Making Conservation Decisions with Ant Community Assessment

Learning Outcomes:

- Conducting science: Students will be able to understand scientific methods used in experimental and descriptive research. These include…
  - Describe modern scientific techniques used in conservation, ecology, and evolution.
  - Differentiate the components of a scientific study (in this lab: data collection and analysis, interpretation of the results).
  - Problem-solve challenges that arise when conducting research (in this lab: molecular barcoding and phylogenetic tree thinking).
- Connecting nature with society: Students will be able to understand ecological and evolutionary processes that influence biodiversity while appreciating the associated ethical and societal issues. This includes…
  - Recognize the development of ecological and evolutionary processes and how they are influenced by environmental change.

What is Biodiversity?

A Comparison of Ant Communities

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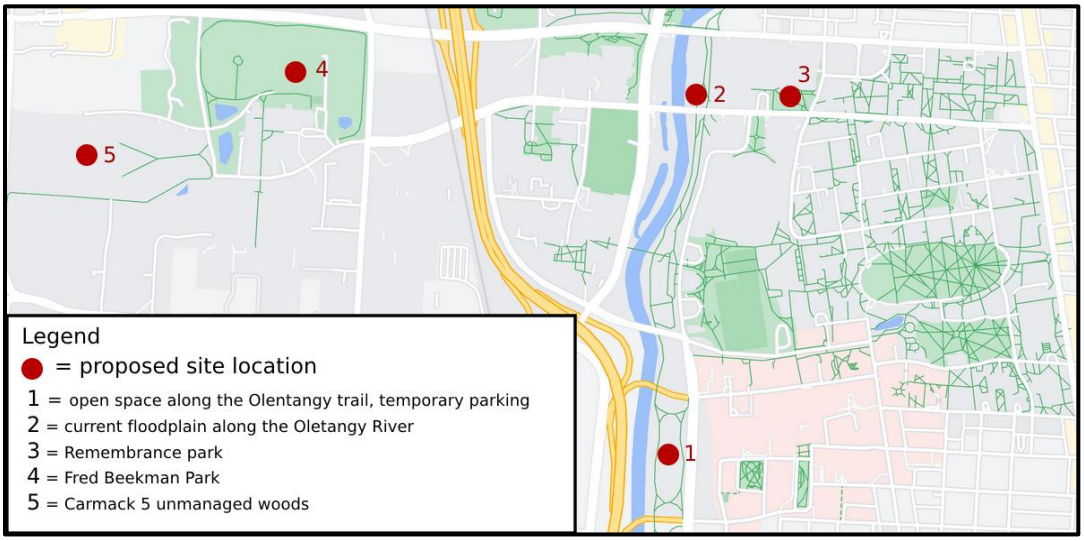
Introduction: Ants are a highly species rich group of invertebrates and play key functional roles in ecosystems. We will evaluate five ant communities, calculate biodiversity indices, and make conservation decisions based on these (and other) outcomes. Within each community, ant collections (Sites 1-5) were normalized to 25 specimens and aligned in rows/columns so that examination, analysis, and identification is easy.

Your goal / The Situation! As OSU continues to grow, so does need for more buildings and supporting infrastructure. The OSU Board of Directors has created a taskforce of scientists from across many disciplines (and you are one of them!) to determine the least ecologically devastating location for a new medical science building. Because of students protesting the destruction of green spaces around campus, the Board is also seeking to identify a location to protect and conserve. The leader of your taskforce, Dr. Rachelle Adams, has decided to assess ant communities at the potential building sites since she knows ants are a good metric for ecosystem health. Your mission is to assess a site with your team, then come back together with the taskforce to decide and justify which site is the most crucial to maintain and which should be destroyed.



Part 1. Identifying putative ant species

Describe different species of ants by using unique morphological characters. Give them a number and easy to remember name so you can communicate with the rest of your team. **Work together** – do not try to identify species from each plot separately since there might be some overlap!

Table 1. Species descriptions. Note: not every row needs to be filled.

Species # and Name	Description
15, Big Chungus	Dark colored ant with gaster much larger than head, one petiole node, no spines on thorax, no striation or hairs on exoskeleton

Part 2. Contrasting ant diversity among sites using calculated indices.

Calculate three different measures of diversity which you can utilize to base your conservation decisions:

- Species richness within each collection site.
- Species diversity within each collection site.
- The similarity of spider communities between collection sites.

EEOB 2260 Glossary:
Biodiversity—the variety of life on Earth at all its levels, from genes to ecosystems, and can encompass the evolutionary, ecological, and cultural processes that sustain life.
Richness—a measure of the number of different kinds of organisms (species) present in a particular area.
Evenness—relative abundance of the different species making up the richness in a given area; compares the similarity of the population size of each of the species present.
Alpha diversity—Species richness or the number of species within an area
Beta diversity—calculates the number of species that are not the same in two different environments.
Gamma diversity—measures biodiversity across a broader geographic area by combining alpha and beta diversity.

Part 2a. **Species richness (α diversity)** is simply the tally of different ant species at each site (or in a collection).

Count the total number of different species for the five sampling sites and record the number of each species in Table 2. ***Tally these using the actual ant site pages***: directly count the number (#) of each ant species in each site

- Total # ants for each site will = 25
- You will use Table 2 throughout the entire exercise, make sure you fill it in completely.

Table 2. Species richness. Note: There may be more species listed than you identified.

	Site 1	Site 2	Site 3	Site 4	Site 5
Species 1					
Species 2					
Species 3					
Species 4					
Species 5					
Species 6					
Species 7					
Species 8					
Species 9					
Species 10					
Species 11					
Species 12					
Species 13					
Species 14					
Species 15					
Total # species					
Total # ants					

✓ In a real situation you would need to take **many** samples as you would not know every species in a site at first look.

Part 2b. **Species diversity** is a more complex concept. We will use an index called Simpson Reciprocal Index (**SRI**). SRI is calculated as "1/*D*" where *D* is as follows: $D = \sum p_i^2$ where p_i = the fractional abundance of the i^{th} species (which is each species) in a community. For example, if a sample contained 10 ants of 2 species and there were 5 individuals of each species, the p_i for species A is 5/10 (total specimens of species A / the total number of spiders in the sample) the p_i for species B is also 5/10. Thus ***SRI*** = 1 / ($(0.5)^2$ + $(0.5)^2$) = **2**. ***For our exercise the denominator for***

all of our species will always be "25" since our data is normalized to 25 total ants per site! For each species represented in **<u>your assigned site</u>** calculate the (p_i^2) as (number of specimens of a species / 25)^2

Using the data from Table 2, Calculate the Simpson Reciprocal Index (SRI) value for the 5 sites

Table 3. Simpson Reciprocal Index values.

Site #1	Site #2	Site #3	Site #4	Site #5

✓ The higher the *SRI* value, the greater the diversity for that site.

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Part 2c. Jaccard coefficient of community similarity (β diversity). Diversity is one thing, distinctiveness is another. We will use a simple measure of community similarity, the Jaccard coefficient of community similarity (CC_J), to contrast community distinctiveness between all possible pairs of sites: This index is calculated as $CC_J = c/S$ where c is the number of species common to both communities and S is the total number of species present in the two communities. For example, if site A contains 2 ant species (species 3 and species 7) and site B contains 2 ant species (species 7 and species 14), one of which is common to both (species 7), the total number of species present in both communities is **3** (species 3, 7 and 14) and the number of species shared between the communities is **1** (species 7).
Thus, the $CC_J = c/S$ which is 1/3 = 0.333

Using the data from table 2, Calculate the Jaccard coefficient CC_J for each pairwise comparison of sites. (That is, compare Site 1 with Site 2, Site 1 with Site 3, …, Site 4 with Site 5 for a total of 10 comparisons and record your results in table 4)

Table 4. Jaccard coefficient values.

	Site #2	Site #3	Site #4	Site #5
Site #1				
Site #2				
Site #3				
Site #4				

✓ CC_J ranges from 0 (indicating that no species are found in common between the 2 communities) to 1 (indicating that all species are found in both communities).
✓ The higher the CC_J value the more closely related the communities are.
✓ You might find it useful to determine the average similarity of one community to all the others, by averaging the CC_J values across each comparison a particular site is included

Part 3. Using all these calculations, address the following:

1. How would your group rank the 5 sites based on conservation priority? Justify why you ranked them in this order.

2. The primary site to be conserved is _____. Why is this site your first choice for conservation?

3. The secondary site to be conserved is _____. Why is this site your second choice for conservation?

4. The least important site to be conserved is _____. Why is this site your least important for conservation?

5. What additional information would you like to have to make a final decision? How would you obtain this information?

Part 4. Creating one additional piece of information is provided - the phylogenetic tree

** Evaluate the phylogenetic diversity of your sites*

1. Draw your tree below.

2. Does this additional information influence your ranking of sites (circle one)?

Yes No

3. In the space below: explain why the phylogenetic tree did or did not influence your ranking of sites.

Part 5. Identifying species using barcodes

Using morphology is useful when organisms are distinct and easy differentiate, but sometimes delimiting morphospecies can be challenging. Additionally, having more lines of evidence to support your conclusions means your conclusions are stronger. In order to confirm your species identities, you have decided to barcode each specimen following a common barcoding protocol: https://dnabarcoding101.org/files/using-dna-barcodes.pdf

Below are the morphospecies you identified and their cytochrome c oxidase subunit 1 (COI or COX1) DNA barcode. You can use these COI sequences to identify species using a **B**asic **L**ocal **A**lignment **S**earch **T**ool (BLAST). BLAST each of these barcodes using the National Institute of Health's BLAST tool here: https://blast.ncbi.nlm.nih.gov/Blast.cgi
Once you identify the species, write its scientific name in the third column.

Table 5. Organism COI sequences and identification

Organism picture	COI	Species name
	ATTTTATACTTTATTTTTGCTATTTGAGCTGGTATGATTGGCTCTTCAATGAGAATAATTATTCGTTTAGAATTAGGTTCTTGTA ATTCATTAATTAATAATGATCAAATTTATAATACCTTAGTTACTAGCCATGCATTTATTATAATTTTCTTTATAGTTATACCATT TATAATTGGAGGATTTGGAAATTTTTTAATTCCCCTAATACTTGGATCCCCTGACATAGCTTTTCCTCGTATAAATAATATAAGA TTCTGACTTCTCCCTCCCTCAATTATATTATTAATATTAAGAAATTTCTTAAGAAACGGGGTTGGAACTGGTTGAACAATTTATC CACCATTAGCTTCTAATATTTTTCACAGGGGTCCCTCAATTGATATATCAATCTTCTCTCTTCACCTAGCAGGAATGTCTTCAAT TCTGGGAGCAATTAATTTTATCTCAACAATTATTAATATACATCACAAATCAATTTCTATAGATAAAACTCCACTAATAGTATGA TCAATTATAATTACAGCAGTACTTCTTCTTCTTTCACTTCCAGTTTTAGCGGGAGCAATTACAATACTTCTAACTGATCGAAATT TAAATACATCATTTTTCGATCCCTCAGGTGGGGGAGACCCAATTCTATACCAACACTTATT	
	ATTTTATATTTTATTTTTGCTATTTGAGCAGGAATAATTGGATCTTCAATAAGTATAATTATTCGCTTAGAATTAGGATCTTGTA ATTCATTAATCAATAATGATCAAATTTATAATACCTTAGTTACTAGTCATGCATTTATTATAATTTTCTTTATAATTATACCTTT TATAATTGGAGGATTTGGAAATTTTTTAGTTCCTCTAATATTAGGATCTCCTGATATAGCCTATCCTCGAATAAATAATATAAGA TTTTGACTCCTTCCCCCCTCAATTATATTACTAATATTAAGAAATTTTTTAAATAATGGAGTTGGTACAGGATGAACAATTTATC CACCATTAGCTTCTAATATTTTTCATAGTGGTCCTTCAATTGACATATCAATTTTTTCACTTCATATAGCTGGAATATCCTCAAT TTTGGGGGCCATCAATTTCATTTCAACTATTATTAATATACATCATAAATCAATCTCTATAGATAAAACTCCTTTAATAGTATGA TCAATTTTAATTACCGCAGTATTACTACTTCTCTCTCTTCCTGTTTTAGCGGGAGCAATTACTATATTATTAACTGAT	
	CTTTACTTCTTATTTGCTATTTGAGCAGGAATAATTGGATCTTCTATAAGTATAATTATTCGCTTAGAATTAGGCTCATCTAATT CATTAATCAATAATGATCAAATTTATAATTCTTTAGTAACTAATCACGCTTTTATTATAATTTTTTTCATAGTAATACCATTTAT AATTGGTGGATTTGGAAATTTTCTAATTCCTTTAATACTAGGATCGCCAGACATAGCATACCCTCGTATAAATAATATAAGATTT TGACTCTTACCTCCTTCAATTACTCTTTTACTTTTAAGAAATTTTATTAATGACGGAACAGGAACAGGATGAACTATTTATCCTC CCTTATCCTCTAATATTTTTCATAATGGTCCTTCTGTAGACTTAACAATTTTTTCTCTTCATATTGCAGGTATATCCTCAATTTT AGGAGCAATTAATTTTATTTCAACAATTCTTAATATACATCATAAAAATTTTTCTATTGATAAAATTCCTTTGCTCGTATGATCA ATTTTAATTACAGCTATCTTACTTCTATTATCCTTACCTGTATTAGCCGGAGCTATTACTATACTATTAACTGATCGAAATTTAA ATACTTCATTCTTTGATCCTTCGGGGGGAGGTGACCCAATTCTATATCAACATTTATT	
	ATTCTTTATTTTTTATTTGCCATTTGAGCCGGAATAATTGGCTCATCTATAAGAATAATTATTCGATTAGAATTAGGTTCTTCTA ATTCATTAATTAACAATGATCAAATCTATAATTCTATAGTTACAAGACATGCATTCATTATAATTTTTTTTATAGTTATACCTTT TATAATTGGGGGATTTGGTAATTTTCTTGTACCTTTAATGTTAGGATCGCCTGATATAGCCTACCCTCGCATAAATAATATAAGA TTCTGACTCTTACCTCCTTCAATCTCTCTACTCCTCTTAAGAAATTTTATTAATGACGGAGTTGGAACAGGATGAACCATTTACC CCCCATTAGCTTCAAATATTTTTCATAATGGCCCCTCAGTTGATTTAACTATTTTTTCTCTACATATTGCTGGGATATCTTCTAT TTTAGGGGCTATTAATTTTATCTCAACCATTATAAATATACATCATAAAAATTTTTCTGTCGATAAAATACCCTTACTTGTATGA TCGATTTTAATCACTGCGATTTTACTTCTTCTATCTCTTCCCGTTCTTGCAGGAGCTATCACCATACTTTTAACTGATCGTAATC TTAATACTTCTTTTTTTGACCCTTCAGGAGGGGGAGACCCTATTTTATATCAAC	
	ATTTTATACTTTATTTTTGCTATTTGAGCTGGTATGATTGGCTCTTCAATGAGAATAATTATTCGTTTAGAATTAGGTTCTTGTA ATTCATTAATTAATAATGATCAAATTTATAATACCTTAGTTACTAGCCATGCATTTATTATAATTTTCTTTATAGTTATACCATT TATAATTGGAGGATTTGGAAATTTTTTAATTCCCCTAATACTTGGATCCCCTGACATAGCTTTTCCTCGTATAAATAATATAAGA TTCTGACTTCTCCCTCCCTCAATTATATTATTAATATTAAGAAATTTCTTAAGAAACGGGGTTGGAACTGGTTGAACAATTTATC CACCATTAGCTTCTAATATTTTTCACAGGGGTCCCTCAATTGATATATCAATCTTCTCTCTTCACCTAGCAGGAATGTCTTCAAT TCTGGGAGCAATTAATTTTATCTCAACAATTATTAATATACATCACAAATCAATTTCTATAGATAAAACTCCACTAATAGTATGA TCAATTATAATTACAGCAGTACTTCTTCTTCTTTCACTTCCAGTTTTAGCGGGAGCAATTACAATACTTCTAACTGATCGAAATT TAAATACATCATTTTTCGATCCCTCAGGTGGGGGAGACCCAATTCTATACCAACACTTATT	
	ATTCTTTATTTTTTATTTGCTATCTGAGCTGGAATAATTGGATCTTCTATAAGTATAATTATTCGATTAGAATTAGGTTCTTCAA ATTCATTAATTAATAATGATCAAATTTATAATTCTTTAGTAACTAATCATGCCTTTATTATAATCTTTTTTATAGTAATACCATT TATAATTGGTGGATTTGGAAATTTTCTAATTCCTTTAATATTAGGATCGCCAGATATAGCTTATCCTCGTATAAATAATATAAGA TTTTGACTTTTACCTCCTTCCATCACTCTATTACTTTTAAGAAACTTTATTAATGATGGTACTGGAACTGGGTGAACTATCTACC CTCCTTTAGCTTCAAATATTTTTCATAATGGGCCTTCTGTAGACTTAACAATTTTTTCTCTTCATATTGCCGGTATATCATCTAT TTTAGGAGCTATTAATTTTATTTCAACAATCCTTAATATACATCATAAAAATTTTTCTATTGATAAAATTCCCCTACTTGTATGA TCTATCTTAATCACTGCAATTTTACTTTTATTATCCCTTCCCGTTTTAGCTGGAGCTATTACAATATTATTAACTGATCGAAACT TAAATACTTCATTTTTTGATCCTTCAGGAGGGGGAGACCCGATTCTATATCAACATTTA	
	CTTAGAATTAGGATCTTGTAATTCATTAATCAATAATGATCAAATTTATAATACCTTAGTTACTAGTCATGCATTTATTATAATT TTCTTTATAATTATACCTTTTATAATTGGAGGATTTGGAAATTTTTTAGTTCCTCTAATATTAGGATCTCCTGATATAGCCTATC CTCGAATAAATAATATAAGATTTTGACTCCTTCCCCCCTCAATTATATTACTAATATTAAGAAATTTTTAAATAATGGAGTTGG TACAGGATGAACAATTTATCCACCATTAGCTTCTAATATTTTTCATAGTGGTCCTTCAATTGACATATCAATTTTTTCTCTTCAT ATAGCTGGAATATCCTCAATTTTAGGGGCCATCAATTTCATTTCAACTATTATTAATATACATCATAAATCAATCTCTATAGATA AAACTCCTTTAATAGTATGATCAATTTTAATTACCGCAGTATTACTACTTCTCTCTCTTCCTGTTTTAGGGGGAGCAATTACTAT ATTATTAACTGATCGAAATCTAAATACTTCTTTCTTTGATCCTTC	

	TATTCTTTACTTCTTATTTGCTATTTGAGCAGGAATAATTGGATCTTCTATAAGTATAATTATTCGTTTAGAATTAGGTTCATCT AATTCATTAATCAATAATGATCAAATTTATAATTCTTTAGTAACTAATCACGCTTTTATTATAATTTTTTTCATAGTAATACCAT TTATAATTGGTGGATTTGGAAATTTTCTAATTCCTTTAATACTAGGATCACCAGACATAGCATACCCTCGTATAAATAATATAAG ATTTTGACTCTTACCTCCTTCAATTACTCTTTTACTTTTAAGAAATTTTATTAATGATGGAACAGGTACAGGATGAACTATTTAT CCTCCTTTATCCTCTAATATTTTTCATAATGGTCCTTCTGTAGATTTAACAATTTTTTCTCTTCATATTGCAGGTATATCCTCAA TTTTAGGAGCAATTAATTTTATTTCAACAATTCTTAATATACATCATAAAAATTTTTCTATTGATAAAATTCCTTTACTCGTATG ATCAATTTTAATTACAGCTATCTTACTCCTATTATCATTACCTGTCTTAGCCGGAGCTATTACTATACTATTAACTGACCGAAAT TTAAATACTTCATTTTTTGATCCTTCAGGAGGAGGTGATCCAATTCTATACCAACATTTATTT	
	TTTTTTATTTGCTATCTGAGCTGGAATAATTGGATCTTCTATAAGTATAATTATTCGATTAGAATTAGGTTCTTCAAATTCATTA ATTAATAATGATCAAATTTATAATTCTTTAGTAACTAATCATGCCTTTATTATAATCTTTTTTATAGTAATACCATTTATAATTG GTGGATTTGGAAATTTTCTAATTCCTTTAATATTAGGATCGCCAGATATAGCTTATCCTCGTATAAATAATATAAGATTTTGACT TTTACCTCCTTCCATCACTCTATTACTTTTAAGAAACTTTATTAATGATGGTACTGGAACTGGGTGAACTATCTACCCTCCTTTA GCTTCAAATATTTTTCATAATGGGCCTTCTGTAGACTTAACAATTTTTTCTCTTCATATTGCCGGTATATCATCTATTTTAGGAG CTATTAATTTTATTTCAACAATCCTTAATATACATCATAAAAATTTTTCTATTGATAAAATTCCCCTACTTGTATGATCTATCTT AATCACTGCAATTTTACTTTTATTATCCCTTCCCGTTTTAGCTGGAGCTATTACAATATTATTAACTGATCGAAACTTAAATACT TCA	
	ATAAGAATAATTATCCGACTAGAATTAGGTTCATCTAATTCATTAATTAATAATGATCAAATTTATAACTCTATAGTTACAAGGC ACGCATTTGTTATAATTTTCTTCATAGTTATACCTTTCATAATTGGTGGATTTGGTAATTTTCTTGTACCTTTAATATTAGGTTC ACCTGATATAGCTTACCCCCGTATAAATAATATAAGATTTTGACTTTTACCCCCCTCTATTTCTCTTCTCCTTTTAAGAAATTTC ATTAATGATGGAGTCGGAACAGGATGAACCGTTTATCCTCCTTTAGCCTCAAATATCTTCCATAATGGCCCTTCAGTTGATTTAA CTATTTTCTCTCTTCACATCGCTGGAATATCTTCTATTTTAGGAGCTATTAATTTTATTTCAACTATTATAAACATACACCATAA AAATTTTTCTATTGATAAAATTCCGCTACTTGTATGATCAATCTTAATTACTGCAATTTTACTACTTCTATCCCTTCCTGTTCTT GCAGGAGCTATTACTATACTTTTAACTGACCGTAACCTTAATACTTCATTTTTTGACCCATCAGGAGGTGGTGATCCTATTTTAT ATCAACATCTTTTCTGATTTTTTGGTCACCCTGAAGTT	

1. How many species are you able to identify with your BLAST? Do you have the same or a different number of species compared to the number you identified in Part 1?

Part 6. Recreating the phylogenetic tree with genetic evidence

Now we will determine how each of these species are related to one another by creating a phylogenetic tree based on the COI barcode gene. Gene phylogenies often (but not always!) agree with morphology phylogenies. One advantage of gene phylogenies is that they can identify closely related species that are morphologically distinct because one species lost or gained a trait. We will use an online tool created by Dr. Kazutaka Katoh at Osaka University to create our phylogeny:
https://mafft.cbrc.jp/alignment/server/index.html

- First, we must align sequences. Alignment matches common features in sequences so that any changes present are fairly compared.
    - What common features do you see? Are there any gaps?

- Next, we resolve a phylogeny. To do this, we must select some sort of evolutionary model. Our online tool lets us use the Neighbor Joining (NJ) and Unweighted Pair Group Method with Arithmetic Mean (UPGMA) models. Within your group, use both models to resolve phylogenies.
    - Different models could give different results. How do your phylogenies compare and contrast?

1. Draw your tree below. Be sure to label species and genera at the appropriate nodes.

Now that we have wealth of evidence, let's revisit Part 3 and definitively declare which site gets funding.

2. How would your group rank the 5 sites based on conservation priority? Justify why you ranked them in this order.

3. The primary site to be conserved is _____. Why is this site your first choice for conservation?

4. The secondary site to be conserved is _____. Why is this site your second choice for conservation?

5. The least important site to be conserved is _____. Why is this site your least important for conservation?

6. Did the additional phylogenetic data change how you assessed conservation priorities? Why or why not?