

# Syllabus

Z620: Quantitative Biodiversity, Indiana University, 2025

## OVERVIEW

Biodiversity refers to the variation among life and extends from within populations to across species and entire ecosystems. Due to one of the most rapid rates of extinction in Earth's history, the world is currently facing a biodiversity crisis. Consequently, it is imperative that we have an understanding of biodiversity and how to characterize and quantify it. A electronic copy of this syllabus with active hyperlinks can be found here: <https://qbiodiversity.netlify.app/>

### Course summary

This course will introduce students to the concepts, patterns, metrics, and tools that are common to the study of biodiversity. Each class meeting will consist of a short lecture followed by computational exercises designed to analyze aspects of biodiversity using data from tree, bird, mammal, and microbial systems. Students will learn how to calculate diversity metrics, generate and quantify diversity relationships, visualize multivariate data, and test hypotheses with an array of statistical techniques. We will learn how to map traits to phylogenetic trees and make inferences about the phylogenetic structure of communities. Concepts related to taxonomic and phylogenetic diversity will be extended to understand spatial and temporal dynamics. Students will be introduced to modern statistical computing and graphics environments, as well as the version control tools Git and GitHub. The class will culminate with student-led team projects.

### Course director

Dr. Jay T. Lennon 261 Biology Building [lennonj@iu.edu](mailto:lennonj@iu.edu)

### Other instructors

Dr. Emma Bueren 073 Biology Building (office) [ebueren@iu.edu](mailto:ebueren@iu.edu)

Dr. Jipeng Luo 073 Biology Building (office) [luojip@iu.edu](mailto:luojip@iu.edu)

### Class meetings

9:30-12:00 Friday, Room 004 in Fine Arts (FA), January 17 - March 7, 2025

### Recommended textbooks

- Measuring Biological Diversity, Magurran (2004) – (available online)
- Biological Diversity, Magurran and McGill (2011) – (available online)
- Numerical Ecology, Legendre and Legendre (2013) – (available online)
- Introductory Statistics with R, Dalgard (2008) – (available online)
- Numerical Ecology with R, Borcard, Gillet, & Legendre (2011) – (available online)

- Functional and Phylogenetic Ecology in R, Swenson (2014) – (available online)
- Phylogenies in Ecology, Cadotte and Davies (2016) - (available online)
- Pro Git, Chacon and Straub (2014) (available online)

## Computational approaches to biodiversity using R and GitHub

In this course, we will be using R and GitHub as complementary tools for learning quantitative biodiversity. R is a free, open-source programming language that is widely used for data visualization and statistics. Specifically, RStudio is an integrated development environment (IDE) that will allow us to interface with other packages, including Markdown and LaTeX. R and RStudio can be downloaded directly to your personal computer, but in the computer laboratory we will be using the cloud version, called Posit.cloud. Last, we will be using GitHub as a version control system to track, record, and recover changes throughout the history of a project. Last, we will be using GitHub as a version control system to track, record, and recover changes throughout the history of a project. GitHub is the premier tool for collaborative and social development of computing-based projects, allowing instructors, students, and collaborators to develop a project (or class) from remote locations. We will use GitHub to host course material including this syllabus, code, and exercises. Each student will have their own GitHub repository and will use GitHub to store and submit their work.

## Other course resources

PDF versions of required papers, along with slides from class lectures can be posted on the IU's learning management system, Canvas.

## Learning objectives

**Quantitative Biodiversity is organized around the following learning objectives.** Upon completion of the course, students will be able to:

1. Identify and discuss core concepts of biodiversity
2. Quantify and compare measures of taxonomic diversity within and among sampled
3. Quantify the distribution of traits and species in a phylogenetic context
4. Evaluate biodiversity in spatial and temporal contexts
5. Use the R programming language to analyze and visualize biodiversity data
6. Use GitHub for conducting and managing reproducible research projects

## Student assessment

- **Assignments:** Students will be given worksheets containing in-class exercises, which will also include assignments that need to be submitted via GitHub.
- **Reading:** When assigned, students will need to read literature prior to class meetings.
- **Group project:** Students will be assigned to groups and will conduct an independent project that will be presented to the class.
- **Participation:** Students will need to attend and actively engage in discussion and computational exercises.

## Late Assignments

We expect that worksheets will be submitted via GitHub on time. We expect that you will let us know in advance if this is not possible. Otherwise, late assignments (<1 week from deadline) will be given partial credit. Assignments submitted >1 week after deadline will receive no credit. You will receive an incomplete

for the course if you receive two or more no-credit evaluations or if you receive four or more half-credit evaluations.

## **Academic Integrity**

As a student at IU, you are expected to adhere to the standards and policies detailed in the Code of Student Rights, Responsibilities, and Conduct. When you submit an assignment with your name on it in this course, you are signifying that the work contained therein is all yours, unless otherwise cited or referenced. Similar standards are assumed for presentations and the generation of web-based media. Any ideas or materials taken from another source for either written or oral use must be fully acknowledged. If you are unsure about the expectations for completing an assignment, be sure to seek clarification beforehand. All suspected violations of the Code will be handled according to University policies. Sanctions for academic misconduct may include a failing grade on the assignment, reduction in your final grade, a failing grade in the course, among other possibilities, and must include a report to the Dean of Students.

## **Attendance**

Given the small number of class meetings and group work involved in the class, in-person attendance is required. If you are sick, please let instructors know, and appropriate accommodations will be made. Unexcused absences will negatively affect a student's grade. Any conflicts should be communicated to the instructor as early as possible, preferably before the beginning of the semester.

## **Special Needs**

Please contact the course director as soon as possible if you have a documented disability or any other issues that will interfere your performance of the activities planned for the class.

## **Schedule**

### **Week 0**

**Introduction to the computing environment** Prior to our first class meeting, students will install software, conduct basic exercises, and read introductory material.

### **Week 1**

#### **Introduction to Quantitative Biodiversity**

What is biodiversity and why do we study it? After introducing the course, we will provide an overview of GitHub and R. Laboratory exercises will include an exercise in GitHub followed by exercises in R such as data manipulations, plotting, and simple statistics.

### **Week 2**

**Diversity within a sample (i.e., alpha-diversity)** We will begin by introducing one the primary ecological data structures: the site-by-species matrix. From this, we will derive the core components of diversity: richness and evenness. We will integrate richness and evenness components by covering diversity metrics and the species abundance distribution (SAD).

### Week 3

**Diversity among samples (i.e., beta-diversity)** We will learn how to quantify diversity among samples (beta-diversity). We will then focus on the visualization of beta-diversity, which will include heatmaps, hierarchical clustering, and multivariate ordination.

### Week 4

**Diversity among samples (i.e., beta-Diversity)** We will continue discussing concepts and tools related to beta-diversity

### Week 5

**Diversity synthesis** We will recap and reinforce concepts from previous weeks while introducing new activities and tools related to data wrangling. We will construct a site-by-species matrix, introduce basic programming methods (e.g., loops), and use simulation methods to sample and analyze biodiversity data.

### Week 6

**Phylogenetic diversity: traits** We will learn how to make phylogenetic trees in R. After this, we will use contributed R packages to map traits onto trees, perform phylogenetically independent contrasts, and test for phylogenetic signal.

### Week 7

**Phylogenetic diversity: communities** We will continue to learn about the integration of phylogenetic for questions related to biodiversity. Specifically, we will think about phylogenetic community ecology, by introducing tools such as unifrac, net-relatedness index (NRI), and nearest taxon index (NTI).

### Week 8

**Group projects: GitOn!** We will use this class period for student presentations of their independent projects while recapping major concepts and tools, in addition to “big data” approaches to addressing global biodiversity issues.