```

If you run into problems you can query the value of `x` in your console, and you can use `length(x)` to check the length of `x`.

6.1   Questions

1. You need to hand in a graph with descriptive axes and with a figure caption. The y-axis on your graph is population size and the x-axis will be created using the `julian()` function. Be sure to label the x-axis differently than you did for the previous assignment. See 1.7.1 for more information. The figure caption in the solutions for this problem is 2 sentences long. [10 marks]

2. You also need to produce an R Script that makes the figure described above. See 1.7.2 for more information. Save this file as *protection-island.R* [5 marks]

Chapter 7

Thurs Sept 24: Protection Island 3

Here is some additional information also taken from: Newcomb, HR. 1940. Ring-necked pheasant studies on Protection Island in the Strait of Juan de Fuca, Washington. MS thesis. Oregon State University.

a. Pheasant chicks are born during the summer.
b. In May 1937, 10 pheasants were introduced to the island. Before the next breeding season there were 35.
c. November 10, 1938 a census estimated 110 pheasants.
d. October 13, 1939 a census estimated 400 pheasants.
e. Between the 1938 and 1939 censuses, Newcomb observed that 17 adult birds died.
f. During the 1938 nesting season there were 5.86 eggs/nest. 83.57% of eggs hatched.
g. During the 1939 nesting season there were 8.73 eggs/nest. 64.58% hatched.
h. During the 1939 nesting season: Average number of chicks per clutch was 6.93.[1]
i. You can assume the sex ratio is 50:50 male to female. Pheasants are a sexually reproducing species.

[1] Note that g. and h. appear to be contradictory.

7.1 Questions

1. Let d be the fraction of population that dies each year. Estimate d for the ring-tailed pheasant population on Protection Island? Write down any assumptions you have made. [3 marks]

2. b is the per capita number of births each year. What is the value of b? Write down any assumptions you have made. [3 marks]

3. Recall that $\lambda = 1 + b - d$. What is the value of λ? Is this population is expected to grow over time? [2 marks]

4. Lets assume that the pheasant population on Protection Island grows geoemetrically (i.e. exponentially but for a discrete time model) where the geometric growth rate, λ, is the value that you estimated in 3. Lets predict the population size each May beginning with May 1937. Let $N_0 = 10$ and let t be the number of years since May 1937. Recall that when a population grows geometrically,

$$N_t = N_0 \lambda^t$$

You can use R to do this calculation as follows (you should use your value of λ from question 5, rather than `lambda <- 3` as in the example below):

```
t <-1
NO <-10
lambda <-3
NO*lambda^t
```

The result of `NO*lambda^t` is N_{t+1}, and with $t = 1$ then $N_{t+1} = N_2$: the population size two years after May 1937. You can change the value of t and repeat the calculation. Unless you have cleared your workspace it won't be necessary to re-input $N_0 = 10$ and $\lambda = 3$. As such, you can calculate N_3 with the following commands:

```
t <-2
NO*lambda^t
```

HAND IN

5. Use R to predict the value of the pheasant population size every year up until May 1940. You only need to hand in the values that you get, not an R Script. [2 marks]

The approach to calculating the pheasant population size in Question 4 is not very organized. In this question, we will learn how to make a data frame, use a for loop, and use the function `rbind()`.

Read Data structures in *Quantitative training for biology*.

Create a one row dataframe called `df`:

```
df <- data.frame(time = 0, popn.size = 10)
```

Query `df` in your `Console` to see the data frame you have created. We would like to add successive values of the population size that we calculate to the data frame. To do this we use the `rbind()` function, which binds rows together.

```
new.result <- data.frame(time = 1, popn.size = 20)
df <- rbind(df, new.result)
```

Here the `rbind()` function takes the `df` dataframe and adds the `new.result` data frame as a new row onto the bottom. Note that the code above *overwrites* the value of `df`: that is, `new.result` is added to the bottom of the `df` dataframe (containing only one row), and the result is called `df` (which now has two rows), and the old dataframe `df` (with one row) is overwritten. As such, each time you run the command `df <- rbind(df, new.result)` another row is added to `df`. Try the following:

```
new.result <- data.frame(time = 1, popn.size = 20)
df <- rbind(df, new.result)
df <- rbind(df, new.result)
df <- rbind(df, new.result)
```

If you query the value of `df` you can see that the several rows, all with identical values have been added because we have run the command `df <- rbind(df, new.result)` multiple times while the value of `new.result` is unchanged. Now let's change the value of `new.result` between each time we run the `df <- rbind(df, new.result)` command.

```
new.result <- data.frame(time = 1, popn.size = 20)
df <- rbind(df, new.result)
new.result <- data.frame(time = 2, popn.size = 30)
df <- rbind(df, new.result)
```

Type `df` into the `Console` to see the resulting dataframe. Finally, when we do calculations for a sequence of values, it is easier to code this using a `for` loop.

```
lambda <- 1.2
N0 <- 10
df <- data.frame(time = 0, popn.size = 10)
for(t in seq(1,4,1)){
  val <- N0*lambda^t
  new.result <- data.frame(time = t, popn.size = val)
  df <- rbind(df, new.result)
}
```

To understand the above code, after copy and pasting it into your `Console`, and running it by clicking `Return`, query the value of `df`: you should see predicted population sizes up until 4 years after May 1937. Now, lets try to understand `seq(1,4,1)`. Let's learn about the `seq()` function by trying it out in the `Console`. What is the result of each of these?

```
seq(-10,10)
seq(-10,5,0.1)
```

The `for` loop works by beginning with `t` equal to the first value of the sequence

and stepping through each value until the final value. The code is written so
that quantities that depend on `t` are inside the `for` loop (i.e., enclosed with in
the `{}` and those that do not depend on `t` are outside the `for` loop). Note that
`val` changes for different values of `t`, `new.result` changes for different values of
`t` (because `new.result` has `time = t` and `pop.size = val`, where `val` depends
on `t`). Finally, `df` also depends on `t`, because `new.result` depends on `t`. In
contrast, `N0` and `lambda` do not change with `t`, so it is more efficient to place
the allocated values for these parameters outside of the loop.

We can also plot the results of our calculations:

```r
lambda <- 2
N0 <- 10
df <- data.frame(time = 0, popn.size = 10)
for(t in seq(1,4,1)){
  val <- N0*lambda^t
  new.result <- data.frame(time = t, popn.size = val)
  df <- rbind(df, new.result)
}
plot(df$time, df$popn.size, typ = "l", xlab = "years since May 1937", ylab = "Populatio
```


If you already have an existing plot you can add new lines using `lines()`. For
example,

```r
plot(seq(1,4), c(1,3,4,2), ylab = "y-axis", xlab = "x-axis")
lines(seq(1,4), seq(1,4))
```

HAND IN

6. Write an R scipt that builds on the file you have previously made *protection-island.R*. Use the `lines()` command to add the predicted population size assuming geometric growth using the commands described in this section. If you have written the code correctly the result should look something like this:

Note that to get years on the x-axis for data from the *protection-island.R* file, I needed to plot `plot(x/365,y)` because with `plot(x,y)` the units on my x-axis were days. Your graph may look slightly different since you may have calculated a slightly different λ value if you made different assumptions to me in questions

1 and 2.

You are to hand in your R Script. See 1.7.2 for more information. [10 marks]

Chapter 8

Fri Sept 25: Exponential growth (continuous time)

8.1 Required reading

Vandermeer, J.H., Goldberg, D.E., 2013. Population Ecology: First Principles (Second Edition). Princeton University Press, Princeton, United States. p4-8. Link

We now have two ways of describing how population size changes with time whereby each individual has the same average number of offspring per unit time and the same probability of dying.

1) Discrete time geometric growth:

$$N_t = N_0 \lambda^t \tag{8.1}$$

and,

2) Continuous time exponential growth:

$$N(t) = N(0)e^{rt} \tag{8.2}$$

Notably, for both these models the per capita birth and death rates do not change change over time, and do not change with density or age.

The notation N_t and $N(t)$ is conventional for discrete time versus continuous time formulations respectively, however, these notations both mean the same: the population size at a particular time, t. When $t = 0$ we have the population size at time 0: N_0 or $N(0)$.

8.2 Discrete or continuous time formulations

Whether it is appropriate to model a population in a discrete time or continous time formulation depends on whether births and deaths are overlapping or neatly partitioned into a distinct time period. For example, for many animals there is a distinct breeding season: a short proportion of the year when offspring are born. As such, there is very little temporal overlap between the times of year when births and deaths occur. Humans are an example of a species that might reasonably be modelled as continuous time because babies are born year round.

8.3 Questions

Please submit the answer to these questions to brightspace, ideally for the next class, but you have until Sept 30 to complete them without penalty.

1. In equation (8.2), what is e? [1 mark]

2. For what values of r does the population size increase over time? [1 mark]

3. As described in the reading, b is a per capita birth rate, and d is a per capita death rate. For continuous time exponential growth, both b and d must be non-negative and can take values bigger than 1. Note that this differs from the discrete time model formulation where $0 \leq d \leq 1$. When $d > 1$ in the continuous time formulation, this means that the average lifespan is less than one time step. For example, when $d = 2$ this means that the average life expectancy for an individual is $1/2$ a time step (i.e., days or year, however, the time unit is defined in the model). When the population size increases over time, what is true of b relative to d? [1 mark]

4. For what value of r does $N(t)$ not change over time? Hint: if $N(t)$ is not changing then $N(t) = N(0)$ for all t. [1 mark]

5. Consider the equation:
$$\frac{dN(t)}{dt} = rN(t).$$

   As described in the reading, this is an alternative way to write the continuous time exponential growth equation. The quantity $\frac{dN(t)}{dt}$ can be understood as the slope of a graph where population size is on the vertical axis and time is on the horizontal axis. As such, if the slope is zero, $\frac{dN(t)}{dt} = 0$, then the population size is not changing. If $\frac{dN(t)}{dt} < 0$, then the population size is decreasing. For what value of r does the population size decrease? What is true about b relative to d in this instance? [2 marks]

6. Which population would be more appropriate to be modelled as a continuous time formulation: *E. coli* bacteria or moose? [1 mark]

Coronavirus deaths in Italy, Spain, the UK and US are increasing more rapidly than they did in China

Cumulative number of deaths, by number of days since 10th death
Nationwide lockdowns: ★

FT graphic: John Burn-Murdoch / @jburnmurdoch
Source: FT analysis of Johns Hopkins University, CSSE; Worldometers; FT research. Data updated March 30, 19:00 GMT
© FT

Figure 8.1: An example of a very well thought out data visualation where the data might demonstrate exponential growth

7. Calculate the formula for the doubling time for continuous time exponential growth ((8.2)). This is the time for the population to double in size. The value of $N(0)$, the population size at $t = 0$ doesn't matter as long as it is a positive number. When the population has doubled, $N(t) = 2N(0)$. To answer this question you need to find t such that $N(t) = 2N(0)$. You may need to revisit some rules about working with logarithms to complete this question (i.e. see here, specifically the *Product, Quotient, Power, and Root* table. Also recall, $Ln(e^x) = x$). Please show your work. [2 marks]

8. Consider the following plot:

In this question, we will find the equation for 'doubles every day'. Our model is equation (8.2). This means that we will calculate the equation for 'doubles every day' under the assumption that cumulative COVID-19 deaths grow exponentially over time.

To begin, we choose the time step for our model as days. The first problem we should consider is what is the value of r if the population doubles every 1 day? Make the appropriate substitutions and re-arrange equation (8.2) to find the value of r.

Now, note that the y-axis on the above graph is on a logarithmic scale. We will assume this is a base e logarithmic scale. Take the natural logarithm of both

sides of equation (8.2). Note that the result should be the formula for a straight line, i.e., $y = mx + c$, but where y is $Ln(N(t))$ and x is t (to match the axes of Figure 8.1). The questions we are left to solve are: what is the slope of the line (i.e., m, or the value of the coefficient that multiplies t), and what is the value of the intercept (i.e., c or the remaining terms on the opposite side of the equals to $Ln(N(t))$ and which are not multiplied by t)?

Show all your work. Your answer is complete when you provide the numerical values of the slope and the intercept for the straight line corresponding to a doubling time of 1 day. Assume $N(0) = 10$. Your answers must be numbers - you will need to substitute the value of r that you calculated in the early part of this question. [2 marks]

9. Provide the values of the slope and the intercept for doubling times of 2, 3, and 7 days. Again assume $N(0) = 10$. You do not need to show your work. [2 marks]

Chapter 9

Tues Sept 29: Doubling time

Today we will make a graph of the current COVID-19 data for Ontario. When only a small fraction of the population is resistant to an infection, the number of daily cases, in absence of any interventions such as physical distancing, is expected to grow exponentially over time. At the end of this exercise you will have calculated the doubling time for the second wave of COVID-19 in Ontario.

Visit the website: https://art-bd.shinyapps.io/covid19canada/, this site is the *front end* for the data we will use which are archived here (also referred to as the *back end*). These data can easily be pulled into R using this command:

```
COVID.data <- data.table::fread('https://raw.githubusercontent.com/ishaberry/Covid19Canada/master
```

To view the data type:

```
head(COVID.data)
```

```
##     province date_active cumulative_cases cumulative_recovered cumulative_deaths
## 1:  Alberta   25-01-2020                0                    0                 0
## 2:  Alberta   26-01-2020                0                    0                 0
## 3:  Alberta   27-01-2020                0                    0                 0
## 4:  Alberta   28-01-2020                0                    0                 0
## 5:  Alberta   29-01-2020                0                    0                 0
## 6:  Alberta   30-01-2020                0                    0                 0
##     active_cases active_cases_change
## 1:             0                   0
## 2:             0                   0
## 3:             0                   0
## 4:             0                   0
## 5:             0                   0
```

```
## 6:              0                    0
```

`head()` is a command that shows the first 6 lines of the quantity inside the round brackets. `COVID.data` is a very large table of data. If I type `COVID.data` into the Console I will get more information than I want, so I instead use `head()`.

So far we have pulled data from an online repository. However, it is good practice to save these data in case later the repository is removed. We can make copy of the data for our records using the following commands:

Note that the above contains the path to folders on my computer and saves `COVID.data` as the file *COVID-data-save.csv*. You will need to replace the path above with correct path to the folder on your own computer where you want to save these data. Setting the path is computer-specific, and so we always have problems with this in class because the solutions vary by student. Some tricks that work for me are:

- type `getwd()` into the Console. This will tell you the current working directory and can give you clues on the format of the path for your computer.

- clicking the `Source` button on a .R file that you have made will print the path to that .R file into the Console.

- elect to save the file somewhere very simple, for example, on your Desktop and then move it to a more organized place later.

Navigate to the folder where you expected to save the data as a .csv file. You should be able to open the .csv file in *Microsoft Excel*.

Now, the data table `COVID.data` contains data for all provinces and we would like to *subset* the data so that only the information pertaining to Ontario is left. We do this as follows:

We should understand what variables are contained in our data set. Query the following in your Console:

```
colnames(data.ON)
```

We will plot confirmed positive cases over time:

```
plot(data.ON$cumulative_cases, ylab = "Cumulative cases", typ = "l")
```
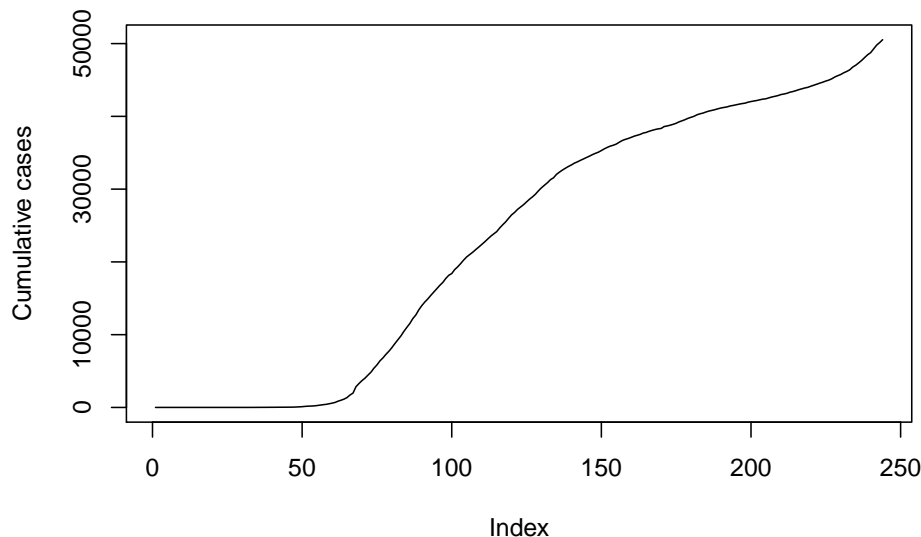
Note that we haven't provided an x-axis argument above. The x-axis should be `date_active`, however, from our previous exercise (Chapter 6), we recognize that dates need to be reformatted to be an appropriate x-axis.

```
head(data.ON$date_active)
```

```
## [1] "25-01-2020" "26-01-2020" "27-01-2020" "28-01-2020" "29-01-2020"
## [6] "30-01-2020"
```

The earliest date is January 25, 2020. We will use this as the origin and calculate the number of days since that time.

```
require(chron)
days.since <- julian(as.Date(data.ON$date_active, format = "%d-%m-%Y"),origin=as.Date("25-01-2020
```

If you get an error this may be because you have not installed the **chron** package. You can do so as `install.packages("chron")`.

On my first attempt at the above code, I tried `julian(data.ON$date_active)`. This generated an error because our dates from the COVID-19 dataset are formatted as a character string "01-25-2020", but the `julian()` function is expecting three numerical arguments `julian(m,d,y)`. As such, `julian(data.ON$Date)` fails to provide three numerical arguments to the function and instead provides a single character string. For this reason the function `as.Date()` needs to be applied to `data.ON$Date` inside the `julian()` function.

We now have a quantity `days.since` that is appropriate for the x-axis of our graph:

```
plot(days.since, data.ON$cumulative_cases, ylab = "cumulative cases", xlab = "days since Jan 25,
```
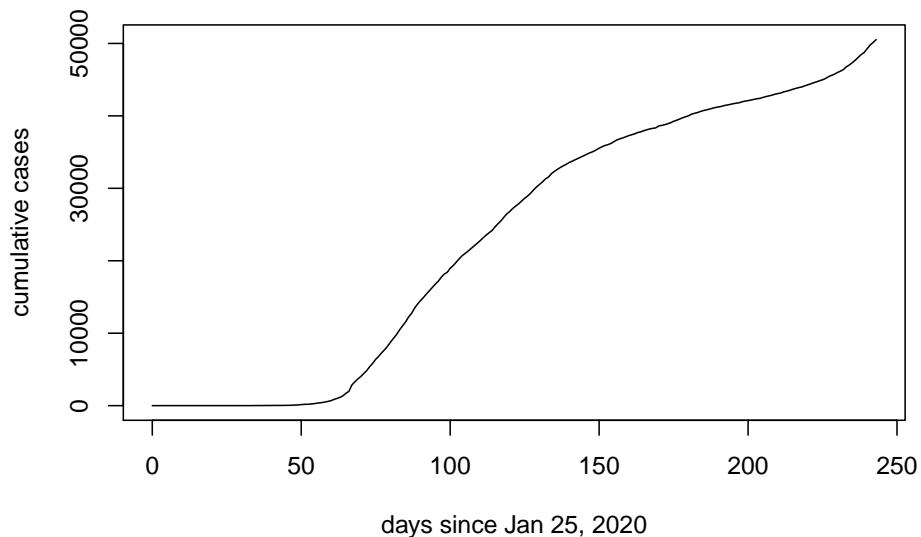
However, rather than calculating cumumlative cases suppose that we might like to plot daily new cases. We do this by subtracting the cumulative cases for the previous day. The function `diff()` subtracts the element previous to the entry of a list and because the first element of the list has not preceeding value we add in a 0.
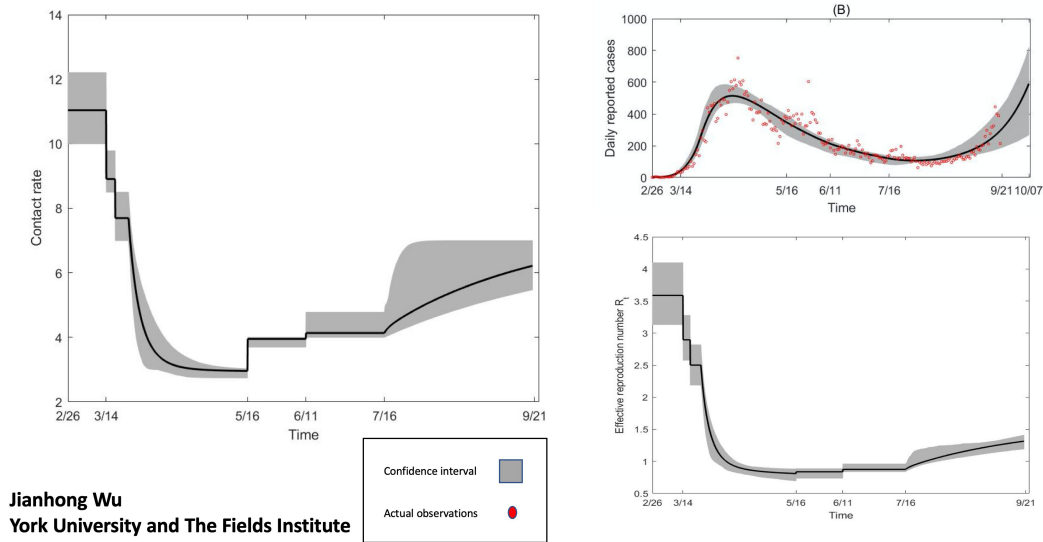
```
new.cases <- diff(c(0,data.ON$cumulative_cases))
plot(days.since, new.cases, ylab = "new cases", xlab = "days since Jan 25, 2020", typ =
```
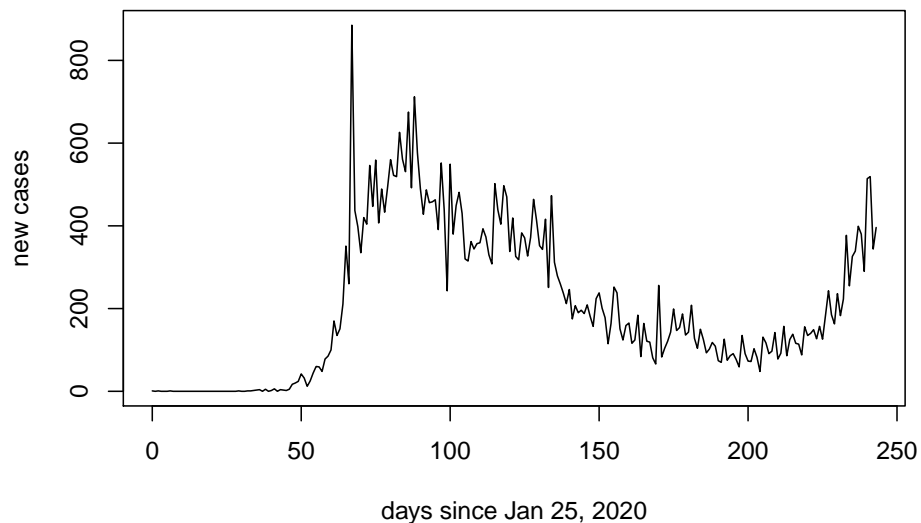

If we have done a good job of our work, it should be consistent with the official graph labelled as (B) below:

Ontario: reproduction number, contacts, daily cases

Jianhong Wu
York University and The Fields Institute

We can also focus in on just the second wave by adjusting the `xlim` argument:

```
plot(days.since[200:max(days.since)], new.cases[200:max(days.since)], ylab = "new cases", xlab =
```
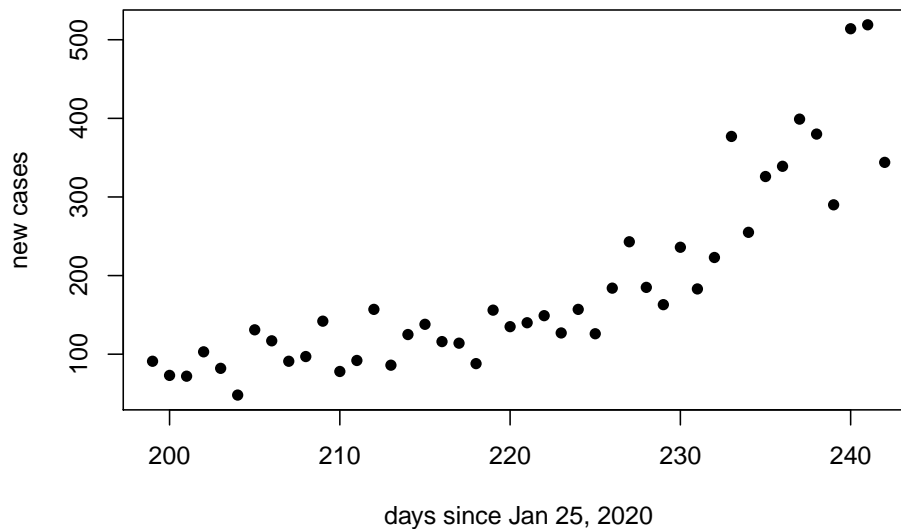

Note that the second wave of COVID-19 in Ontario appears to be consistent with exponential growth. Recall that when the y-axis of the graph is on a logarithmic scale, exponential growth will be represented as a straight line.

We can estimate the doubling time of the number of new cases for the second

Figure 9.1: Straight lines illustrate exponential growth with different doubling times when the y-axis is plotted on a logarithmic scale

wave of COVID-19 in Ontario by perfoming a linear regression on the natural logarithm of the number of new cases. Below, we consider only the data 224 days after January 25 and onwards. The function `lm()` performs the linear regression and `abline()` plots the regression.

```
since.225 <- days.since[225:max(days.since)]
log.cases.225 <- log(new.cases[225:max(days.since)])
plot(since.225,log.cases.225, ylab = "log(new cases)", xlab = "days since Jan 25, 2020"
reg <- lm(log.cases.225~since.225)
abline(reg)
```

days since Jan 25, 2020
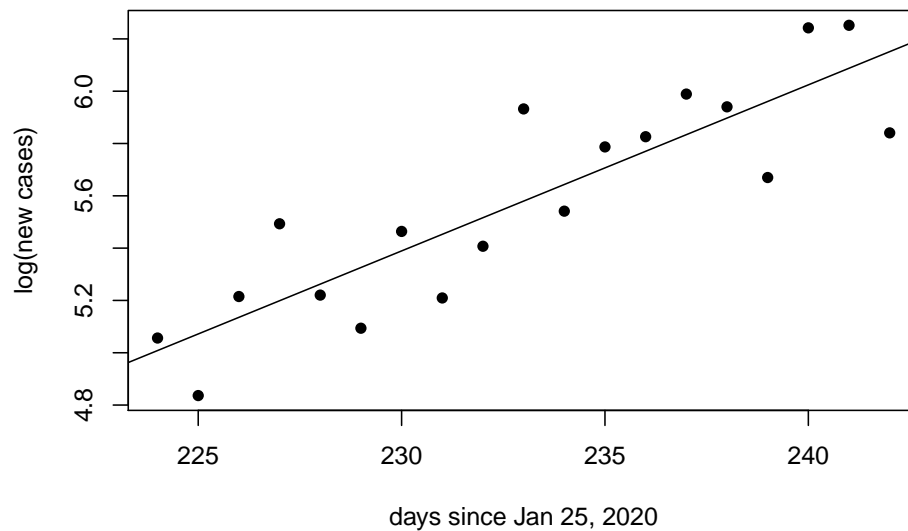
```
summary(reg)
```

```
##
## Call:
## lm(formula = log.cases.225 ~ since.225)
##
## Residuals:
##      Min       1Q   Median       3Q      Max
## -0.31056 -0.17056  0.04794  0.11769  0.35249
##
## Coefficients:
##              Estimate Std. Error t value Pr(>|t|)
## (Intercept) -9.214443   1.993026  -4.623 0.000243 ***
## since.225    0.063494   0.008551   7.425 9.92e-07 ***
## ---
## Signif. codes:  0 '***' 0.001 '**' 0.01 '*' 0.05 '.' 0.1 ' ' 1
##
## Residual standard error: 0.2042 on 17 degrees of freedom
## Multiple R-squared:  0.7643, Adjusted R-squared:  0.7505
## F-statistic: 55.13 on 1 and 17 DF,  p-value: 9.923e-07
```

From the summary of the linear regression we are interested in the slope, because in the previous class we estimated the relationship between this slope and the doubling time.

```
Call:
lm(formula = log.cases.225 ~ since.225)

Residuals:
     Min       1Q   Median       3Q      Max
-0.34767 -0.12710  0.03244  0.10027  0.33219

Coefficients:
             Estimate Std. Error t value Pr(>|t|)
(Intercept) -10.612982   2.026825  -5.236 8.15e-05 ***
since.225     0.069584   0.008715   7.984 5.69e-07 ***
---
Signif. codes:  0 '***' 0.001 '**' 0.01 '*' 0.05 '.' 0.1 ' ' 1

Residual standard error: 0.1918 on 16 degrees of freedom
Multiple R-squared:  0.7994,    Adjusted R-squared:  0.7868
F-statistic: 63.75 on 1 and 16 DF,  p-value: 5.691e-07
```

Figure 9.2: The above output shows the slope of the regression as 0.0695 log cases per day

9.1   Questions

1. How many observations and how many variables are there in the `COVID.data` and the `data.ON` files? (see the *Environment* tab) [1 mark]

2. What command did you use to save the data as a .csv file? [1 mark]

3. What do you estimate the doubling time of the second wave of COVID-19 in Ontario to be? Show your calculations [3 marks]

4. Write an R Script that performs the linear regression as illustrated above. Your script must make the figure including the regression line [7 marks]

Chapter 10

Thurs Oct 1: [DRAFT] Density dependence and logistic growth

10.1 Required reading

Vandermeer, J.H., Goldberg, D.E., 2013. Population Ecology: First Principles (Second Edition). Princeton University Press, Princeton, United States. p9-17. Link

10.2 Questions

1. What is the equation for continous time logistic growth? Define all the symbols in the equation.

2. What does dN/dt mean?

3. Equibrium values

Chapter 11

Fri Oct 2: Solving the logistic growth equation using a computer

Numerical solutions to CT logistic growth

Chapter 12

Tues Oct 6: Data and the logistic equation

Density dependence + data

12.1   Questions

1. Question 1.9 on p12 of Vandermeer and Gordon.
2. Question 1.10 on p12 of Vandermeer and Gordon.

Chapter 13

Thurs Oct 8: Discrete time models with density dependence using a computer

Chapter 14

Thurs Oct 15: Solving the discrete time models with density dependence using a computer

Chapter 15

Tues Oct 20: Density-yield and density dependence in births versus deaths

Chapter 16

Thurs Oct 22: Stage-structured models

- The idea of stage-structured models.
- Multiplying matrices.
- Eigenvalues of 2 x 2 matrix

Chapter 17

Fri Oct 23:
Stage-structured dynamics

- Eigenvalues and eigenvectors
- Diagrams

Chapter 18

Tues Oct 27: Yellow columbine

Chapter 19

Thurs Oct 29-Fri Oct 30: Midterm [due Fri Nov 6 at 5pm]

Chapter 20

Thurs Nov 5: Evolutionary ecology

Chapter 21

Thurs Nov 5: Evolutionary ecology

Chapter 22

Fri Nov 6: Evolutionary ecology

Chapter 23

Tues Nov 10: Evolutionary ecology

Chapter 24

Thurs Nov 12: Evolutionary ecology

Chapter 25

Fri Nov 13: Evolutionary ecology

Chapter 26

Tues Nov 17: Evolutionary ecology

Chapter 27

Thurs Nov 19: Evolutionary ecology

Chapter 28

Fri Nov 20: Evolutionary ecology

Chapter 29

Final project ideas

[DRAFT]

For your final project you may choose either:

1. Review paper: Read and synthesize information on a new topic in population and evolutionary ecology that we have not considered in class.

or,

2. Analysis: Download and visualize a dataset relevant to population and evolutionary ecology. Discuss your graphs in the context of a principle in population and evolutionary ecology.

Use Dias et al. 1996 *Sources and sinks in population biology* as a guide for what a final project that is a *Review* should aspire to look like.

If you choose to do a final project that is an *Analysis* you should use some of the exercises we have completed for class as a guide (for example, the Doubling time, Protection Island, Yellow columbine, or balsam fir analyses). Note that you will need to write your final project as a report, rather than a series of questions.

Some examples of final project topics are:

Review paper: - Population dynamics in warming environments. - Population dynamics in seasonal environments. - Spatial population dynamics. - Metapopulations.

Analysis:

29.1   How to read scientific papers

Please consult How to Read a Scientific Paper (2014) for the recommended
approach to 'reading' journal articles. Steps 1,2, and 4 are good advice, but step
3 may not be relevant for some readings.

29.2   Sources for datasets

29.3   Grading Rubric: Review

29.4   Grading Rubric: Analysis