TIEE Issues – Data Set Submission Form – Volume 7

**1. Data Set Homepage**

**Title**: Diseasebots: A hands-on agent-based model to simulate effects of host density on contact rates and transmission of pathogens or mutualist symbionts

**The Ecological Question:** How do intraspecific contact rates change with population density, and how does this affect transmission of pathogens or mutualist symbionts between hosts?

**Ecological Content:** Host-pathogen interactions, mutualism, density dependence

**What Students Do:** Students use agent-based models for disease and mutualism to explore the effects of population density on contact rate and transmission. The activity consists of three parts:

1. A hands-on stochastic simulation using tiny robots to simulate how contact rates and transmission of pathogens (or mutualists) changes with host density.
2. Computer simulations of a general agent-based disease transmission model
3. Analysis of real ecological data on host contact rates in a snail-ectosymbiont system

**Student-active Approaches:** Open-inquiry group projects; manipulative models (‘beanbag biology’)

**Skills:** Experimental design, data visualization, data analysis, manipulating mathematical models of ecological processes, designing questions that can be answered with models, using software (NetLogo)

**Assessable Outcomes:** Proposed experimental designs, figures with captions.

**Source**: Unpublished data from Hopkins et al.

**Author(s):** Arietta Fleming-Davies1,2 and Skylar Hopkins2,3

**Institution(s):** 1 University of San Diego 2 Radford University 3Virginia Tech 4University of California at Santa Barbara

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Thanks to the QUBES (Quantitative Undergraduate Biology Education and Synthesis; <https://qubeshub.org>) and ESA faculty mentoring network “DIG into Data” for support in this project. The original diseasebot activity was used by A. Fleming-Davies in her course on infectious disease ecology at Radford University, and the idea to use the *Physa*-*Chaetogaster* system as a real life equivalent originally came from Jeremy Wojdak.

**Relevant Cover Image:**

Physa\_Hopkins.png

Diseasebots.mp4 (video)

**2. Overview**

In parts one and two of this module, students use hands-on and computational agent-based models to create simulated data sets exploring the effects of population density on contact rate and transmission of pathogens. Using tiny robots or their computer simulated equivalents in NetLogo, students manipulate host density and/or other population features and measure effects on contact rate and disease transmission. In Part three, students analyze an empirical data set similar to those they simulated with the agent-based models, containing ecological data on how snail contact rates change with population density. The data here are from a study by Hopkins et al. examining contact rates and transmission of an ectosymbiotic worm (*Chaetogaster limnaei*) among individual snail hosts of the species *Physa gyrina*, a common North American aquatic snail. *Chaetogaster* are small segmented worms that live externally on the headfoot of many snail species, on every continent except Antarctica (Smythe et al. 2015). *Chaetogaster* are primarily transmitted during direct contacts (Hopkins et al. 2015). To quantify how per capita contact rates change with host density in *Physa gyrina* snails, Hopkins et al. manipulated snail density in replicate tanks in the laboratory, using snails collected from Montgomery County, VA. Snails were placed in densities of 1,2,3,4,…14,16, or 18 individuals per container, and researchers observed each container for 45 minutes, counting the number of contacts per individual. Three replicates of each density treatment were observed over six days of trials.

**3. The Data Sets**

HopkinsSnaildata.csv (Real ecological data collected by S. Hopkins et. al)

NetlogoExample.csv (An example NetLogo output, generated from the model diseasebots.nlogo by A. Fleming-Davies)

Skylar Hopkins, Cari McGregor, Lisa Belden, and Jeremy Wojdak give permission for this data set to be posted and distributed on the TIEE website. Collection of these data was funded by the National Science Foundation (DEB-1501466, DEB-0918960, DEB-0918656).

**Additional files:**

diseasebots.nlogo (NetLogo diseasebot model, can be opened in the free NetLogo software (<https://ccl.northwestern.edu/netlogo/download.shtml>)

**4. Student Instructions:**

***Note to faculty:***

*This exercise has three parts, and the handouts correspond to each part. Please see faculty notes for different possible arrangements (for example, using parts 1 and 3 but not 2):*

1. *Hands-on simulation of a disease transmission model*
2. *Computer simulations of a general agent-based disease transmission model*
3. *Analysis of real ecological data on host contact rates in a snail-ectosymbiont system*

**Diseasebots Part 1: Hands-on stochastic model of infectious disease**

*Learning Objectives:*

1. Simulate a very simple disease model in a hands-on simulation and explore how host density affects contact rates and disease transmission

2. Design an experiment to explore basic biology of diseases, by manipulating a factor affecting disease transmission

3. Become familiar with how to use mathematical models to answer experimental questions

4. Describe the difference between stochastic and deterministic models

5. Practice collecting and visualizing data to show the results of experimental manipulations

Population density plays a role in many ecological processes, from logistic population growth, to predator-prey dynamics, to interactions with mutualists. Host population density is one of the key factors that influences the spread of disease and whether an outbreak (epidemic) will occur. In ecological systems in which disease transmission occurs through direct contact between infected and uninfected hosts, transmission is often density dependent. In these systems, as host population density increases, contact rate also increases, leading to higher transmission.

Disease ecology, the study of how infectious diseases spread in populations, is a field in which very simple mathematical models can be extremely useful, both for understanding the processes in nature as well as for making public health predictions like whether an outbreak will occur. You might be familiar with the classic SIR (Susceptible-Infected-Recovered) model. In **deterministic** disease models, like the SIR model, we can always predict a single outcome for a given set of parameters (e.g., rate of disease transmission between individuals) and initial conditions (e.g., starting number of infected individuals). For example, if we know the transmission and recovery rates of a disease, for any initial fraction of infected individuals in the population we can determine whether an epidemic will occur and how many individuals will get the disease. Unlike deterministic models, **stochastic** models recognize that events such as transmission happen with a certain probability, and therefore we can expect that each time we simulate the model, we will see one of many possible outcomes, which might differ substantially from the mean outcome.

In stochastic models, unlike deterministic models, you will get a different outcome every time, and thus it is necessary to simulate the model many times from the same initial conditions to determine the distribution of possible outcomes and reach a general conclusion. For example, if you flip a coin 10 times, you know that on average you will get heads 5 times, but you don’t expect to get exactly 5 heads each time. Instead, you could get anywhere from 0 to 10 heads, but some of those outcomes are more likely to occur than others (i.e., getting 10 heads won’t happen as often as 6 heads). Therefore, if we want to figure out which outcomes are most probable, we will need to simulate our model many times, rather than drawing conclusions from a single simulation.

Agent-based models (ABMs) or individual-based models (IBMs) are a specific type of stochastic model, in which we simulate individuals in a population, each behaving according to certain decision rules. General patterns at the population level arise from individual behavior.

In the first part of this activity, we will simulate a very simple disease transmission model in a hands-on simulation using mini-robots to see the effect of population density on contact rate and spread of the disease. We will introduce one infected individual into populations of different sizes. To simplify logistics, individuals will stay infectious forever rather than recovering. Because no one recovers, the infection will spread very quickly, until all individuals are infected.

#  Whole class simulation using robots

1. In the first simulation, we will collect data as a class on how population density affects contact rates and the spread of disease. We need to decide which population sizes to use, how many replicates per population size, and what response variable to measure. Working in groups of ~4 people, come up with a strategy for data collection, and briefly describe your methods in writing. We will run no more than 20 trials total.
2. Now fill in the rows in the table below with the different population sizes the class decided to measure, and fill in the response variable as the third column heading. If the class decided to run one simulation several times for each population size, make sure to repeat that population size in the table.

|  |  |  |
| --- | --- | --- |
| **Trial****number** | **Population size** |  |
| 12345 |  |  |
| 678910 |  |  |
| 1112131415 |  |  |
| 1617181920 |  |  |

**Group experiments**

In the next part of the activity you will modify the environment or population in some way, to test the effect this modification has on the number of contacts and the spread of disease. What ‘real world features’ could you add that this model currently leaves out?

Some ideas for processes or scenarios to model (note: this is just a starting point): Patchy environment, divided populations, quarantine, vaccination, high-risk and low-risk hosts

Some facts about the robots (also just a starting point): They move very slowly on paper; they can be slowed down by weighting them; you can mark them with stickers; permanent modifications are **not** allowed (i.e. no, you can’t cut the legs off).

1. Please describe your experimental plan in the space below (notes and bullet points are fine; full sentences are not necessary). This should include: 1) A description of the ‘real world’ feature that you would like to model 2) A description of the modifications you will make to the bugs or their environment to model this feature 3) Your experimental question 4) The response variable(s) that you will measure 5) Sample sizes including number of trials and replicates per treatment level
2. Please fill in the second and third column headings with the experimental variables you will manipulate (2nd column) and measure (3rd column). Then conduct your simulations and use the table to collect data.

|  |  |  |
| --- | --- | --- |
| **Trial****number** |  |  |
| 12345 |  |  |
| 678910 |  |  |
| 1112131415 |  |  |
| 1617181920 |  |  |

1. Now plot your collected data in a graph to demonstrate the main pattern. The graph should clearly communicate the experimental evidence to answer your experimental question. Please include a figure caption that summarizes your main result. What did you learn from your model? What assumptions went into the model, and how did it differ from the real world?

**Diseasebots Part 2: Computer simulations of agent-based models**

*Learning Objectives:*

1. Use the software NetLogo to simulate a simple agent-based model of a biological process
2. Explore how host density affects contact rates and disease transmission in a stochastic model
3. Design an experiment to collect data over multiple simulations of the computer model, and explain why multiple simulations are necessary for data collection in stochastic models
4. Practice collecting and visualizing data to show the results of experimental manipulations

As you saw in the hands-on simulation of a stochastic disease model, the limitation of stochastic models is that you need to simulate the ecological scenario multiple times in order to understand the effect of your manipulation on your response variable, which can be very time consuming. Computer simulations allow us to speed up this process.

The computer version of this simulation runs in the program “NetLogo.” Your group will run the same experiment you conducted with the mini-robots, this time using NetLogo.

There are two ways to run this program: installing NetLogo on your laptop, or running it remotely through the QUBES website. Your instructor will indicate which set of instructions to follow. You can download an electronic version of this pdf file from your course website so that you don’t have to type in all of the links.

*To run NetLogo on the QUBES website:*

1. To run the software, you first need to create an account on the QUBES website. Goto [https://qubeshub.org](https://qubeshub.org/) and click “Login,” then follow the prompts to create an account by linking your gmail/google account. At least one person per group needs to create an account in order to open the software.
2. Next, go to <https://qubeshub.org/groups/teaching_with_netlogo> and click the “Join” button on the upper left. Make sure you are logged in to your QUBES account.
3. Now you are ready to open the software! Click this link: <https://qubeshub.org/tools/netlogo/invoke?params=file:/data/groups/teaching_with_netlogo/diseasebots.nlogo> to launch NetLogo with the diseasebot model already loaded. You might need to adjust your browser zoom a little and/or adjust the size of the internal window in order to see the whole thing. Congratulations, you are now using a supercomputer!

*To install NetLogo locally:*

1. Go to <https://ccl.northwestern.edu/netlogo/download.shtml> and download and install the appropriate version for your operating system.
2. Go to your course website and download the file diseasebots.nlogo. Open this model in NetLogo.

**Now with modeling software!**

1. Once you have the model open in NetLogo, play around with the sliders to change model parameters. To run the model, first click “setup” and then click “go”. The simulation will run until you click “go” again. Set up the sliders and options to match your ‘real world’ experiment. In NetLogo, the agents (i.e. our diseasebots) are always called turtles, so that’s why they are turtle-shaped.
2. To run your model multiple times, you will use a tool called Behavior Space. Go to Tools and select Behavior Space in the top menu. Then click “New” in the pop up box to create a new experiment.
3. Now find the variable that you want to change in your experiment in the top box, and type in the range you want to vary it over. For example, to change the amount of vaccination, you would modify the first line in the top box. Right now, it looks something like this: ["number-to-vaccinate" 5]. This means that the number of robots to vaccinate is set at 5. If you want to vary that from 0 to 20 robots, increasing by 5 each time, you’d replace 5 with [0 5 20]. So it would now look like ["number-to-vaccinate" [0 5 20]]. Make sure to leave all of the other variables in that box the same–only change the one that you want to vary over your experiments.
4. Choose how many times to repeat each experiment, and type it into the Repetitions box. Try starting with 100 repetitions.
5. Decide what variable you are measuring and type it in the “Measure runs using these reporters” box. For example, to measure the fraction infected, type in %infected.
6. Choose a time limit (when to cut off your simulations) and type it into the “Time limit” box. Try starting with 1000 time steps.
7. Click OK. You have now created a new experiment. Click “Run” to run. In the box that pops up, uncheck the “Spreadsheet” box and check the “Table” box, then click OK. Name your file, and click OK again.
8. Once your experiment runs, download your Excel file and plot the data in a graph to demonstrate the main pattern. The graph should clearly answer your experimental question. Please include a figure caption that summarizes your main result. If you completed Part 1, the same graph type should work here. Are your results similar to the results of your ‘real-world’ experiment with the disease bots? What is different?
9. How many times (repetitions) did you choose to simulate your experiment? What happens if you increase the number of repetitions? Why? Please explain your answer briefly in the document containing your results figure.

**Diseasebots Part 3: Disease? These are mutualists!**

*Learning Objectives:*

1. Explore the effects of host population density on contact rates using a real ecological data set.

2. Connect host-pathogen interactions to the larger context of interspecific interactions, including mutualism

3. Practice analyzing and visualizing real ecological data to answer a research question.

4. Explain how host density effects on interspecific interactions affect other key ecological processes such as density-dependent population growth

You might remember from your intro bio course that interspecific interactions can change from mutualism (+/+ interactions where both species benefit) to commensalism (+/0 interactions) to parasitism (+/- interactions; infectious disease is a type of parasitism) depending on the ecological context. Changes in contact rate with host density affect transfer of mutualists between hosts just as they affect transfer of parasites or pathogens between hosts. In fact, many ecological models can be used for both mutualism and parasitism. And in some cases, the same symbiont or partner species can act as either commensalist, mutualist, or parasite depending on nutrient availability, developmental stage of the individuals, temperature, presence of other species, or other biotic or abiotic factors. For example, mycorrhizal fungi are often assumed to be mutualistic, donating nutrients that lead to increased growth of their host plants, but under certain conditions can act as parasites or commensalists (Johnson et al. 1997).

In Part 3, we will analyze real ecological data to determine how host density affects snail contact rates, which should determine transmission rates of a mutualist symbiont: *Chaetogaster limnaei. Chaetogaster* are small segmented worms that live externally on the headfoot of many snail species (Figure 1), on every continent except Antarctica (Smythe et al. 2015). The data here are from a study by Hopkins et al. examining contact rates that affect transmission of *Chaetogaster* between individuals of the species *Physa gyrina*, a common North American aquatic snail. In a previous study, Hopkins et al. (2015) glued tiny tethers to snails, and found that *Chaetogaster* would not disperse if snails were tethered so that they could not touch. Therefore, *Chaetogaster* are thought to be primarily transmitted within and between species during direct contacts (Hopkins et al. 2015). Therefore, the probability that a snail acquires *Chaetogaster* should be closely linked to the number and/or quality of direct contacts that the snail has with other snails in the community.



Figure 1: Arrows point to two of the many *Chaetogaster* symbionts present on this planorbid snail (can you find the others?). *Photo: Neil Phillips.*

To quantify how per capita contact rates change with host density in *Physa gyrina* snails, Hopkins et al. manipulated snail density in replicate tanks in the laboratory, using snails they collected from Montgomery County, VA (Figure 2). Snails were placed in densities of 1,2,3,4,…14,16, or 18 individuals per container, and researchers observed each container for 45 minutes, counting the number of contacts per individual. In order to distinguish between individuals, snails were marked with unique codes using nail polish (Figure 2). Three replicates of each density treatment were observed over six days of trials.

 

Figure 2: Left panel: collecting *P. gyrina* snails in the field, Montgomery County, Virginia. Right panel: *P. gyrina* marked for easy identification during contact rate experiments. *Photos: S Hopkins.*

1. Researchers wanted to answer the question: how does *P. gyrina* population density affect intraspecific contact rates? Based on your observations in Parts 1 and 2 (if applicable), how do you expect contact rate to change as population density of *P. gyrina* increases*?* Why?
2. Using the data file provided by your instructor, plot the data in a graph that clearly answers the researchers’ experimental question. Please include a figure caption that summarizes your main result. If you completed Parts 1 and/or 2, what features of this graph resembles your results in those parts? Do the ‘real’ data resemble a stochastic process? Why?
3. Biotic factors such as interactions with other species can contribute to density-dependent patterns of population growth. In logistic growth, population growth slows down as a population nears its carrying capacity, which can result from either *decreased* birth rates or *increased* death rates at higher population densities. Based on the pattern in contact rates you observed in your graph, would you expect the *Chaetogaster-Physa* mutualism to contribute to the ‘classic’ density dependence population growth (i.e., higher death rates at higher population densities)? Why or why not?

**5. Faculty Notes:**

*Timeline:*

The whole three-part activity can fit nicely into a 3-4 hour lab period. It can also be broken up over several classes, or the pieces can be used independently. For students with limited computer skills or who might be more easily frustrated by technology, you can skip the second part (computer simulations using NetLogo) entirely, and go straight from Part 1 to Part 3. We recommend starting with Part 1, as the hands-on element tends to generate student interest and enthusiasm. If time or student computer skills are limiting, you can also demonstrate the NetLogo model for the class but not ask students to complete it on their own. Alternatively, for a class in which students are quite comfortable with technology, Part 2 or 3 could be assigned for completion out-of-class. Part 3 can also be used as a standalone data analysis activity, and should take 30 minutes to one hour if used alone.

*Part 1 tips*

*Materials:*

1.Tiny robots such as “Nanobots”: The ‘mini-robots’ used for the original diseasebot activity were Nanobot toys, which can be purchased at a variety of places (~$20 for 5 at the time of publication). A class population of 25 robots works well for a class section of up to 24 students. Student groups can share the robot populations for the individual experiments—they will need at least 5 per group to collect data, although this depends on the size of the robot ‘arena.’ Of course, if you have a student MakerSpace or collaborations with an engineering department, the robots can also be homemade (e.g., combine a battery, vibration motor, and the end of a toothbrush), or as complicated as you wish.

2. Flags to mark robots: We used small pieces cut from file tabs to pre-mark the robots. It is easy to then attach stickers or flags to that tab during the simulation to indicate infection. Assigning each student a robot to watch and mark in the whole class simulation works well and can also be a ‘team-building’ exercise, as students crowd around the arena together.

3. Arenas: We used premade arenas that we had on hand for another lab. These were whiteboard squares with a one inch tall wood barrier around the edge, and were approximately 1 m2 in size for the smaller student areas, and about 1.5 x 1.5 m for the larger whole class arena. It is not necessary to build arenas specifically for this lab, however. A variety of options will work, including taping paper barriers on to a lab table, or repurposing a 1 m2 . quadrat. If your robot population is large enough or you are willing to wait longer for successful contacts, letting them loose on the floor in a smaller classroom also works.

4. Assorted materials for modifications: For the student-designed diseasebot experiments in Part 1, provide students with an assortment of materials to modify the diseasebots or their environment. For example, copier paper, masking tape, cardboard paper towel tubes, stickers to mark vaccinated diseasebots, modeling clay or pennies to slow down some robots. The robots will slow down significantly on paper ‘islands’, or it can also be used to create hard or reflective barriers. If you are using Part 2 as well, you might check students’ designs to make sure there is a close equivalent of their ‘real world’ design in the NetLogo model. See Part 2 tips below for a list of potential modifications in the NetLogo model. Or if your students are more experienced with writing code (perhaps if they have used NetLogo before), they can also change the NetLogo code to allow a larger range of modifications, rather than simply using the sliders.

*Other Part 1 tips:*

Students will vary in their choices of experimental designs for the whole class simulation. Some groups might need to be reminded of the importance of multiple replicates within each treatment/density.

There are several good choices for useful response variables. Populations tend to get infected quickly, and since it is an SI model, everyone will get infected eventually. Measuring number infected after a very short cutoff time or measuring the length of time until 100% of the population is infected can work. Alternatively, to measure contact rates, students can either choose one ‘indicator’ robot and measure the number of its contacts, or each student can follow a different robot and they can average them (this is a good opportunity for discussing why different robots in the same arena aren’t statistically independent, and for emphasizing that outcomes represent a distribution—some robots might have 10 contacts, while others have only 4).

*Part 2 tips*

The NetLogo model allows for the following modifications to the ‘real world’ robot simulation (where transmission occurs in 100% of contacts, in a 1m2 arena). You can provide this list to your students, or it is often more effective to help them brainstorm it as a class after exploring the model on their own:

* Up to 4 patches or ‘islands’ that either slow down individuals (can be created by laying down paper squares) or are reflective (any type of hard barrier)
* Varying percentages of slower moving individuals (can be created by taping pennies or sticking modeling clay to robots)
* Vaccination of varying percentages of the population (vaccinated individuals cannot become infected; can be indicated in the real world with a sticker)
* Transmission only occurs at some lower percentage of contacts (this is difficult to mimic in the ‘real world’ robot version, but is clearly a more realistic approximation of pathogen or symbiont transmission in nature)

See the file netlogoexample.csv for an example of the Behavior Space data generated by NetLogo. Some students will struggle with interpreting the output or manipulating the Excel file. Note that the correct export option is actually “Table,” not “Spreadsheet.” To graph in R or JMP will require some manipulation of the Excel file so that the column headings are in row 1 (removing the extra information at the top). Students might also need help interpreting the column headings. We strongly suggest that students start with manipulating only one variable at a time, as the output rapidly becomes more complicated.

The NetLogo software allows for manipulation of the model using sliders (i.e., a “point and click” graphical interface), or more advanced students can also modify the code directly.

*Part 3 tips*

1. We do not include software-specific instructions for the graphs and leave that at the discretion of the instructor. See assessment section below for sample graphs.

2. If students are working in R, you might make their lives easier by providing the data as a csv instead of an Excel file, with ‘R friendly’ column headings (no special characters, etc.).

3. For more advanced students, the Hopkins et al. 2015 paper can be assigned as a reading either prior to or as a follow up to Part 3.

*Student-active Approaches:*

* **Open-inquiry:** Students come up with their own experimental questions and experimental designs. Some students may struggle with the elements of good experimental design, such as replication, controlling for confounding factors, varying only one variable at a time, and randomly assigning treatments. Others struggle with the concept of stochastic models (or of randomness in general), such as the ability to draw general conclusions about how different factors affect contact rate or spread of disease, even though we get a different outcome every time we run an experiment. Even choosing an informative response variable can be challenging for some students.
* **Manipulative models:** In Part 1, students manipulate a hands-on equivalent of an agent-based model. Manipulative models, or ‘beanbag biology’ (Jungck et al. 2010), can increase students’ comfort with models by providing an intuitive, hands-on version for them to explore. It also frees them from the additional cognitive load of working with new software. Presenting mathematical models without equations can also help math anxious students engage more fully. Working with the diseasebot robots, students practice coming up with questions that can be answered using a model, which is often one of the most challenging steps when working with mathematical models for the first time.

*Assessable Outcomes*

The main assessable outcomes are experimental designs and graphs produced from student data or from the provided dataset. Student groups can present their experimental designs from Part 1 to the class, and critique each other’s designs. Alternatively, you can ask students to submit a more formal write-up of either the experimental design or the entire group experiment and results, including the NetLogo results if applicable.

Students can make graphs in your preferred software for the course. We recommend R or JMP, but they can also be made directly in Excel. Asking students to submit a clean figure in a Word document, including a descriptive caption, can work well in assessing student completion and understanding of the key learning objectives, without the more intensive time requirements (for both student and instructor) of a complete lab writeup.

  

Above, we show two potential figures for the *Physa*-*Chaetogaster* dataset (Part 3). On the left, each trial is plotted in a different color and each snail is shown as a different datapoint. On the right, contact rates have been averaged across snails within a tank, which will require slightly more processing by the students (either using a pivot table in Excel or using summary stats in R or JMP, etc.).

Adding a statistical analysis to the graph creation is one way to increase the difficulty for more advanced courses and students. Note that individual snails (or robots) within tanks are not independent, so students should analyze data with tank (or robot arena) as the unit of replication, assuming they are not yet ready for mixed effects models. This can also be a good opportunity to discuss statistical independence and how to avoid pseudoreplication.

**References**

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