CourseSource Lesson Manuscript: **APPLYING NGS TECHNOLOGIES IN BIODIVERSITY DISCOVERY**

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Abstract

This lesson will bridge the gap between disciples and fields that sometimes seem unrelated to undergraduates, such as biodiversity, genetic, evolution, and conservation biology. Students will be engaged in active learning through hands on activities including using web resources, analyzing and using genetic data in tree construction, and finally using the genetic and tree hypothesis to predict the presence of new species.

Students will initially work in pairs and then discussion and debate will be among all students. We expect that this two level approach will foster collaboration, participation, and inclusive diversity.

Article Context:

Course
- Evolution

Course Level
- Introductory

Class Type
- Lecture/lab

Audience
- Life Sciences Major
- University

Class Size
- 1 – 50

Assessment Type
- Answer multiple choice question(s)
- Interpret data

Lesson Length
- One class period

Key Scientific Process Skills
- Asking a question
- Analyzing data
- Interpreting results/data
- Communicating results

Pedagogical Approaches
- Think-Pair-Share
- Collaborative Work
- Computer Model
- Pre/Post Questions

Bloom's Cognitive Level (based on learning objectives & assessments)
- Foundational: factual knowledge & comprehension
- Application & Analysis
- Principles of how people learn
- Develops supportive community of learners
- Leverages differences among learners

Vision and Change Core Concepts
- Evolution
- Structure and Function

Vision and Change Core Competencies
- Ability to tap into the interdisciplinary nature of science
- Ability to communicate and collaborate with other disciplines
- Ability to understand the relationship between science and society

KeyWords: cryptic speciation, DNA, conservation

Learning Goal(s)

- *Students will understand NGS.*
- *Students will appreciate the importance of phylogenetic analyses for conservation biology.*

Learning Objective(s)

For example:

- *Students will be able to compare DNA sequences and identify genes.*
- *Students will be able to determine how many genetic units represent new species and its impact on their conservation status.*

Introduction

Humans are witnessing for the first time in our history the extinction of an entire class of organisms: Amphibians (i.e., frogs, salamanders, and caecilians), an extinction only rivaling that of the extinction of the dinosaurs. At the same time that amphibians are disappearing, there are many species that remain unknown to science. Confounding this loss of biodiversity is the existence of 'cryptic species'. Cryptic species are morphologically indistinguishable; however, they represent separate evolutionary lineages. Fortunately, their evolutionary history is imprinted in their DNA. During this period we will examine genetic material and their utility in building phylogenetic trees that in turn will assist to identify separate evolving lineages misunderstood as a single species. Usually, species with wide geographic distributions are categorized as species of 'least concern' by the IUCN. Consequently, if this wide spread species represents complexes of 'cryptic species' then the conservation status must be reconsidered.

Intended Audience

The intended audience would be undergraduate students interested in the biological sciences and specifically the conservation of biodiversity during this time of mass extinction.

Required Learning Time

3 hrs Lecture/lab.

Pre-requisite student knowledge

General or introductory biology course with lab.

Scientific Teaching Themes

Active Learning

Students will work in pairs to examine sequences provided against Genbank to determine what they may correspond (e.g., nuclear coding gene, mitochondrial). Class with contrast and discuss their findings. Subsequently, students use the sequences to build a phylogeny and learning tree construction.

Assessment

Students will be evaluated on their competency and understanding in using tools such as Genbank Blast, for example what is the difference between % of sequence cover vs. % of sequence identity and how to determined genetic distances between pair of species and clades.

Teacher will assess use and understanding of Genbank and students thinking process in identifying monophyletic groups in the resulting tree.

Inclusive Teaching

To facilitate engagement of all class members, students will work in pairs encouraging collaboration and active participation of students in the process of analyzing sequence data and building trees; activities that required active discussion between the pair of studetns.

Lesson Plan

Pre-class preparation: students will be given an article where DNA sequences were used to build a phylogenetic tree.

30 minutes Lecture/discussion:

Discussion on paper and faculty providing additional background information as well as assessing the class overall knowledge and encourage student inquiry.

DNA SEQUENCE DATA. Pairs of students will be given four Sequences of DNA (sequences will be different among groups, e.g., coding, noncoding and mitochondrial sequences) from a geographically widely distributed species. First, they would blast the sequences to learn and get familiar with Gene Bank resources and applications. They will be expected to understand values such % of coverage vs. % of identity. They will also be expected to classify the organism to Phylum and get basic information (e.g. distribution, habitat) with Genbank, as well as other web-based databanks, resources (e.g., IUCN, etc).

TREE BUILDING. Students will compile all sequences from the class into single fasta files by DNA marker since they will need to be aligned by marker. The importance of the alignments in tree construction as well as simple ways to improve the alignments will be discussed. Students will be encouraged to discuss the significance and use (or not) of indels (insertions/deletions) in the alignments. The improved alignments will be used to build trees, both single maker trees and concatenated trees; students will discuss differences between trees. Faculty will present examples of rooted and unrooted trees asking the students the differences they see and what could be the explanations. Subsequently, we would discuss the role of outgroup selection in tree construction. For tree building, data will be run in SATE (web-based free software).

GENETICS AND CONSERVATIONA BIOLOGY. Based on examination of the resulting tree, students will be asked if they think the taxa represent a single or a complex of cryptic species considering in their discussion the knowledge they have previously collected regarding the species distribution. Student pairs will dedicate 15 minutes to exchange ideas and develop arguments to support a single or multiple species position. Then the floor will be open for entire class debate.

ASSESSMENT. At the end of the period, students will be given a short evaluation (consisting of multiple choice and interpretation of data) covering the concepts that were focused on during this learning period.

Modules	Duration
Preliminary Lecture	40 minutes
DNA Sequencing	40 minutes
Tree Building	45 minutes
Genetic and Conservation Biology	30 minutes
Assessment	25 minutes

Teaching Discussion

Share your observations about the Lesson's effectiveness in achieving the stated learning goals and objectives, student reactions to the Lesson, and your suggestions for possible improvements or adaptations to different courses or student populations. Subheadings can be included within the sections above to increase readability and clarity, following the embedded styles in Microsoft word:

Heading 2

Heading 3

Heading 4

Acknowledgments

Begin the Acknowledgements on a new page. The acknowledgements can include multiple paragraphs.

References

* Cite references in the parenthesis in text, in the order in which they appear.

1. Begin the reference list on a new page. The reference list is comprehensive and spans the text, figure captions, and materials.

2. Number references in the order in which they appear in the text. Follow ASM style and abbreviate names of journals according to the journals list in NCBI. List all authors of the reference.

Examples of reference style:

1. **Knight JK, Wood WB.** 2005. Teaching more by lecturing less. Cell Biol Educ. **4**:298-310.
2. **Samford University.** How to get the most out of studying: A video series. www.samford.edu/how-to-study/. Accessed August 20, 2013.
3. **Handelsman J, Miller S, Pfund C.** 2006. *Scientific Teaching*. New York, NY:W.H. Freeman.

3. Please add text notes to the end of the reference list; do not mix in references with explanatory notes.

Figure and Table Legends

Begin legends on a new page.

* **A separate file for each figure, table, and supplemental material item should be uploaded. Do not embed them in this text file.**

Tables

Table 1. Table legends should contain a short description of the table.

Figures

Figure 1. The figure legend should begin with a sentence that describes the overall “take home message” of the figure. Figure parts are indicated with capital letters (**A**).

Supplemental Materials Files

** Wherever possible, ensure that the article title and authors are visible when a reader opens the file, either in a header, on the first page/first slide, or as a “Notes” sheet in a workbook of spreadsheets.

Title supplemental materials as follows:

1. “Supplemental File S1.”
2. Short version of your article title (so that readers can easily tell which article a supplemental material is from). For example, shorten “Why Meiosis Matters: The case of the fatherless snake,” to “Why Meiosis Matters”.

Examples:

Supplemental File S1: Why Meiosis Matters,-Lecture Presentation Slides

Supplemental File S2: Bad Cell Reception-Assignment Worksheet

Supplemental File S3: Teaching PCR-Demonstration video showing how to use multi-colored yarn to create models of supercoiled DNA