

A CURE in traits and species distributions

Reproductive modes, ranges sizes, and natural history collections

Overview and Background

Understanding the distributions of species in nature is a driving theme in the natural sciences, one that has remained elusive for centuries. Multiple forces shape species distributions, including habitat dynamics, species' ability to move, and interspecies interactions, but the way they contribute on their own and together remains incompletely understood. What we do know about species distributions is based predominantly on studies of large plants and animals, and processes discovered in those groups may not be the same as for other organisms. Smaller, sessile, symbiotic organisms, like lichens, remain a mystery. Their complicated reproductive biology and dispersal strategies, and obligate symbiotic relationship make understanding how various factors shape their distributions particularly challenging.

Lichens reproduce and disperse in three fundamentally different ways. They produce exact clones of both the fungal and algal partner, along with the complete microbiome via **lichenized asexual propagules** like isidia, soredia, and lobules. The fungal partner may produce **conidia**, which act as both mitotic propagules (i.e., they are an exact genetic clone of the fungal parent and produced by mitosis) and as spermatia, effectively dispersing the fungal individual to connect with individuals with complementary mating types. The fungal partner may also reproduce sexually via **ascospores**. Some species may reproduce using only one of these three modes, others may use all three modes. Quantifying the proportion of individuals engaging in each reproductive mode in lichen species has never before been attempted. Our task is to generate the first such dataset using lichen species from the Appalachian Mountains as a study system.

The Appalachian Mountains are a North-South oriented mountain range that span from New York to Alabama. They formed roughly 480 million years ago, making them one of the oldest mountain ranges on Earth. Some portions of the Appalachian Mountains have remained continually exposed since their initial formation, through Ice Ages, drastic changes in sea-level, and continental drifts and collisions. The age of the mountains, geological history, climate, diversity of rocks and soils are many of the factors that lead to them being a biodiversity hotspot. More recently, the Appalachian Mountains have been heavily impacted by anthropogenic change, including repeated, near-complete clear-cutting events, mountain-top removal mining, fracking, severe air pollution, and development. Thus, given their unique history, wealth of biodiversity, and recent rapid change, they are a perfect natural laboratory to research how diverse factors shape species' distributions – and in the case for this class, lichen distributions specifically.

Learning Objectives

By engaging in this project students will:

- Develop hypotheses regarding the relationship of reproductive biology with evolutionary and/or ecological processes,
- Create a morphological trait dataset using digitized herbarium specimens,
- Summarize, visualize, and analyze data,
- Write a research report discussing their hypotheses, methods, and results,
- Present a research project using a PowerPoint.

Step 1: Form groups and develop a hypothesis, or multiple hypotheses

Using the comparative framework below, consider questions you might ask about how reproductive modes and reproductive biology of organisms may relate to their distributions, range sizes, ecological niches, other aspects of their biology, and many other traits. Discuss with your group members potential research questions and hypotheses. Develop one or two hypotheses or research questions that you want to explore during this project.

See **‘Hypothesis and Sampling Design’** tutorial. And **‘annotated bibliography’** assignment.

Step 2: Generate Dataset

You will access images of specimens via The New York Botanical Garden virtual herbarium. Then, you will record character states in a google sheet with your group mates. The characters you choose to record and how you record them will depend on your hypotheses. Recording data will require careful organization.

See the **‘How to generate your dataset’** and **‘A guide to species and structures’** tutorials for further instructions.

Step 3: Mapping Distributions and Calculating Range Sizes in QGIS

Once you finish generating your trait dataset you will then map the occurrences, learn how to change the symbology in a map to visualize data, and calculate range sizes. This step will generate figures for your final presentation and paper, and will allow you to complete your dataset for statistical analysis.

See the **‘Cartography and spatial analysis’** tutorial for further instructions.

Step 4: Statistical Analyses

At this point your dataset will be completely assembled. The next step will be to perform appropriate statistical tests. Depending on the hypotheses your group developed you may use t-tests, ANOVAs, spearman correlation, linear regression, or another statistical analysis.

See **‘Statistical analyses in JASP’** tutorial for further instructions.

Step 5: Communicating Results

You will communicate your findings through writing a scientific paper and giving an oral presentation. Your written results will take the typical form of a scientific primary literature and included a title, authors, abstract, introduction, methods, results, discussion, and literature cited sections. Oral presentations will be similarly organized.

See **‘Research report’** and **‘Oral presentation’** instructions for additional details.