

## Measuring Animal Populations in a Natural Habitat Assessing Organisms in the Wild

### Objectives

1. Students will collect samples from different field environments.
2. Students will use a taxonomic key to identify organisms collected in the field.
3. Students will compare and contrast environments.
4. Students will assess species density and the relative abundance of species.

### Field Sampling

*Why do we need to sample?* When we want to learn about specific plants and animals in a particular area and how many there are of each species, it is impossible to go and count every individual present unless those individuals are quite large. Even then, counting every individual poses real problems. Instead, scientists usually take a number of samples from around the habitat, making the necessary assumption that these samples are representative of the habitat in general. Samples are usually taken using a standard sampling unit of some kind. This ensures that all of the samples represent the same area or volume of the habitat each time. The usual sampling unit is a **quadrat**, which normally consists of a square frame. The purpose of using a quadrat is to enable comparable samples of consistent size and shape to be obtained from an area. We will use a quadrat that is 0.5 m<sup>2</sup>. The quadrat must be randomly placed in the area to be sampled.

*How will we sample organisms in the field?* In order to sample the environment, the researcher must take preliminary samples to determine whether the organisms he or she is interested in studying appear in that area, and in what density they appear. We are taking these preliminary samples. We will collect samples from two types of environments. From these samples, we will determine what organisms live in each environment and how many live in each environment. We will collect in these environments:

1. a 0.5 m square of leaf litter in the **open forest**, including 3 cm of dirt
2. a 0.5 m square of leaf litter **next to a rotting log**, including 3 cm of dirt

*How do we identify the organisms?* In the lab, you will have access a taxonomic key. Please remember, your TA does not have “the right answer” to the identity of all the organisms. Use the picture keys also available to aid in your identifying. We will identify our organisms to the most specific level possible. However, due to limited time and your limited expertise, most organisms will only be keyed to *order*. We will make a big assumption: that all the similar looking members of a group can be called a single species. Then we will use our “species numbers” for our data analysis.

### Procedure for today’s lab

Each GROUP should start with:

- one PVC quadrat
- bucket
- two beakers

- 1) Working in groups of 2-3, you will collect samples in the open forest OR from an area next to a rotting log. Your TA will tell you which area you will be sampling.
- 2) Haphazardly toss your quadrat into your sample area.
- 3) Collect the leaf litter and the top 3 cm of soil, and place it in your bucket. Make sure you have collected enough material before walking back, as this could affect the outcome of your data analysis.
- 4) Back in the lab, pour the contents of your bucket directly onto your cleared bench top. Gloves are available from your TA if you wish to use them. Carefully (but quickly) sort through the material, collecting all of the living animals you find in a beaker. Be careful that none escape from the container.
- 5) Separate your animals into what appear to be similar groups of organisms. Use your dichotomous key and picture key to find the most specific taxonomic classification that you are able to find. *If you need help, ask your TA.*
- 6) Record in **Table 1** the name and the number of each “species” you have collected. *(Although we are not sure if you have separated the organisms into individual species, we are going to use that term for this lab.)*
- 7) Before proceeding to the Processing the Data section, *clean your bench*. Every bit of leaf litter and dirt should be placed in a bag provided by the TA at the front of the room. Empty the organisms in your collection beaker into the large bag as well. (These will later be replaced in the forest.) Use water and paper towels to wipe your bench top clean. Check the floor to make sure all debris is cleaned up. Rinse your containers at the sink and put them back on your bench for the next lab section.

## Data

Table 1. Species Data

	Species	Number		Species	Number
1			8		
2			9		
3			10		
4			11		
5			12		
6			13		
7			14		

## Processing the Data

You can use the back of this page as scratch paper if needed.

- 1) Your group's **Total Area of Leaf Litter Sampled (TALL)** =  
 (area of your quadrat) x (# of quadrats sampled)

*Reminder: area = length x width*

Your TALL: \_\_\_\_\_

2. For *each* "species" calculate the **Density** of individuals sampled (**D**) =  
 (# of individuals/ area of quadrat)
3. For *each* "species" calculate the **Relative Abundance** of each species (**RA**) =  
 (# of individuals/ total # of species sampled)
4. Record your results for 2 and 3 in **Table 2**. Calculate your average D and RA, and record on the board. Complete **Table 3** with the other groups' data and class averages.

Table 2. Group Calculations

Species Name	Density	Relative Abundance
1		
2		
3		
4		
5		
6		
7		
8		
9		
10		
11		
12		
13		
14		
<b>Your Group's Averages:</b>		

Table 3. Class Averages

<b>Open Forest Groups ↓</b>	<b>Density</b>	<b>Relative Abundance</b>
<i>Average Open Forest →</i>		
<b>Rotted Log Groups ↓</b>		
<i>Average Rotted Log →</i>		

### Questions

1. How many different species did you find? Did you expect to find this many species?
2. How many individuals would you estimate to be in an area twice as large as the sample you collected? Explain why you feel comfortable making this estimate.
3. After comparing the class averages for D and RA (Table 3) for both the open forest groups and rotted log groups, which environment do you think has the greatest diversity and why?
4. (Just for fun...) What were your favorite organisms and why? Which were your least favorite?