What factors affect speciation?
1. The Galapagos Archipelago consists of a dozen islands all within 64 km of their nearest neighbor. From 1 to 11 of the 13 species of Darwin’s finches live on each island. Many evolutionary biologists believe that if there had been only one island, there would be only one species of finch. This view is supported by the fact that Cocos Island is isolated (by several hundred kilometers of open ocean) from all other islands in the archipelago, and only one species of finch is found there.
   a. How does the existence of an archipelago promote speciation? Explain or provide an example.

b. Is the mode of speciation that occurred on these islands more likely to have been allopatric or sympatric? Explain.

c. Is the type of speciation seen on the Galapagos Archipelago more likely to be the result of anagenesis or cladogenesis? Explain.
2. Hybrids formed by mating two different species are often incapable of reproducing successfully with each other or with members of their parent populations. Explain why this is the case. (*Hint*: Consider what you know about chromosome numbers and meiosis.)

3. Because most hybrids can’t reproduce, their genes and alleles (and the alleles of their parents) are functionally removed from the population. Only the alleles of individuals who interbreed remain in the population. This implies that there is a strong selective advantage for genes and alleles that enable individual organisms to recognize members of their own species. A wide range of reproductive isolating mechanisms have been identified.

Each of the following scenarios describes a reproductive isolating mechanism. Indicate whether each is a prezygotic or postzygotic isolating mechanism. Explain your answers.

   a. Crickets use species-specific chirp patterns to identify a mate of their own species.
   b. Two species of butterfly mate where their ranges overlap and produce fertile offspring, but the hybrids are less viable than the parental forms.
   c. Two species of a plant cannot interbreed because their flowers differ in size and shape and require pollination by different species of bee.
   d. Two species of firefly occupy the same prairie and have similar flash patterns, but one is active for a half-hour around sunset while the other doesn’t become active until an hour after sunset.

4. Do you think the concept of a species is a useful biological tool? Why or why not?
How are phylogenies constructed?
Construct a modified concept map to relate the ideas of phylogeny and systematics, below, to the cladogram on the next page.

- Begin by writing each term on a separate Post-it note or piece of paper.
- Then indicate how the terms are associated or related to each other and to the cladogram on the next page.
- Be sure to include definitions or descriptions of all the terms as you use them to explain these relationships.

TERMS TO KNOW:

- clade
- cladistics
- cladogram
- homologous
- analogous
- monophyletic
- paraphyletic
- convergent evolution
- symplesiomorphy
- synapomorphy
- outgroup
- ingroup
- taxonomy
- phylogeny
- allopatric
- sympatric
- anagenesis
- cladogenesis
Ancestral vertebrate

- Vertebral column
- Jaws; Two sets of paired appendages; Mineralized (ossified) skeletons and teeth
- Lungs or lung derivatives
- Legs
- Anniotic egg
- Milk
- Osteichthyes (bony fishes)
- Diaph (ray-finned fishes)
- Actinopterygii (ray-finned fishes)
- Chondrichthyes (cartilaginous fishes; sharks and rays)
- Cephalaspidomorphi (lampreys)
- Myxii (hagfishes)

Feathers
1. On the cladogram shown on the previous page, is the group that contain humans, whales, crocodiles, and birds a monophyletic or paraphyletic group? Explain.

2. Considering only the individual organisms in the cladogram, which traits can be used as good examples of analogy or convergent evolution? As good examples of homology? Explain your reasoning.

3. In recent years, DNA sequence data has been used to understand phylogenetic relationships among organisms and to modify our existing cladograms.
   a. What type of DNA has been used most commonly in this analysis? Why was this chosen over others?
   b. The phylogenies developed using DNA sequence analysis may differ from those constructed using morphology and physiology. How do evolutionary biologists know which is more correct?
Something for fun:

Put yourself in the professor’s shoes: What questions would you ask?

A great way to study for an exam is to put yourself in the professor’s shoes. For example, ask yourself: What questions would I ask about the material if I were the Professor? Asking and answering such questions are good practice for taking the actual exam because it forces you to organize the major ideas and concepts you have studied.

Write three exam questions designed to test how well a student understands the major concepts in phylogeny and speciation. Indicate the correct answer to each question and also tell the reason why each alternative answer is incorrect. Your questions should be of the following types:

I. Problem solving or application of a concept or principle to a problem
For example: The little-known hypothetical organism *Skyscra parius* is a long-necked animal that feeds on the leaves of Australian trees that grow to heights of 30 feet. Being a hooved animal, *S. parius* cannot climb trees, so it feeds much like modern-day giraffes do. Fossil evidence indicates that the ancestors of *S. parius* had fairly short necks. Read the arguments presented below. For each, indicate whether or not the factors described could have affected neck length or tree height over the course of evolution of *S. parius*. [A = factors described could have affected neck length; B = factors described probably did not affect neck length]

1. ________ *S. parius* ancestors likely demonstrated significant variation in neck length, with some having shorter necks and others having longer necks.

2. ________ When first born, juveniles of *S. parius* were much shorter than adults, so they were not able to compete successfully with adults that had longer necks.

3. ________ Female *S. parius* preferentially mate with longer-necked males.

II. Translation: the ability to recognize concepts restated in a different form or to restate concepts in a different form
For example: In what ways are the structure and function of the reptile egg and the amniotic egg (in this example, the chicken’s egg) similar? In what ways are they different?

T/F 1. Both the reptile and the chicken’s egg contain stored food for development of the embryo.

T/F 2. When laid by the chicken or reptile, both the reptiles and the chicken’s egg contain a partially developed diploid embryo/offspring generation.

T/F 3. The shells of the egg help prevent desiccation (water loss) in a similar fashion/

T/F 4. Gestation time is the same for reptiles and chickens.

Write/type your exam questions on a separate sheet of paper.

Exam Question 1:

*Answer:*

Exam Question 2:

*Answer:*

Exam Question 3:

*Answer:
Classification I

Purposes for classification:
1. **Practicality** (Operationality, ease, stability)
2. **Information Content** (Optimal summarization of what is known about entities)
3. **Predictivity** (Of unknown features of entities)
4. **Function In Theories** (Should "capture" entities acting in, or resulting from, natural processes)

Classification vs. taxonomy vs. systematics?

The majority view is that "systematics" is the more general term, being defined as the study of organismal diversity, whereas "taxonomy" is more narrowly the set of procedures and rules for naming organisms and organismal entities (taxa) and producing "classifications" (ordering and/or nesting of taxa).

How would you define cladistics in this grouping?

Natural classification

All three schools of systematics want to produce "natural" classifications, but disagree on what counts as "natural":
1. **Pheneticists** view natural groups as those taxa linked by the greatest similarity to each other; characters not weighted. Note that "phenetic" vs. "phylogenetic" is not the same distinction as "phenotypic" vs. "genetic" (an unfortunate similarity in sound).
2. **To evolutionary systematists**, "natural" groups are defined by gaps between taxa in characters for which an evolutionary scenario can be argued. Characters are weighted by adaptive significance.
3. **Cladists** consider natural groups to be monophyletic, and thus "natural" classifications reflect the tree of life. Note that "cladist" does not equal "parsimony advocate" -- the former term reflects a philosophy of classification, the latter term reflects a preference for one of several related character-based approaches to tree-building, all of which yield cladograms.

The winning argument for phylogenetic classifications

The debate over classification has a long and checkered history (see Hull 1988; Stevens, 1994). A conceptual upheaval in the 1970's and 80's resulted in a true scientific revolution -- Hennigian Phylogenetic Systematics. Many issues were at stake in that era, foremost of which was the nature of taxa. Are they just convenient groupings of organisms with similar features, or are they lineages, marked by homologies? A general, if not completely universal consensus has been reached, that taxa are (or at least should be) the latter (Hennig, 1966; Nelson, 1973; Farris, 1983; Sober, 1988).

A summary of the arguments for why formal taxonomic names should be used solely to represent phylogenetic groups is as follows: evolution is the single most powerful and general process underlying biological diversity. The major outcome of the evolutionary process is the production of an ever-branching phylogenetic tree, through descent with modification along the branches. This results in life being organized as a hierarchy of nested monophyletic groups. Since the most effective and natural classification systems are those that "capture" entities resulting from processes generating the things being classified, the general biological classification system should be used to reflect the tree of life.

The German entomologist Willi Hennig codified the meaning of these evolutionary outcomes for systematics, in what has been called the Hennig Principle (Hennig, 1965, 1966). Hennig's seminal contribution was to note that in a system evolving via descent with modification and splitting of lineages, characters that changed state along a particular lineage can serve to indicate the prior existence of that lineage, even after further splitting occurs. The "Hennig Principle" follows from this: homologous similarities among organisms come in two basic kinds, synapomorphies due to immediate shared ancestry (i.e., a common ancestor at a specific phylogenetic level), and symplesiomorphies due to more distant ancestry. Only the former are useful for...
reconstructing the relative order of branching events in phylogeny. A corollary of the Hennig Principle is that classification should reflect reconstructed branching order; only monophyletic groups should be formally named. Phylogenetic taxa will thus be "natural" in the sense that they are the result of the evolutionary process.

This isn't to say that phylogeny is the only important organizing principle in biology. There are many ways of classifying organisms into a hierarchy, because of the many biological processes impinging on organisms. Many kinds of non-phylogenetic biological groupings are unquestionably useful for special purposes (e.g., "producers," "rain forests," "hummingbird pollinated plants," "bacteria"). However, it is generally agreed that there should be one consistent, general-purpose, reference system, for which the Linnaean hierarchy should be reserved. Phylogeny is the best criterion for the general purpose classification, both theoretically (the tree of life is the single universal outcome of the evolutionary process) and practically (phylogenetic relationship is the best criterion for summarizing known data about attributes of organisms and predicting unknown attributes). The other possible ways to classify can be used simultaneously, but should be regarded as special purpose classifications and clearly distinguished from phylogenetic formal taxa.

**Phylogenetic classification in detail:**

1. Three ways of defining a name: **Node-, Stem-, or Apomorphy-based.**
2. Different ways of defining **monophyly:**
   a. **Synchronic** (i.e., "all and only descendants of a common ancestor") or,
   b. **Diachronic** (i.e., "an ancestor and all of its descendants"). Which is better? Should the word "species" appear in the definition of monophyly? Does it matter?
3. **Clade versus Lineage** (see next page for illustration). They are not the same thing -- "clade" is a synchronic concept, a snapshot of a lineage -- while a lineage is a diachronic concept, a series of replicators.

**Three major logical phases of a phylogenetic analysis:**

(1) **Pre-cladistic phase** (synthetic, inductive)
   • The elements of a cladistic data matrix (i.e., characters, and character-states) are assembled.
   • This complex process involves considerable reciprocal illumination (since developing hypotheses of distinct, independent characters with discrete states goes hand in hand with developing hypotheses of homogeneous characteristics).

(2) **Cladistic analysis** (analytic, deductive)
   • The data matrix is translated into a cladogram using a parsimony model.
   • Reciprocal illumination is often involved here as well, since incongruence between characters or odd behavior may lead to a return to phase 1 (a reexamination of characters, and models) primarily to check for fit to assumptions of the cladistic method:
     • Homogeneous characters should be employed, and be the result of a diverging process rather than a reticulating process; characters should be discrete, heritable, and independent.

(3) **Classification and evolutionary studies**
   • The cladogram is translated into a classification, based on an assessment of the relative support for different clades.
   • Formal taxa (including species) are named here, on the basis of clear support for their existence as monophyletic cross-sections of a lineage, and for their utility in developing and discussing process theories.