EEB319H1S – Population Ecology

LAB 5 - Dynamics of Infectious Diseases

**To do before Lab 5:**  *see detailed instructions below*

1) Choose an infectious disease in a non-human animal species. *Examples of infectious diseases, some of which I will mention briefly in lectures: canine parvovirus in wolves, myxomatosis in Australian rabbits, brucellosis in bisons, rabies in racoons, arctic fox and bats, sea star wasting disease in starfish and other echinoderms, Tasmanian devil facial tumour disease (a transmissible cancer) in Tasmanian devils, poxviruses (smallpox in humans, monkeypox, rabbitpox, cowpox, etc.) and influenza viruses in a wide variety of animals, including marine mammals, chronic wasting disease in elk and deer, white-nose syndrome in bats, lyme disease in a wide variety of mammals, etc.*

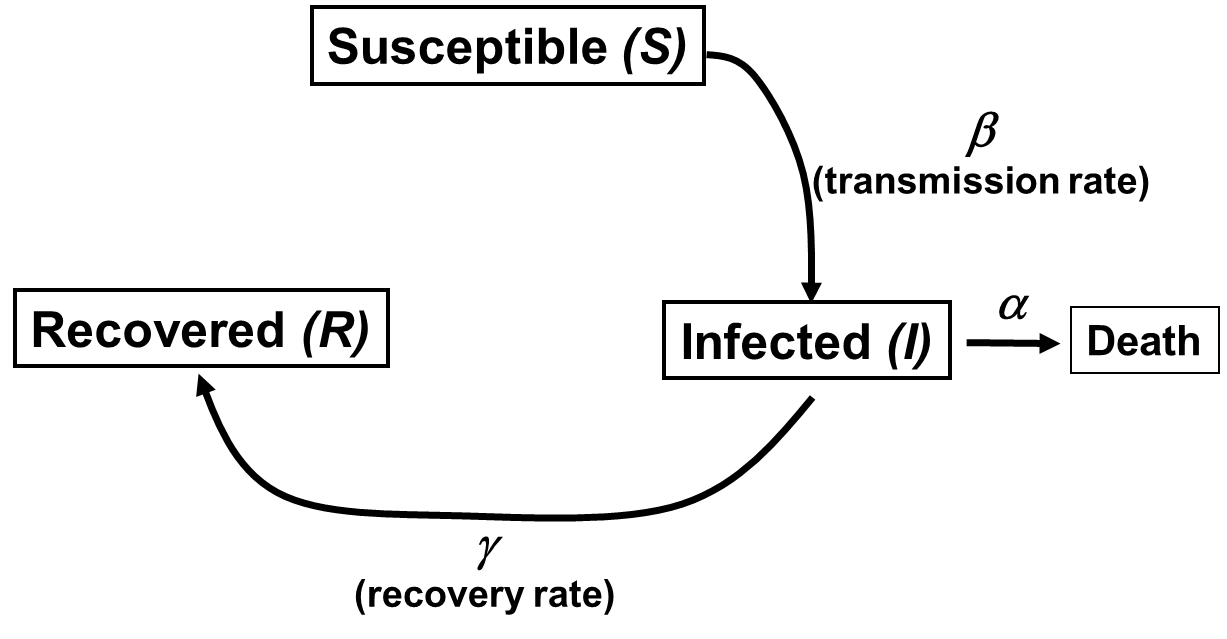
2) Find published measurements of transmission rate (β), mortality rate from disease (α) and recovery rate (γ) in chosen host species.

*Note: your TA is available during scheduled labs and weekly office hours to help you if you have questions.*

**Background**

Kermack and McKendrick (1927) proposed the SIR Model, a simple model that provides useful insights into the dynamics of infectious diseases. Using this model, the authors refuted two commonly held beliefs at the time about the conditions necessary to end an epidemic: 1) an epidemic will only end when all susceptible individuals are removed (i.e., everybody gets sick and risks dying), and 2) the virulence of the infectious organism decreases progressively over the course of the epidemic. Instead, their SIR Model suggested the existence of a Threshold host density for persistence of the disease. The SIR Model offers a way to help understand and manage epidemics. Several extensions of the model (SIS, SEIR, etc.) have been proposed to better fit more complex disease systems, but the basic SIR Model is still valued for its simplicity.

The SIR Model is a compartmental model, in that it assumes that individuals in a closed host population are either Susceptible (S), Infected (I), or Removed (R), and that movement between these three states is described by fixed parameters (β, α, γ):



All individuals are considered “*Susceptible*” until they become “*Infected*”, and the rate at which S individuals become I is modeled with a density-dependent (or mass action) transmission function *β* ×*[S* × *I]*, where *β* is transmission rate and *[S × I]* suggests random encounter between susceptible and infected individuals. Once an individual is “*Infected*”, it becomes contagious immediately and the only way out of the group is to be “*Removed*” through recovery or death. α is death rate from the disease (Note: α is different from natural death, *d*) and γ is rate of recovery. Once an individual has “*Recovered*”, it is permanently immune. The SIR Model may also include natural birth (*b*) and natural death (*d*) rates, which balance each other (i.e. host population is fixed, *r* = 0). Birth and death rates are usually assumed to be negligible (*b* = *d* = 0) over the time scale a disease will spread (e.g. disease that spread over a few weeks while the host reproduces every few years).

Important assumptions of the SIR Model are:

1. closed host population (no immigration, no emigration)
2. host population is fixed (at equilibrium; *b* = *d*)
3. all individuals are equally susceptible to the disease
4. homogeneous mixing of population (no clustering), with equal probability of individuals to come in contact with one another
5. no latent period; a new infected individual becomes contagious immediately
6. host is completely immunized from a single infection (recovery is permanent)
7. no inherited immunity
8. no evolution in the infectious organism (disease parameters are fixed)

Change in the number of individuals in each state (S, I, R) is modeled as:

Where *S(t)* = number of susceptible individuals at time t, *I(t)* = number of infected individuals at time *t*, and *R(t)* = number of recovered individuals at time t. SIR models are written in continuous time, meaning that they are comprised of differential equations, wherein we’re interested in the change of a state variable (S, I, or R) over time as a continuous variable () rather than discrete (, where “” is the discretization interval). *β* is transmission rate (i.e. probability that a random encounter between one S and one I results in infection of S), *α* is death rate of infected individuals from the disease (i.e. probability that an individual in the “I” compartment of the model will die from the disease) and *γ* is recovery rate of infected individuals (i.e. probability that an individual in the “I” compartment of the model will recover and become permanently immune to the disease). These rates are probabilities so they take on values between 0 and 1.

The derivatives in equations 1-3 above can be discretize with Euler approximations:

I

where *dt* is the time interval used (discretization interval).

Reference

Kermack, W.O., and McKendrick, A.G. 1927. A contribution to the mathematical theory of epidemics. Proceedings of the Royal Society of London. Series A, Containing Papers of a Mathematical and Physical Character. 115 (772): 700–721.

**Lab Goals**

1. Apply the SIR Model to a non-human animal host species.

2. Understand how SIR Model parameters (β, α, γ) are measured.

3. Use the SIR Model to understand disease dynamics in your animal species.

4. Use the SIR Model to manage/control an epidemic in your animal population.

5. Evaluate the impact of uncertainties in the published parameters on your results.

6. Evaluate the assumptions of your SIR Model for your host species.

**A. Finding data** *(to do before Lab 5)*

Once you have decided on a disease of interest that infects a non-human animal host species, you need to find measurements of the three SIR Model parameters: transmission rate (*β*, beta), death rate from the disease (*α*, alpha) and recovery rate (*γ*, gamma). These measurements can be from a single study or from different studies, but they need to be measured from field or lab data on your host species.

You can use Google Scholar or *Web of Knowledge* to search for each SIR parameter (by name) for your given [disease] and [host]. NOTE: To use Web of Knowledge off campus, you’ll need to use U of T’s VPN (Google Scholar is also easier to use if you’re using U of T’s VPN), which you can read about and download here: https://onesearch.library.utoronto.ca/ic-faq-categories/utorvpn. *β* may be called transmission rate, transmission coefficient or infection rate. You can also search for SIR (or other) models developed for your chosen disease and host. If you find parameter values from published models, make sure these come from measurements. Go back to the original source of data so you can understand and evaluate how these parameters were measured. Focus on the way they acquired the field or lab data instead of the statistical analyses used to estimate the parameters from the data.

Record uncertainties associated with each parameter so you can account for these when running your analysis. For e.g., a study may provide a range of parameter values or errors associated with mean parameter values, or different studies may provide different values for a given parameter.

Please also note that many articles you come across may include alternative forms of the SIR model, comprised of parameters you are unfamiliar with, or cannot directly map onto your model. Make sure to explain how your reference article’s parameters differ from yours, and how those differences may alter parameter values and results.

**B. Setting up your SIR model**

Set up your SIR model in R Markdown using the equations above and the (β, α, γ) parameters you found in the literature. Pay attention to time units and decide on *dt*, the time step you will use to run your model.

Please resist the temptation to make the basic SIR model more complex. Instead, note which assumptions of the basic SIR Model are violated in your system and discuss in your report how this might affect your results.

**C. Running your SIR model**

**1. Disease dynamics**

Use your SIR model to determine disease dynamics in your host population. If one individual in the population becomes infected, how will the disease spread through the population (i.e., how will S, I and R change over time) and how will it affect population size (N = S+I+R)?

Plot S, I, R and total population number (N) over time in one figure. *Remember to connect the points of each time series, label your axes (with units), and create a legend.* Describe the trends for each category and for the overall population. Are the trends as you expected? Why or why not? Does the number of infected individuals peak? If so, when? Does the initial size of the host population affect the outcome?

**2. Parameter uncertainties**

Determine the effect of parameter uncertainties on your results. For example if authors provide an average and a range of values for a given parameter, try to run the model with these three values to see how this affects your results. Alternatively, if you did not find uncertainty measurements in the literature, you can run a simple **sensitivity analysis** to estimate how important deviations in each parameter would affect your results (e.g. what would be the impact of doubling/halving transmission rate?)

**3. Host density threshold for persistence of disease**

The Net Reproduction rate (R0) of your infectious disease is the ratio between what increases *I* (transmission rate *β*) and what removes *I* from the host population (death rate *α* and recovery rate *γ*):

R0 = β / (α + γ) (7)

Calculate the Net Reproduction rate (R0) for your population. What does this value suggest? Will the disease spread or not through your population?

Using a similar logic, we can calculate the host density threshold for persistence of the disease by figuring out the equilibrium for *I*, or dI/dt = 0. We know that when dI/dt = 0, the number of *I* will remain stable. Using equation 2 above:

ST = (α + γ) / β (9)

where *ST* is the threshold relative to the size of the original population (*N*) when all individuals were susceptible (i.e. healthy). The host density threshold (*NT*) is then calculated as:

NT = ST × N (10)

So, if the original healthy population is *N* = 100 and *ST* is 1.5, the host density threshold (*NT*) is 150, much higher than the initial population, so an epidemic will not develop. If the transmission rate increases and *ST* becomes 0.7, *NT* is now 70 and an epidemic will develop. **Note that both *R0*and *NT* only apply to the original fully susceptible population (i.e., without vaccination).**

Calculate *NT* for your population and check that you get the expected dynamics. How does *NT* change relative to your original population if you increase/lower transmission, mortality or recovery rates. Within the uncertainty associated with your parameter values, does *NT* ever drop below *N*?

**4. Controlling disease spread**

Trying to control the spread of disease has become an increasingly important challenge for wildlife biologists. Within our simple SIR model, recall that below the critical host density threshold *NT* (where *R0* = 1), disease is unable to spread.

Provide three realistic options to manage the disease in your animal population. Think about all parameters you could manipulate and how one could do this in a real field population. Imagine you are working with the Ministry of Natural Resources and make realistic proposals. For e.g., if you are working with an endangered or exploited population, it may not be appropriate to suggest culling unless there are no other options. In urban areas (including cottage country), culling will also likely be opposed by the residents/cottagers and spreading baited vaccines may put children and pets at risk.

Prepare graphs to show the expected impact of each management option compared to what you found in (1) above. Summarize your results in a table, where you present β, α, γ, R0 and NT (with uncertainties where relevant) from the published data you gathered and for your three management options.

**Lab 5 Full Lab Report (individual)**

*Prepare your Report in R Markdown and submit on Quercus with any required supporting files.*

*Note: 300 words is ~1 double-spaced page with 12pt font.*

**1. Abstract** (max. 250 words)

The abstract contains one sentence about the general problem your are addressing, one sentence about the goal of your study, one sentence about the methods used, 3-4 sentences about results (1 per item in section C) and one concluding sentence.

**2. Introduction** (300 words max.)

Describe the (non-human) animal species and infectious disease you chose. How does the disease spread? What does it do to the host? How common is this disease / where is it found? Provide specifics that you can refer to when discussing the assumptions of the SIR Model as applied to your host population.

**3. Method** (300 words max.)

Describe briefly but thoroughly how each of the published parameter values (β, α, γ) you are using were measured. Field observations? Experiments? Number of observations? What type of population compared to yours? Describe any uncertainty (range) associated with these parameter values.

No need to describe the SIR model since we are all using the same equations listed in the lab handout.

**3. Results** (600 words max., plus tables and figures)

Present all results from section C above. Include all tables and figures (with legends; number consecutively as: Table 1, 2, 3… and Fig. 1, 2, 3…) and organize the results under the four subheadings. The text should briefly explain what is shown and refer to all graphs and figures.

**4. Discussion** (600-900 words)

Discuss your plan to control the epidemic in your animal population. Explain pros/cons of each management option. How does it compare to what is being done in wildlife populations? Were these successful or not?

Discuss the importance of uncertainties in your parameter values (e.g., does it change disease dynamics?) and in the structure of the basic SIR model. How realistic are the SIR Model assumption for your system? Provide some details about deviations from these assumptions.

**Resources**Here are some links you may find useful to produce your report in R Markdown *(the bolded items are especially good)*:

* **R Markdown: The Definitive Guide:**[https://bookdown.org/yihui/rmarkdown/markdown-syntax.html](https://can01.safelinks.protection.outlook.com/?url=https%3A%2F%2Fbookdown.org%2Fyihui%2Frmarkdown%2Fmarkdown-syntax.html&data=04%7C01%7Chelene.cyr%40utoronto.ca%7C31e4fee67c404e0071bd08d9f30e7f9e%7C78aac2262f034b4d9037b46d56c55210%7C0%7C0%7C637808065853803686%7CUnknown%7CTWFpbGZsb3d8eyJWIjoiMC4wLjAwMDAiLCJQIjoiV2luMzIiLCJBTiI6Ik1haWwiLCJXVCI6Mn0%3D%7C3000&sdata=ZBlYn59E3DFctJ%2FbHqEWTxFO6iv2OYVnE2%2F0mgBWQg4%3D&reserved=0) *Section 2.5.3 is mathematical expressions, but the whole page is useful/all you could ever need.*
* **Mathematics in R Markdown:**[https://rpruim.github.io/s341/S19/from-class/MathinRmd.html](https://can01.safelinks.protection.outlook.com/?url=https%3A%2F%2Frpruim.github.io%2Fs341%2FS19%2Ffrom-class%2FMathinRmd.html&data=04%7C01%7Chelene.cyr%40utoronto.ca%7C31e4fee67c404e0071bd08d9f30e7f9e%7C78aac2262f034b4d9037b46d56c55210%7C0%7C0%7C637808065853803686%7CUnknown%7CTWFpbGZsb3d8eyJWIjoiMC4wLjAwMDAiLCJQIjoiV2luMzIiLCJBTiI6Ik1haWwiLCJXVCI6Mn0%3D%7C3000&sdata=rPovEYlqhN%2Btnf7Za6G7PoclyQp3UpEl4sqnco2eRtw%3D&reserved=0) *This one is a quicker reference than the last one, so great if you just have a quick question about aesthetics.*
* The Base Plotting System in R:  [https://rstudio-pubs-static.s3.amazonaws.com/84527\_6b8334fd3d9348579681b24d156e7e9d.html](https://can01.safelinks.protection.outlook.com/?url=https%3A%2F%2Frstudio-pubs-static.s3.amazonaws.com%2F84527_6b8334fd3d9348579681b24d156e7e9d.html&data=04%7C01%7Chelene.cyr%40utoronto.ca%7C31e4fee67c404e0071bd08d9f30e7f9e%7C78aac2262f034b4d9037b46d56c55210%7C0%7C0%7C637808065853803686%7CUnknown%7CTWFpbGZsb3d8eyJWIjoiMC4wLjAwMDAiLCJQIjoiV2luMzIiLCJBTiI6Ik1haWwiLCJXVCI6Mn0%3D%7C3000&sdata=XK13r33myjO%2FoQkcMTgUI7k%2B0ELD3L0YalBTypwsv2E%3D&reserved=0)
* **Base Plotting in R:**[https://towardsdatascience.com/base-plotting-in-r-eb365da06b22](https://can01.safelinks.protection.outlook.com/?url=https%3A%2F%2Ftowardsdatascience.com%2Fbase-plotting-in-r-eb365da06b22&data=04%7C01%7Chelene.cyr%40utoronto.ca%7C31e4fee67c404e0071bd08d9f30e7f9e%7C78aac2262f034b4d9037b46d56c55210%7C0%7C0%7C637808065853803686%7CUnknown%7CTWFpbGZsb3d8eyJWIjoiMC4wLjAwMDAiLCJQIjoiV2luMzIiLCJBTiI6Ik1haWwiLCJXVCI6Mn0%3D%7C3000&sdata=eVi9veGcE3GQGhiv1Hqy%2FvIlkciAHOQWn8bbXv9wl3A%3D&reserved=0) *This is a great plotting resource; Towards Data Science is, in general, a great resource.*
* R Base Graphs: [http://www.sthda.com/english/wiki/r-base-graphs](https://can01.safelinks.protection.outlook.com/?url=http%3A%2F%2Fwww.sthda.com%2Fenglish%2Fwiki%2Fr-base-graphs&data=04%7C01%7Chelene.cyr%40utoronto.ca%7C31e4fee67c404e0071bd08d9f30e7f9e%7C78aac2262f034b4d9037b46d56c55210%7C0%7C0%7C637808065853803686%7CUnknown%7CTWFpbGZsb3d8eyJWIjoiMC4wLjAwMDAiLCJQIjoiV2luMzIiLCJBTiI6Ik1haWwiLCJXVCI6Mn0%3D%7C3000&sdata=15sSjtCmLwO68Ksq%2F1%2F1NgM%2Fug%2BV8z0BslrdQRTpmBA%3D&reserved=0)
* A Practical Guide to ggplot2 (for any students who favour the tidyverse):  
  [http://www.sthda.com/english/wiki/be-awesome-in-ggplot2-a-practical-guide-to-be-highly-effective-r-software-and-data-visualization](https://can01.safelinks.protection.outlook.com/?url=http%3A%2F%2Fwww.sthda.com%2Fenglish%2Fwiki%2Fbe-awesome-in-ggplot2-a-practical-guide-to-be-highly-effective-r-software-and-data-visualization&data=04%7C01%7Chelene.cyr%40utoronto.ca%7C31e4fee67c404e0071bd08d9f30e7f9e%7C78aac2262f034b4d9037b46d56c55210%7C0%7C0%7C637808065853803686%7CUnknown%7CTWFpbGZsb3d8eyJWIjoiMC4wLjAwMDAiLCJQIjoiV2luMzIiLCJBTiI6Ik1haWwiLCJXVCI6Mn0%3D%7C3000&sdata=LOJ%2BLqWiEZyUY0yP4hX62WmTUHu6ns6Wg0obMbn6CA4%3D&reserved=0)
* ggplot2 Cheatsheet:  [https://ggplot2.tidyverse.org](https://can01.safelinks.protection.outlook.com/?url=https%3A%2F%2Fggplot2.tidyverse.org%2F&data=04%7C01%7Chelene.cyr%40utoronto.ca%7C31e4fee67c404e0071bd08d9f30e7f9e%7C78aac2262f034b4d9037b46d56c55210%7C0%7C0%7C637808065853803686%7CUnknown%7CTWFpbGZsb3d8eyJWIjoiMC4wLjAwMDAiLCJQIjoiV2luMzIiLCJBTiI6Ik1haWwiLCJXVCI6Mn0%3D%7C3000&sdata=DL3JjY5luXAE1osVEyYUJJSSS%2FbOvwpS1yjCQ5ihFus%3D&reserved=0)
* Data Visualisation with ggplot2:  [https://datacarpentry.org/R-ecology-lesson/04-visualization-ggplot2.html](https://can01.safelinks.protection.outlook.com/?url=https%3A%2F%2Fdatacarpentry.org%2FR-ecology-lesson%2F04-visualization-ggplot2.html&data=04%7C01%7Chelene.cyr%40utoronto.ca%7C31e4fee67c404e0071bd08d9f30e7f9e%7C78aac2262f034b4d9037b46d56c55210%7C0%7C0%7C637808065853803686%7CUnknown%7CTWFpbGZsb3d8eyJWIjoiMC4wLjAwMDAiLCJQIjoiV2luMzIiLCJBTiI6Ik1haWwiLCJXVCI6Mn0%3D%7C3000&sdata=3YLveDC%2FM9%2BOUGHxucX0U7Uqs5TgnkiQNS9LWyFzTMo%3D&reserved=0)
* **A ggplot2 Tutorial for Beautiful Plotting in R:**[https://www.cedricscherer.com/2019/08/05/a-ggplot2-tutorial-for-beautiful-plotting-in-r/](https://can01.safelinks.protection.outlook.com/?url=https%3A%2F%2Fwww.cedricscherer.com%2F2019%2F08%2F05%2Fa-ggplot2-tutorial-for-beautiful-plotting-in-r%2F&data=04%7C01%7Chelene.cyr%40utoronto.ca%7C31e4fee67c404e0071bd08d9f30e7f9e%7C78aac2262f034b4d9037b46d56c55210%7C0%7C0%7C637808065853803686%7CUnknown%7CTWFpbGZsb3d8eyJWIjoiMC4wLjAwMDAiLCJQIjoiV2luMzIiLCJBTiI6Ik1haWwiLCJXVCI6Mn0%3D%7C3000&sdata=oeDHnrJAnIUjXhSLFqcvGdjHa%2FA0Ek0w9YupLf0T71s%3D&reserved=0)
* **R Markdown Cheatsheet:**<https://www.rstudio.com/wp-content/uploads/2015/02/rmarkdown-cheatsheet.pdf>