

# Bio 1M: Midterm 1 extra notes (complete)

## 1 Phylogeny

- *Bioskills are in the back of your book*
- Phylogeny is the evolutionary history of a group of organisms
- Based on the idea that organisms are related by evolution
- Understanding these relationships is critical to our understanding of both evolution, and how biological processes work

### Phylogenetic trees

- A **phylogenetic tree** is a model of how a group of organisms descended from a common ancestor
- The model consists of **nodes**, where groups split, **branches** where evolution occurs, and **tips** representing observed **taxa** which are the endpoints of the process we are trying to model.
- A point where more than two branches diverge is called a *polytomy*.
  - Polytomies mean we don't know which event happened first.

### Monophyletic group

- A **monophyletic group** is a group *defined by* a single common ancestor
  - All descendants of the ancestor must be in the group
- Monophyletic groups can also be called **clades** or **taxa**.
- As biologists, we should try to think in terms of clades
  - Are flying vertebrates a clade?
  - What are some prominent groups that are not clades?
    - \* **Answer:** apes, reptiles, trees

### Sister taxa

- Sister taxa can be a useful way of thinking about trees
  - two taxa that share a common node
  - You need to take the whole taxon
- E.g., sisters of: *Homo sapiens*; *Homo erectus*; humans?
  - **Answer:** *Homo neanderthalensis*; *Hn* and *Hs*; *Paranthropus*

## Reading phylogenetic trees

- The tree indicates the pattern of branching of **lineages** (evolving lines)
- Tips are *assumed* by the model to be monophyletic
- A tree is a model of how evolution occurred
  - Trees that correspond to the same model are considered equivalent

## Order of species

- Except for the branching pattern, we don't interpret anything about the order of a tree
  - No species are higher or lower than others, according to the tree
  - We've all been evolving for the same amount of time
- How do we judge how closely related two organisms are, according to a tree?
  - **Answer:** By looking for their common ancestor

### 1.1 Constructing phylogenetic trees

- First, measure **characteristics** (or **characters**) of the taxa of interest – i.e., anything that seems useful to measure
  - Can be **morphological** (i.e., physical) or genetic
- Then infer (make an educated guess about) the phylogenetic relationships.
  - **Phenetic** approaches use measures of distance between organisms
  - **Cladistic** approaches are based on modeling how evolution occurs on the tree

## Morphological vs. genetic characteristics

- Should we use morphological or genetic characteristics to infer phylogenies?
  - We usually have more information from genetic characteristics, and this information is easier to measure precisely
- When should we use morphological characteristics?
  - **Answer:** When genetic information is not available
    - \* **Answer:** Most fossil organisms
  - **Comment:** Some viruses evolve so fast that morphological characteristics can be more stable than genetic characteristics

## Phenetic vs. cladistic analysis

- Cladistic analysis makes use of the phylogenetic model of organisms evolving from each other to infer phylogenies
- Phenetic analysis ignores the phylogenetic model of organisms evolving from each other while inferring phylogenies
- Which is better?
  - **Answer:** Cladistic analysis
- When should we use the other one?
  - **Answer:** When our data are only distances, with no characters available – e.g., certain molecular techniques

## Synapomorphies

- Classical cladistic analysis is based on **synapomorphies** – shared, **derived** characters
  - as evidence that two taxa are related
- Why do we focus on derived characters?
  - **Answer:** These are things that evolved in the relevant context
  - **Answer:** So they are the things our model (the phylogenies) must explain

## Flight as evidence

- Oaks and fish don't fly, but birds do
  - **Answer:** We're pretty sure that the common ancestor didn't fly
  - **Answer:** No evidence (any model will have flight evolve once)
  - **Answer:** Flight evolved once in either case
- Mosquitoes and birds fly, but fish don't
  - **Answer:** Evidence (flight might have evolved once or twice on this tree)
  - **Answer:** But this evidence points in the wrong direction
    - \* **Answer:** This is why we combine evidence from different sources

## What characters are derived?

- Derived compared to what?
  - The common ancestor (characteristics of the common ancestor are called **basal** or **ancestral** characters).
    - \* What if our flight example was ostriches, hawks, and sparrows?
    - \* **Answer:** No evidence for similarity between hawks and sparrows
  - A **derived** character is a character not shared by the common ancestor of the group that we are currently thinking about
  - One way to think about cladistic vs. phenetic analysis is that phenetic analysis treats derived and basal characters equally

## Inferring the common ancestor

- We want to know what the common ancestor was like, so we can tell which characters are derived (as opposed to basal)
- This can be done sometimes by common sense
- Inferring the common ancestor statistically is difficult, for technical reasons
  - We can make use of an **outgroup** to study a group. An outgroup is an organism closely related to, but outside, the group being studied.
  - We assume that the the **root**, or beginning, of the tree is where the outgroup branches from the group

## Confusing the phylogeny

- Two species may have the same trait because the trait evolved twice independently – **convergent evolution**
  - **Answer:** Flight, trees, dolphins and ichthyosaurs
- An organism may lack a character that its ancestors had – **secondary loss**
  - This can be even more confusing
- Similarities that are not homologies (ie., not due to common ancestry) are called **homoplasies**

## Parsimony

- Classical cladistic analysis is based on searching for the tree that can explain the observed data most **parsimoniously** – with the fewest number of changes necessary.
- How do we address the problem of convergent evolution and homoplasy?
  - **Answer:** Make use of many different characteristics, when possible
  - **Answer:** It may also help to use many different taxa
- *Comment:* Modern approaches that use genetic data may use more sophisticated approaches, rather than simple parsimony