**Natural History, Biodiversity, and the Growth of Evolutionary Thought: Syllabus (BSC XXXX)**

**Time:** 2hrs daily, Tu, W, Tr

**Location:** TBD

**Prerequisites:** none, open to non-majors

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Office Hours: TBD

**Course Description:** “There is grandeur in this view of life, … [that] from so simple a beginning endless forms most beautiful and most wonderful have been, and are being, evolved” is how Darwin concluded the Origin of Species. This class will explore Darwin’s world and demonstrate why this statement is even more apt today. The foundation for all of modern biology is evolution, and evolutionary thought stands out from other important scientific principles by the way in which it transformed how science and the society in general view the natural world. This class will trace the origins of biological thought from the explosion of discoveries about biological diversity arising from the Age of Exploration by northern European countries, especially the UK, the early development of natural history as a field and specifically of natural history museums as a repository of those discoveries, and how these museums and global exploration set the stage for the intellectual transformation that followed. In the first half we will dissect the writing of Charles Darwin as the best example of that unfolding realization — because it was a tour de force explanation of evolution — and as a mirror to the societal and intellectual perspectives of the era. With that as context, we will then bring the field to the present by summarizing the core concepts of modern evolutionary biology (and use the discoveries over the last 150 years to test the hypotheses of Darwin and his contemporaries), and survey the major elements of diversity of life on earth.

The great transformations in science are more often due to new ways of seeing nature than due to new data, but both were key to the growth of evolutionary thought. Therefore students will come to evaluate how the new data from exploration and collecting expeditions showing the vastness of biological diversity stimulated a fundamentally new and transformative model for understanding the history of life on Earth. The class will discuss how the models have changed over time as has the philosophy of science.

**Course Objectives:**  
By the end of this course, the student will be able to:

- Pose evolutionary hypotheses based on systematic classifications and the underlying scientific principle of common descent.
- Use modern phylogenetic methods and DNA sequence data to test and evaluate the claim of common descent.
- Analyze and interpret research results using appropriate phylogenetic methods.
- Summarize the broad outline of biodiversity and the relationships among selected major groups.
• Contrast the primary pre-evolutionary hypotheses for the history of life with the
current model of evolutionary thought, illustrate how each was reflected in the
development of natural history collections, and evaluate support for them.
• Demonstrate a basic mastery of the central concepts of evolutionary biology:
natural selection and phylogeny.

Liberal Studies for the 21st Century
The Liberal Studies for the 21st Century Program at Florida State University builds an
educational foundation that will enable FSU graduates to thrive intellectually and
materially and to engage critically and effectively in their communities. In this way
your Liberal Studies courses provide a comprehensive intellectual foundation and
transformative educational experience. This course has been approved as meeting the
Liberal Studies requirements for Natural Sciences and thus is designed to help you
become an effective interpreter of scientific results and critical analyst of claims
about the natural world.

Additional short readings may be assigned through the course Blackboard website.

Web Site: The course will use BlackBoard to provide a web interface. In it you will find
information about the class, schedule, handouts, links to web sites for the
assignments, links to interesting sites or other resources, any corrections, additions, or
news for the course, and access to the class e-mail list.

Attendance: Due to the interactive nature of lectures, attendance is mandatory. Class will
start promptly and important topics will often be discussed during the first five
minutes. You will be responsible for any information presented during class,
from the assigned reading, and for obtaining any handouts.

Excursions: There will be at least three visits to natural history collections, two as a
class to tour the collections themselves (herbarium and animal collection) and one to
conduct assignments individually using public exhibits.

Assignments: A series of take-home or museum-based assignments will be conducted
individually by students (see attached appendix).

Grading: There will be one final of 100 points, two quizzes of 20 pts each, and four
assignments of 40 pts each, plus 30 points for participation in class discussions,
yielding a total of 330 pts. The final grade will be based on cumulative points, with
90-100% an A-/A, 80-89% a B-/B/B+, 70-79% a C-/C/C+, and 60-69% a D-/D/D+.
For example, B+ is 0.899-0.87, B is 0.869-0.83, B- is 0.829-0.80. I reserve the right
to raise a grade under particular circumstances when the student has made unusual
efforts or improvements.

Exams: The exam will include multiple choice, short answer, short essay, and problem
solving questions. Make-up exams will be allowed only if the absence was
unavoidable and at the discretion of the instructor. Make-up exams may have a
different content and format.
Cell phones, smart phones, graphing calculators (including those often suggested for
physics classes) and similar text-compliant electronic devices are not allowed during
tests, only numeric calculators.
**General Policies:**

1. I expect you to be familiar with and adhere to the university's academic honor code as described in the FSU Student Handbook and below. Any claim of ignorance of the honor code is unacceptable. While I encourage students to help each other on assignments and studying, each student must turn in independent work. Obviously shared answers or photocopied printouts on assignments will be considered cases of copying.

2. You are responsible for everything covered in lectures and assigned readings. Note that for some topics, the assigned reading may not have extensive overlap with the lecture material. This means that you may encounter exam questions on material that is covered in the text but was not discussed in lecture. I expect you to know and understand the assigned material regardless of its origin (textbook or lecture). Of course, office hours and review sessions may be used for questions about any required material.

3. You are free to ask for a re-evaluation of any part of any examination or assignment (i.e. a "re-grade") under these conditions. First, your request must be turned in to me no later than one week after your graded examination or assignment is returned to you; no requests will be accepted after the one-week deadline. Second, your request must be in written form explaining why you believe your answer was graded incorrectly or why the question was unfair, etc. Third, all re-grading decisions are final.

4. If you must miss a scheduled examination you must notify me no later than one week before the examination. If you miss a scheduled examination due to illness or unanticipated circumstances you must bring a doctor's note to verify the illness or other documentation for other circumstances. When you present that material to me, we will schedule a make-up examination for you. If there are other circumstances that create a problem for you in taking an examination on the scheduled day, please talk to me about them.

5. If you wish to be excused from class to observe a religious holy day in your faith, please notify me in advance so that we can arrange for you to make up the work you will miss.

6. I will call your attention to these policies on the first day of class and thereafter expect you to be familiar with them.

**UNIVERSITY POLICIES**

**University Attendance Policy:** Excused absences include documented illness, deaths in the family and other documented crises, call to active military duty or jury duty, religious holy days, and official University activities. These absences will be accommodated in a way that does not arbitrarily penalize students who have a valid excuse. Consideration will also be given to students whose dependent children experience serious illness.

**Religious Holidays:** Each student shall be excused from class to observe a religious holy day of his/her faith. Please notify the professor early in this semester if this applies to
you, and make arrangements ahead of time to make up any missed work. See: http://registrar.fsu.edu/bulletin/undergrad/info/integrity.htm.

**Academic Honor Policy:** The Florida State University Academic Honor Policy outlines the University’s expectations for the integrity of students’ academic work, the procedures for resolving alleged violations of those expectations, and the rights and responsibilities of students and faculty members throughout the process. Students are responsible for reading the Academic Honor Policy and for living up to their pledge to “. . . be honest and truthful and . . . [to] strive for personal and institutional integrity at Florida State University.” (Florida State University Academic Honor Policy, found at http://fda.fsu.edu/Academics/Academic-Honor-Policy.)

**Americans With Disabilities Act:** Students with disabilities needing academic accommodation should: (1) register with and provide documentation to the Student Disability Resource Center; and (2) bring a letter to the instructor indicating the need for accommodation and what type. Please note that instructors are not allowed to provide classroom accommodation to a student until appropriate verification from the Student Disability Resource Center has been provided. This syllabus and other class materials are available in alternative format upon request.

For more information about services available to FSU students with disabilities, contact the: Student Disability Resource Center, 874 Traditions Way 108, Student Services Building, Florida State University, Tallahassee, FL 32306-4167. (850) 644-9566 (voice) (850) 644-8504 (TDD). sdrc@admin.fsu.edu. http://www.disabilitycenter.fsu.edu/

**Free Tutoring from FSU:** For tutoring and writing help in any course at Florida State University, visit the Academic Center for Excellence (ACE) Tutoring Services’ comprehensive list of tutoring options - see http://ace.fsu.edu/tutoring or contact tutor@fsu.edu for more information. High-quality tutoring is available by appointment and on a walk-in basis. These services are offered by tutors trained to encourage the highest level of individual academic success while upholding personal academic integrity.

**Sexual Harassment Policy:**
It is the policy of the University that its employees and students neither commit nor condone sexual harassment in any form. Refer to: http://registrar.fsu.edu/bulletin/grad/info/university_notices.htm

**Syllabus Change Policy:** Except for changes that substantially affect implementation of the evaluation (grading) statement, this syllabus is a guide for the course and is subject to change with advance notice.
Course Schedule

Summary of topics and associated in-class activities, out of class assignments, and readings.

1) Models of the history of life from Plato through the mid 19th century
   a) Classical essentialism, Plato through early 19th century
   b) Merging of essentialism and religion into Natural Theology
   c) Iconography and revolutions in science

   Assignment 1: Tree of Life, a web-based exploration of the diversity of life and introduction to tree thinking.

2) Age of Exploration and the discovery of biological diversity
   a) Pre-scientific explorers
   b) Naturalists and the creation of Natural History and biogeography
      e.g., Alexander von Humboldt, Alfred R. Wallace
   c) Parallel growth of the natural sciences, especially geology (Uniformitarianism, deep time)

   Reading: Ruse, Michael, selected readings. Darwin Ch. 11, Geographic Distribution.

3) “Cabinets of Curiosity” and the development of natural history collections
   a) 17th and 18th centuries, Sir Hans Soane

   Activity: visit museum, e.g., Viktor Wynd Museum
      Behind the scenes tour of natural history museum, (e.g., Natural History Museum, London, or UFL Museum of Natural History)

   Assignment 2: Natural History Museum Scavenger Hunt and the Changing Nature of Exhibits.

   Reading: Bell, Ch. 1, The Evidence for Evolution. Darwin Ch. 9, The Geologic Record.

4) Darwin, the “Origin of Species,” and the transformation of biology
   a) The voyage of the Beagle and exploration by colleagues
   b) Darwin’s transformative insights: population thinking, tree thinking, evolutionary change as such, natural selection
   c) Darwin’s critique of his own model, roadmap to testing hypotheses

   Activity: visit Down House (Darwin’s home)
   Activity: visit herbarium (e.g., Kew Gardens or Godfrey Herbarium)

   Reading: Darwin Ch. 3-6, 8., Bell Ch. 2, The Engine of Evolution, Ch. 6, The Origin of Variation.

5) Evolution since Darwin and the three pillars of modern evolutionary biology
   a) natural selection (population thinking)
   b) speciation, and
   c) phylogeny (tree thinking)
Activity: classroom population genetics

Assignment 3: Natural Selection essay.

Reading: Bell Ch. 7, The Origin of Species, Darwin Ch. 6, Difficulties for the Theory

6) **Biodiversity and the Tree of Life**
   a) Basic phylogenetic methods
   b) A tour of the Tree of Life:
      1 - the three domains
      2 - plant diversity
      3 - invertebrate diversity
      4 - vertebrate diversity

Activity: Reassembling the Tree of Life from Assignment 1

Assignment 4: Testing Phylogenetic Hypotheses in Mammals

Reading: Bell Ch. 3, The Tree of Life, Ch. 4, The Diversity of Life, Darwin Ch. 13, Classification

7) **Natural history collections in the modern era**
   a) Modern practices of collecting, curation, scientific applications, and education
   b) Quick guide to the practice of systematics; testing hypotheses, the discovery and communication of biodiversity

Reading: Bell Ch. 5, The Ancestry of Life.
Assignment Descriptions

Assignment 1: Climbing Around in the Tree of Life

Learning Objectives:
After this activity, students will be able to:
1. Use phylogenetic trees to summarize the evolutionary history and diversity of living organisms.
2. Explain how the current branching structure of the tree of life (the “Tree”) has become much more complex than the traditional kingdoms of older classifications.

Introduction:
This activity is intended to increase your familiarity with biological diversity, particularly the vast numbers of groups of organisms to which we seldom are exposed, and how that diversity is organized by phylogenetics. For example, the three kingdoms of older classifications — plants, animals, and fungi — together form just a small branch at the tip of one of the major divisions — Eukaryota— used in modern classifications. Even within the familiar groups, most branches are unfamiliar even to biologists. Systematists have spent much of the last two centuries working out the relationships among organisms so that we can classify them. In the last few decades that effort explicitly searches for evidence of evolutionary relationship and the branching structure of our Tree has become much more complex — and consequently, our understanding much richer. As you do this activity, I strongly encourage you to explore some of the side branches along the way (you will be amazed).

A second objective is to start you along the road to mastering “tree thinking,” a fundamental scientific approach to visualize, “quantify,” and describe biological diversity. Phylogenetic relationship forms the underlying framework for all of comparative biology, and phylogeny is the Tree. Here you will work with one way of drawing phylogenies, a cladogram, that shows the branching order of lineages, that is their “family tree.”

You will be using the Tree of Life Project (http://tolweb.org). It is an international collaborative project (organized by twins David and Wayne Maddison) with each group of organisms or branch of the Tree being written by an expert on that group. The branches are connected by links that effectively let you climb up and down the Tree one set of branches at a time. This is almost the same as moving forwards and backwards through the time in the history of life. On each page is information about the taxon (a taxon is a unit of classification, e.g., Phylum Arthropoda, Class Mammalia, Order Primates). Check them out as you explore. Note: each web page will have a small phylogeny that this assignment will call a “tree” (in lower case) which is just a small piece of the “Tree” (of Life, capitalized).

Procedure overview:
Each person will pick up 6 slips of paper. One is a From species with the URL for its page in the Tree of Life. The other 5 are To species without URLs. The From and To species will belong to different Domains, or basal trunks, in the Tree (Archaea, Eubacteria, Eukaryota). Your assignment is to start at the From species by typing its URL into your web browser. Then follow links down the Tree to the Root (“Life on Earth”) and then go back up a different branch to find the To species. There are millions of possible combinations of species, so each student’s set will be different. At each step, write down on a blank sheet of paper name of the taxon for that page/branch and any defining characteristics. Each taxon name is connected by lines (forming the entirety of the branch). After reaching the first “To” species. Look at the next
“To” species. “Climb” down the branch until you reach where you think the lineage to your second species branches off, and follow the links back up the Tree until you reach that species. Repeat for all 5 species. When you are done, you will have a simplified phylogeny or tree, of Life of Earth. Then redraw the tree to make it neat and to fit on the page, and label as instructed. Write down the URLs of each “To” species as proof that you found them via the Tree. Later, the class will combine all of the students’ individual trees into one big tree to illustrate how they all fit together.

Rubric:
Every tree will be different, but will be compared to the known phylogeny and where needed, reference to the Tree of Life website for confirmation. Grading as follows:
1) Accuracy of the tree structure (5 branching points, 2 points each correct)
2) Correct documentation of non-branching nodes (named taxa) on the tree (number of nodes varies with species chosen from approximately 20 to 70, and so the percentage of correct nodes for their particular tree times 20 points total)
3) Correct URLs for the To species(5 points)
4) Quality of graphical presentation (5 points)

Assignment 2: Natural History Museum Scavenger Hunt and the Changing Nature of Exhibits
Learning Objectives:
After this activity, students will be able to:
1. Explain how the display of material in natural history exhibits changed from a pre-evolutionary to post-evolutionary (current) time periods.
2. Identify and explain the primary scientific principle that is used to organize exhibits today and provide examples from those exhibits of its application.

Introduction:
What we as individuals or as a people save to cherish is a reflection of what we consider important, and thus a reflection of how we see the world. Museums and collections are primary examples. From the 16th to early 19th centuries, personal collections predominated, to evolve into institutions built around first sharing with the public and increasingly preserving for posterity important aspects of our world. In this assignment you will visit natural history exhibits on your own, starting in a scavenger hunt tracking down clues, while at the same time taking note of how biological materials and biodiversity is presented at those museums. In addition to learning about the evolution of natural history museums, this assignment will also expose you to the diversity of life to enhance your appreciation of that diversity.

Procedure overview:
You will first visit the Sloane collections at the Viktor Wynd Museum, or refer to lecture notes if the museum is not accessible. While following the clues, take note of the organization of the items on display. How are items grouped? Taxonomically? Geographically? By date of collection? Or some other eclectic criterion? After completing the section on the Sloan collection, visit the Natural History Museum.

For each clue below, answer the associated question, provide the exhibit case number to indicate the precise location in an exhibit hall, and, where appropriate, provide the scientific name for the species or taxon.
Sample clues:
Find the shrunken head. Where is it from? What bird was collected from the same island and exhibited nearby?

This pterosaur is only represented by a skull and was named after a French explorer.

What species of tree is the tallest in the world? Where does its live?

This family of beetles is famous for their iridescent green bodies. Find the exhibit of about 20 of them. Briefly explain how iridescence is produced.

In addition to the scavenger hunt clues, 10 points will be based on questions requiring evaluation of the evidence presented in some of the exhibits. Answering these questions will require finding evidence not only specific to a single exhibit, but will require finding and synthesizing evidence from other exhibits.

Sample synthesis question:
The pterosaurs in case “XX” are reported to have diversified initially around 225 million years ago. What evidence is presented to support this date? Cite and describe the exhibits that are the source of the evidence. Which evidence consists of direct observation and which requires indirect inference?

Note: If taught in London, this activity would involve visiting the Viktor Wynd and Natural History Museums outside of class individually, both museums being accessible by public transit or on foot. If taught in Tallahassee, the students would refer to lecture notes regarding 18th century collections and complete the assignment as part of a class field trip to the Florida Natural History Museum.

Rubric:
Scavenger hunt type questions are 2 or 3 points each for those only involving identifying the sought after exhibit, and 4 points each when some interpretation of the exhibit is involved (2 points for fully correct interpretation, 1 point off for interpretations that name the correct issue but either lack an explanation or have an incorrect explanation). Scavenger hunt questions, 25 points total.

Synthetic questions will be 5 points each (15 points total). Full credit requires correctly extracting from the lectures or the textbook the relevant features (synapomorphies) and briefly describing them, identifying the exhibit(s), describing the features as they actually appear in the specimens on display, and correctly explaining how the presence of those features provides evidence of relationship. One-half to 1 point deductions for the following: not citing or describing the feature to be sought, not citing the feature seen in the displayed specimens, not including some or all of the exhibits that highlight specimens with the feature, poorly explaining how synapomorphies provide evidence of relationship, or if the answer focuses on a feature diagnostic of a slightly more or less inclusive group (i.e., a synapomorphy from a node above or below the target node).

Assignment 3: Natural Selection Essay
Learning Objectives:
After this activity, students will be able to:
1. Clearly and concisely explain the process of natural selection.
2. Evaluate the relative contributions of alternative evolutionary processes.
**Introduction:**
In the evolution of life, the single most important mechanism that causes change in a population of species is natural selection. It was Darwin’s most famous insight (although not necessarily his most important). As such, it is important that any study of biology understand the process in its basic form. However, natural selection is not the only process that causes evolutionary changes. Genetic drift, migration, and a few minor processes like mutation can also produce evolution. A rich body of mathematical theory has been developed to quantify, explain, and predict all of these processes under a wide variety of conditions. The large majority of that theory is beyond the focus of this class, but some of the most basic equations are easily accessible. In addition, the concepts underlying that mathematics can be understood in fairly common terms. Therefore, an expectation for this class is that students will develop an understanding of the basics of natural selection and the primary additional processes, and be able to compare them for their relative contribution under normal or common situations.

**Procedure overview:**
Write an essay on the following question. It must be typed or computer printout, between 500 and 600 words long, approximately 2 double-spaced pages. Although the format is similar to a long essay question on a test, this is different because you will have ample opportunity to think long and carefully about what you say and to revise the essay. Therefore, I expect the essay to be well-crafted and written without spelling or grammatical errors. There should be topic sentences and a clear and logical argument. The writing must be succinct. Answer the questions directly. Edit out all unnecessary words, phrases, and sentences. You should expect that to get a good grade that you will have to revise the essay 2-3 times. Think carefully about what is important and how you present your information. This is not an English essay, but a scientific one, so avoid “setting the stage,” providing excessive background, or wordiness (for example, do not even mention Charles Darwin; he is irrelevant to the question). The grading of the assignment will reflect your ability to express ideas clearly and to synthesize information in your own words.

**Question:** Define and explain the process of natural selection. Briefly describe how two other primary processes of evolution — genetic drift and migration — may act to either strengthen or counteract the effects of selection, and under which conditions they do so.

**Rubric:**
The grading of the assignment in part reflects your ability to express ideas clearly and to synthesize information in your own words. I will also take off points for grammatical errors and lack of conciseness of your writing.

**Definition of natural selection:**
I am looking for a mechanistic explanation of natural selection that is not straight out of the book or other source. Full credit must state that selection acts on individuals – who survives and who leaves offspring, while the effects are seen only in populations. Listing Darwin’s Four Postulates is helpful, explaining how they apply to biology a bonus. Detailed, but accurate. (20 points)

**Discussion of factors that interact with natural selection:**
Partial credit for defining the processes, but full credit required discussion of whether each factor counteracts or enhances selection and under what circumstances. Points will be deducted without an explicit discussion. (10 points for each mechanism).

Genetic Drift:
Genetic drift can either counteract the effects of natural selection or can enhance natural selection. Its effect depends on the strength of selection, the population size and the frequency of
alleles being selected for. It will counteract selection if drift results in fixation of an allele that is not the best fit. Drift can enhance natural selection if the allele that happens to be fixed is the one favored by selection.

Common incorrect answers are that genetic drift counteracts selection because it decreases genetic diversity in the population. However, the end result of selection is not to create genetic diversity but that the most-fit allele becomes fixed in the population. Both processes actually reduce the genetic variation.

Migration:
Migration counteracts selection by reducing the genetic differentiation among populations that may be the result of natural selection. Explaining Founder Effect a bonus if both aspects are explained; being the product of migration, and resulting in strong genetic drift through small population size.

Assignment 4: Testing Phylogenetic Hypotheses in Mammals

Learning Objectives:
After this activity, students will be able to:
1. Conduct a phylogenetic analysis of DNA sequence data using the principle of maximum parsimony.
2. Formulate and rigorously test phylogenetic hypotheses.
3. Evaluate whether a given set of evidence provides support for a fundamental concept of science.

Introduction:
This assignment will give you the opportunity to test the fundamental model of evolution, that of common descent, meaning that species share an actual phylogenetic history, one of the most important hypotheses in all of science. Second, you will test several phylogenetic hypotheses that you formulate based on prior classifications. Third, you will gain experience actually conducting a phylogenetic analysis using the program PAUP* (Phylogenetic Analysis Using Parsimony, v.4.0), the most widely used software for this purpose. As much as possible, I have replicated what any researcher would do who assembles a data set from publicly available sequences stored on GenBank (the primary archive of DNA sequence data). You choose the data to use, you choose which hypotheses to test, you gather the data (with help from me), and you analyze them.

This project will use DNA sequence data that have been acquired for a wide variety of mammals. Each gene can be used separately to test phylogenetic hypotheses based on other genes or other characters (for example, morphology, or a classification). Every phylogenetic analysis can be used to test many hypotheses because each branch on the tree is an hypothesis that a group of species is related. So if a previously hypothesized group is not present in a tree, then that tree does not support the hypothesis. If the group is present, then the tree does support the hypothesis.

Procedure overview:
For this assignment, you will form into groups of three or four people. You will choose as a group which 20 species to include in the study out of a possible 40, then each member of the group will choose a different gene to work with. Then, you will download the sequences from a custom website designed to make this step easy, and combine them into one file. Next you will run a basic phylogenetic analysis on a computer, after which the group will meet to compare results and write up the results, particularly answering key questions. Finally, the entire class will discuss all the groups’ results and more generally, what constitutes a formal test in science.

Assignment detail excerpts (key sections are included below):
Guide to PAUP

This guide is intended for the first time user of PAUP* (Phylogenetic Analysis Using Parsimony) 4.0b. Specific PAUP menu commands will be highlighted in Helvetica, e.g., (Get trees from file).

Each data file has the following format. #Nexus starts each file. Next, after any comments, enter "begin data;" starts the Data block. The data block tells PAUP what format the data is in, and includes the data matrix. Only two command lines are required: dimensions, which defines the matrix size using ntax= and nchar=, and format, which includes datatype=, missing= and gap= " ". For example:

#NEXUS

BEGIN DATA;
   DIMENSIONS NTAX=4 NCHAR=17;
   FORMAT DATATYPE=DNA MISSING=? GAP=- ;
MATRIX
   Species_1    ATCCTGGATATCTCTGA [17]
   Species_2    ATCTTGGATATCTCCGA [17]
   Species_3    ATCCCTGGGTATCTCAGA [17]
   Species_4    ??TCTGAGCATCTCAGA [17]
;
END;

ntax is the number of rows, nchar is the number of columns (characters), missing is used when data is incomplete or uncertain, and gap tells what symbol is used to keep DNA sequences in alignment when there have been insertions or deletions in some species.

The start of the data matrix is indicated with matrix, no semi-colon. (Note: keep track of your semi-colons.) Tabs and spaces are used to separate the species name from the sequence data. There can be no spaces in species names however, so underscores ("_") must be used. Anything inside [brackets] is ignored by PAUP. Brackets are used for notes to yourself.

For this assignment, you will have 20 species (ntax=20), and the number of characters is the length of the DNA sequence for your chosen gene (the genes range from 900 to 3000 characters long).

3: Go to the Sequence Browser (click on the link, or go to http://bio.fsu.edu/steppan/SequenceBrowser/SeqBrowser.html). The first thing you will see is a classification of the species. To see a picture, just click on a species name and a picture of the animal (or representative species) will pop up. These should help you to choose which species your group will use. After you have become familiar with the species, choose as a group 20 of the species using the following guidelines:
1) You must include all marsupials (there will only be 1 or 2).
2) At least 4 orders must be represented by 2 or more species.
3) You must include the following minimum number of orders from the major clades:
   Xenarthra — 2
   Afrotheria — 2
   Laurasiatheria — 3
   Euarchontognires — 3
4) One order must be represented by at least 4 species.

Be very careful to satisfy all 4 guidelines.
You will want to select species that you are interested in (this assignment should be both fun and enlightening). As a general rule, in order to test whether a hypothesized taxon is monophyletic, you must have at least two members of it in the analysis. By following the guidelines above, you will be able to test many different phylogenetic hypotheses. For example, you will be able to test the monophyly of marsupials and placentals, of each of the 4 major clades, and of at least 4 orders (each of those represents a hypothesis based on previous data). Think carefully about what hypotheses you want to test. Your sampling will also allow you to test relationships among orders.

6: Meet as a group and compare your data.

1: Now you will test your trees for congruence, meaning do they agree in terms of topology (branching sequence)? First, everybody should label the major groups and taxa on each gene tree to the right of the species names (that is, identify any clades that correspond to the major groups like Afrotheria or Rodentia and each order).

2: Do a pairwise comparison of the clades shared between each group member’s phylogeny. Each member of the group should lay out their printed trees to do this comparison. Put two trees side-by-side and find and count all the clades (a node and all descendants) that are the same between both trees. When finished with the first comparison, continue with each possible student’s tree in turn. For each comparison, tabulate the number of clades in common to both and the number of clades present in the first that are missing in the second. You can use the form below as a guide for all pairwise comparisons among 4 genes (some groups will have three genes and do not need the rows that compare to a 4th gene).

<table>
<thead>
<tr>
<th>Gene 1 name</th>
<th>Gene 2 name</th>
<th># clades same</th>
<th># clades missing</th>
</tr>
</thead>
<tbody>
<tr>
<td>Gene 1 name</td>
<td>Gene 2 name</td>
<td># clades same</td>
<td># clades missing</td>
</tr>
<tr>
<td>Gene 1 name</td>
<td>Gene 3 name</td>
<td># clades same</td>
<td># clades missing</td>
</tr>
<tr>
<td>Gene 1 name</td>
<td>Gene 4 name</td>
<td># clades same</td>
<td># clades missing</td>
</tr>
<tr>
<td>Gene 2 name</td>
<td>Gene 3 name</td>
<td># clades same</td>
<td># clades missing</td>
</tr>
<tr>
<td>Gene 2 name</td>
<td>Gene 4 name</td>
<td># clades same</td>
<td># clades missing</td>
</tr>
<tr>
<td>Gene 3 name</td>
<td>Gene 4 name</td>
<td># clades same</td>
<td># clades missing</td>
</tr>
</tbody>
</table>

Q2. Would you say that the different genes corroborate each other? Each gene essentially tests the hypotheses from the other genes, so do the three genes (generally) confirm or reject the other’s hypotheses? Discuss in detail, including several examples if possible of key areas of agreement or disagreement.

Q3. Do these data support or reject the predictions of common ancestry among mammal species? Explain your reasoning.

Rubric:

1. Introduction
   a. Brief statement about phylogenetic analysis (Addresses Learning Objective 1; 2 points)
   b. Brief statement about the main questions/goals of the study. (Addresses Learning Objective 1; 1 point)
   c. State hypotheses: which species will form clades? State null hypothesis. (Addresses Learning Objective 1; 7 points, typically 1 point each, depending on the set of species selected)
   d. Predicted tree topology. (Addresses Learning Objective 1; 2 points)

2. Results
   a. State which hypotheses are corroborated and which are not in your personal gene tree (Addresses Learning Objectives 1 and 3; 8 points based on percentage of correct assignments)
Compare gene trees in your group to each other.

b. Similarity of gene trees based on clade counting (Addresses Learning Objective 3; 5 points)

c. Description of agreement in topology (Addresses Learning Objective 3; 5 points)

d. Answering of specific questions in the handout. (Addresses Learning Objective 2; 4 points)

3. Discussion

Is there a shared history of mammals? (Addresses Learning Objective 2; graded by how well the answer is reasoned and whether the results support the conclusion; high score given for evaluating whether complete agreement is needed or what criteria should be applied to accept or reject; 6 points)

Grading expectations:

a. Excellent (35-40 points)
   i. Conclusions consistent with results
   ii. Argument draws on multiple points of evidence
   iii. Conclusions address question/goals/hypotheses listed in Introduction

b. Good (30-34 points)
   i. Conclusions consistent with results
   ii. Argument misses some pieces of evidence
   iii. Conclusions address some but not all question/goals/hypotheses

c. Fair (25-29 points)
   i. Conclusions consistent with results
   ii. No argument or little engagement with results
   iii. Conclusions do not or mostly do not address questions/goals/hypotheses

d. Poor (<25 points)
   i. Conclusions not consistent with results, results in conflict with expectations such as to indicate a major error in procedures

Note regarding Liberal Studies Competencies:

This assignment, a simplified version of a set of assignments that I have used with biology undergraduates for years, was originally designed to address the very same competencies that now form the basis for the Natural Science competencies for Liberal Studies. I use this assignment because it is so effective at teaching students about applying the scientific method to historical data and events, and demonstrates that the scientific process is not limited to experimental systems. Therefore, this assignment is discussed below in relation to three different Course Objectives (1-3). In addition, Learning Objectives 2 and 3 (based on Natural Sciences competencies 2 and 3), are naturally achieved in a unified, coordinated fashion; evaluating claims (Objective 2) results in large part from proper analysis and subsequent interpretation of research results (Objective 3).
Appendix: Assessment of Liberal Studies Learning Objectives

Learning Objective 1: Pose evolutionary hypotheses based on systematic classifications and the underlying scientific principle of common descent.

The primary organizing principle for this course is the common descent of species. That concept developed out of the era of exploration and was needed to make sense of the greatly increased diversity that was discovered. It was Darwin’s singular contribution, the framework in which modern science now organizes the description of biodiversity, and the cornerstone of modern biology in general. It is also a very challenging concept for most students, encompassing deep time and thousands of interconnections among species; the genealogical description of which is called the Tree of Life. Most students struggle to develop even a superficial conceptualization. In addition, it is the single most socially controversial concept in science, and especially for non-biological science majors, understanding the scientific explanation for biodiversity prepares the students to draw their own conclusions. Both because common descent is such a powerful scientific concept and because it carries such emotional resonance (or dissonance), it presents an excellent model for evaluating the role of science in society, and more clearly exposes the nature of scientific inquiry itself.

Although the processes leading to common descent largely played out in the past, the overarching generality of this concept makes it well suited to developing hypotheses and predictions based on the model and testing those hypotheses. No laboratory or manipulative experiments are needed. Under this model, if species share a common history, then the heritable traits that changed (evolved) along this history should reflect it. Therefore, one set of traits should predict the status of other traits, and phylogenies based on different sets of traits should largely agree.

I will assess this objective most directly through the Introduction portion of Assignment 4, Testing Phylogenetic Hypotheses in Mammals. After establishing the central model of common descent, students must apply that model to biological diversity. They must translate the classification of mammals into a graphical, phylogenetic set of predictions for a novel data set that they will assemble. Each data set will be unique; it is unlikely that the specific combination of species and genes have ever been analyzed anywhere before, and each student’s set is different. They must recognize the generality of the model and apply it to specific data. This assignment makes up 40 points, 12% of the total, and the initial hypotheses formulation accounts for 4% of the total points in the class. Furthermore, the students must demonstrate the ability to distinguish multiple, sometimes overlapping predictions by correctly assessing topological concordance between their predictions and their resulting trees, as required in the interpretation of the results. The students will evaluate support for each predicted clade (a clade is a monophyletic group, that is, a single branch on a tree and all of its descendants), and compare their results to those of their group-mates. Therefore, they must demonstrate the ability to not only make predictions for their data set, but to evaluate the predictions of other students for their data sets. I will assess their competency by tabulating whether they make the correct number of predictions, whether the predictions are properly formulated, and by how well they justify their predictions in the text of the write-up. Independent of grading, I will also help the students refine their abilities through group discussion of the predictions and results.

Learning Objective 2: Use modern phylogenetic methods and DNA sequence data to test and evaluate the claim of common descent.

As discussed above for Learning Objective 1, the central tenant of modern biology is the common descent of species. Therefore, much of the material presented in this class, including Assignments 1 and 3, builds towards a direct test of this model. Specifically, I will illustrate how society’s understanding of biological diversity had changed over the centuries, and how that understanding crystallized into the common descent model. The lectures and readings then demonstrate the scope of the model — that is how far reaching and multifaceted its predictions are — and how it provides an organizing principle for our classifications, museums, and other mechanisms of scientific communication.
I will assess this objective in two parts: first through the questions forming the second half of Assignment 2, Natural History Museum Scavenger Hunt and the Changing Nature of Exhibits, and then through the Results and Discussion portions of Assignment 4, Testing Phylogenetic Hypotheses in Mammals. In the synthetic questions of Assignment 2, which together account for 15 points (5% of the total), the students must identify those characters from the textbook that are predicted to be shared derived characters (synapomorphies) of clades, and thus would constitute evidence for common descent. There are numerous examples that could be identified in the public displays in the Natural History Museum. Working on their own, students will search through the displays for examples that match the predictions, and then photograph and cite those examples as documentation. One of many of those examples is the presence of two sets of paired limbs that articulate with the vertebral system in tetrapods (Tetrapoda). Another is the presence of three sepals and three petals in the flowers of the taxon Monocotyledoneae (the monocots, like lilies and irises). The students will then be asked to evaluate whether their survey of life in the museum supports those predictions. The answers can range from the simple documentation of such characters to more synthetic and sophisticated recognition that exceptions to these predictions do exist and whether these exceptions falsify the model or merely require the addition of ad hoc mechanisms (for example, whales and snakes have lost one or both pairs of limbs, respectively). I will assess their competency through their ability to identify the characters and their explanations of the taxonomic distribution of those characters in the context of the model.

Assignment 4 is structured to directly assess how well students can apply scientific methods, recognize evidence, and evaluate claims (or support) for predictions about biodiversity. In this case, the methods consist of assembling DNA sequence data to create data sets and then running phylogenetic analyses. The evidence that they must first recognize as such and then subsequently evaluate is the set of clades estimated by the phylogenetic analyses. The most conceptually challenging aspect of the assignment requires students to evaluate not only whether the model has been supported or rejected, but the degree of support, and whether or not complete agreement is necessary for model acceptance. That is, does any conflicting result for a sub-prediction provide the basis for rejection of the entire model? I will assess the students’ success through the Results and Discussion in the write-up (28 points, 8.5% of the total; did they build their data sets correctly (the raw data will be turned in), did they run the analyses properly (as evidenced by realistic topologies and branch length distributions), did they correctly define tests, and did their explanations of their decisions demonstrate an ability to evaluate the degree to which the evidence support the claims? Although not a basis for grading, I will further assess and reinforce their competency by leading a class discussion comparing the results for the different students and their groups.

Learning Objective 3: Analyze and interpret research results using appropriate phylogenetic methods.

Assignment 4, Testing Phylogenetic Hypotheses in Mammals, provides the most direct means to assess this objective. The students will demonstrate the ability to conduct sophisticated phylogenetic analyses using specialized software that is actually one of the most widely used by practicing scientists. Although a powerful and versatile program, PAUP also employs a graphical user interface with most parameters set to appropriate defaults, and therefore the program is accessible to undergraduates. Nonetheless, the application of parsimony or maximum likelihood as optimality criteria, and understanding how these are applied to character data, requires the students to master important biological and statistical concepts. The correct interpretation of phylogenetic results requires synthesizing the concepts of deep time, common descent, and evolutionary change within lineages (via natural selection and genetic drift), as well as the ability to mentally translate historical genealogical associations into a graphical iconography.

Assignment 1, Climbing Around in the Tree of Life, while not employed here to directly assess this objective, is an important exercise to train students in “tree thinking,” the graphical iconography of evolution history, a skill critical to Assignment 4. Assignment 3, Natural Selection Essay, while likewise not a direct assessment of this objective, is a critical exercise to
train the students, through their multiple revisions of their own understanding, in “population thinking.” Population thinking is the conceptual foundation necessary to explain the mechanisms of divergence that result in phylogenetic trees, and is the concept that underlies the mechanisms of natural selection and genetic drift. Like tree thinking, population thinking is only superficially intuitive for most people at best, but its internalization by students is necessary to a full mastery of the diversification of life.

I will assess this objective through the Results and Discussion portions of Assignment 4. Grading will be based on the accuracy of the students’ phylogenetic results (demonstrating the ability to conduct scientific analyses; this is not part of the assessment for Learning Objective 2) and how well they demonstrate the ability to evaluate and interpret those results in the context of the tested model, common descent.

Learning Objective 4: Summarize the broad outline of biodiversity and the relationships among selected major groups.

The primary organizing principle for this course is the common descent of species, and modern classifications of life are organized around our understanding of the phylogenetic tree. Perhaps of more direct utility to non-scientists is simply an appreciation for the enormity of biological diversity and the major groups that are often mentioned in news reports, at zoos, etc… Even working biologists are ignorant of many significant (and fascinating) groups. This objective therefore addresses both scientific knowledge as well as a more emotional appreciation that may have a longer-term impact on their lives than the knowledge-based aspect.

I will assess the students’ competency in this objective principally through Assignment 1: Climbing Around in the Tree of Life, and secondarily through one or two test questions. In Assignment 1, students must navigate through the Tree and classification, thus experiencing the phylogeny rather than just memorizing it. By making many wrong turns, they inadvertently discover other groups of organisms, and because they are encouraged to explore when they see something interesting, an appreciation for life is fostered. The transcription of the tree in the write-up reinforces the learning experience, and the ungraded class discussion that synthesizes all the individual trees (each students’ portion of the Tree is different) provides additional reinforcement. This assignment makes up 40 points, 12% of the total. Students will be graded on the accuracy of the tree structure (5 branching points, 2 points each correct), correct documentation of non-branching nodes (named taxa) on the tree (number of nodes varies with species chosen from approximately 20 to 70, and so the percentage of correct nodes for their particular tree times 20 points total), successfully finding the To (target) species and demonstrating that with correct URLs (5 points) and clear graphical presentation (5 points).

Learning Objective 5: Contrast the primary pre-evolutionary hypotheses for the history of life with the current model of evolutionary thought, illustrate how each was reflected in the development of natural history collections, and evaluate support for them.

There have been two principal hypotheses for the history of life that have been widely applied in western civilization, and one transitional one. These are: (1) thousands to millions of special creation events with no diversification and no evolutionary change (the Biblical account), (2) millions or more special creation events with no diversification but with strong evolutionary change within lineages (Lamarck’s evolution model), and (3) a single origination event with diversification and evolutionary change (the modern scientific model). Two models (1 and 3) have dominated human understanding of the natural world. The transition between the two was initiated by the accumulating evidence of biological diversity and finalized by the presentation of a new conceptual model. Natural history collections reflected these models. Pre-evolutionary cabinets of curiosity were eclectically organized, each different reflecting the interests of the original collector. Modern natural history museums are nearly universally organized around phylogeny. Collecting efforts are now also systematically organized around phylogenetics. Finally, primary support for the modern model comes from the abundant derived characters
shared by related species and the fossil record. These features can often be recognized in the specimens displayed in natural history exhibits.

I will assess this objective through a portion of Assignment 2: Natural History Museum Scavenger Hunt and the Changing Nature of Exhibits as well as a short essay question on the test. Several synthesis questions ask the students to identify shared derived features (“synapomorphies”) from their lectures and readings and then search the exhibits for organisms displaying those features. Documentation will be in the form of photos (usually shot on cell phones) and careful documentation of cases. Students will be graded by whether the selected traits are synapomorphies and whether the photographed examples correctly document those features. A simple percentage will be applied for grading. These synthetic questions will account for 15 of the 40 points in the assignment. The test question, directly asking the students to contrast the models, will constitute 10 points, 3% of the total.

Learning Objective 6: Demonstrate a basic mastery of the central concepts of evolutionary biology: natural selection and phylogeny.

As pointed out here repeatedly, the central organizing concept of modern biology is common descent. But in addition, the primary explanatory process is natural selection. Natural selection was the pivotal insight that united Darwin’s and Wallace’s ideas about evolution by providing the mechanism that explained how common descent could work and explain the diversity of life. The basis of the concept is well known — “survival of the fittest” is the common caricature — but in practice is poorly understood. The difficulty most people have with mastering the concept is their unfamiliarity with “population thinking.” This mode of thinking requires the recognition that change takes place in the mean attributes of sets of organisms; the organisms don’t change, the populations do. This is a statistical concept. Properly taught, this concept can be mastered. However, in addition to natural selection, two other mechanisms are important, genetic drift and migration. The latter is quite easy to understand (organisms move from population to population, bringing their traits with them). The former is also strongly dependent on population thinking and statistical or sampling theory, that some change will inevitably be random. These alternative mechanisms can either enhance the effects of natural selection or retard them, depending upon the circumstances. A sophisticated understanding of evolutionary change requires not only an understanding of how natural selection works but a more synthetic evaluation of the interactions between these mechanisms.

I will assess Learning Objective 6 directly though Assignment 3: Natural Selection Essay. That assignment constitutes 40 points, 15% of the total. The concept of phylogeny is well assessed in several aspects separately through Learning Objectives 1-4, which are discussed above.