Course Syllabus (Spring 2015)

Z620: Quantitative Biodiversity, Indiana University

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 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.

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. Last, we will learn how to map traits to phylogenetic trees and make inferences about the phylogenetic structure of communities. Students will be introduced to modern statistical computing and graphics environments, as well as the version control tools Git and GitHub.

Course Director

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Other Instructors

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Class meetings

9:30-12:00 Friday, room 155 in the Public Health (PH) Building, Janurary 16 - March 2, 2015

Course Website

http://documentup.com/QuantitativeBiodiversity/QuantitativeBiodiversity

Student Portal

IU GitHub (https://github.iu.edu/2015-QuantitativeBiodiversity/)

Recommended Textbooks

- Measuring Biological Diversity, Anne E. Magurran (2004) – (available online and on reserve in Life Science Library)
- Biological Diversity, Magurran and McGill (2011) – (available online soon! and on reserve in Life Science Library)

- 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)

Computational Approaches to Biodiversity Using R And GitHub

In this course, we will be using R and GitHub as complimentary 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. 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 IU's GitHub to host course material including this syllabus, code, and exercises. Each student will have their own private GitHub repository and will use GitHub to store and submit their work.

Other Course Resources

We will be assembling course literature, including reading assignments in our Quantiative Biodiversity Mendeley group. PDF versions of required papers, along with slides from class lectures will be posted on the IU's learning management system, Canvas. We will also use Canvas's etherpad tool, which is a real-time editor that will facilitate collaboraiton and problem solving inside and outside the classroom.

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 samples 3. Quantify the distribution of traits and species in a phylogenetic context 4. Use the R programming language to analyze and visualize biodiversity data 5. Use GitHub for conducting and managing reproducible research projects

Student Assessment

- **Assignments:** Students will be assigned in-class exercises, which will have problem sets that need to be submitted via GitHub.
- **Reading:** Students will be expected to read assigned papers from the primary literature prior to class meetings.
- **Participation:** Students will need to attend and actively engage in discussion and computational exercise.

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, attendence is required. Absences will negatively affect a student's grade. Any conflicts should be communicated to the instructor as early as possible.

Special Needs

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

Schedule

Note: This is a somewhat tentative schedule. The materials taught each week are subject to minor changes.

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. Last, we will highlight statistical approaches that allow one to test hypotheses about beta-diversity.

Week 4

Geographic divesity We will introduce ways to quantify the dispersion and aggregation of species in space. We will then learn about some of the major geographic patterns of biodiversity, including the spatial species abundance distribution (sSAD), distance decay (DD), and the species area relationship (SAR). We will conclude by using variance partitioning to quantify the contribution of geographic distance and the enviroment to species distributions.

Week 5

Null, Neutral, and Niche Perspectives on Biodiversity We will compare and contrast null, neutral, and niche-based explanations for biodiversity patterns using simple individual-based models. We will then use this framework to explore patterns of biodiversity (SAD, SAR, DD, SSAD, measures of alpha & beta-diversity).

Week 6

Introduction to Phylogenetic Diversity We will learn how to make phylogenetic trees in R. After this, we will use contributed R packages to map traits onto trees, peform phylogenteically independent contrasts, and test for phylogenetic signal.

Week 7

More on Phylogenetic Diversity We will continue to learn about the intergration 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

Synthesis We will use this class period for recapping major concepts and tools, in addition to "big data" aproaches to addressing global biodiversity issues. We will also devote class time to transferring IU GitHub respositories to a public GitHub site.