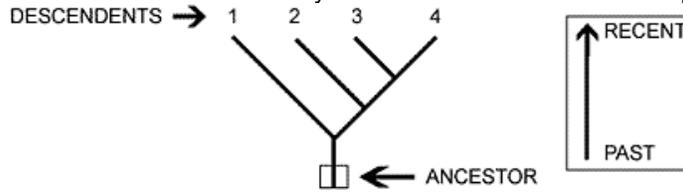


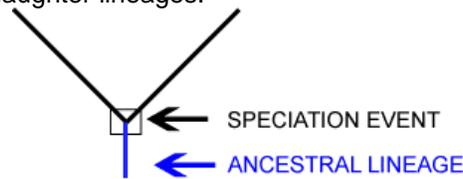
Phylogenies

The process of evolution produces a pattern of relationships between species. As lineages evolve and split and modifications are inherited, their evolutionary paths diverge. This produces a branching pattern of evolutionary relationships. By studying inherited species' characteristics, we can reconstruct evolutionary relationships and represent them on a "family tree," called a **phylogeny**.

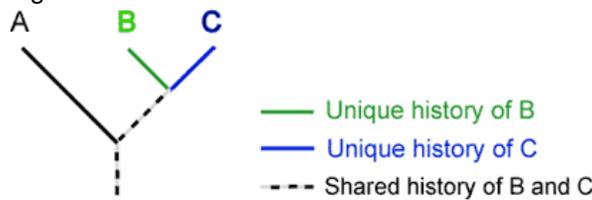
Understanding a phylogeny is a lot like reading a family tree. The root of the tree represents the ancestral lineage, and the tips of the branches represent the descendants of that ancestor. As you move from the root to the tips, you are moving forward in time.



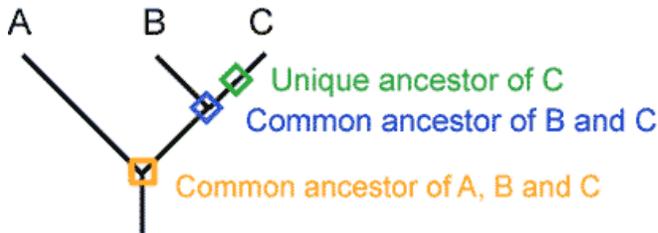
When a lineage splits (speciation), it is represented as branching on a phylogeny. When a speciation event occurs, a single ancestral lineage gives rise to two or more daughter lineages.



Phylogenies trace patterns of shared ancestry between lineages. Each lineage has a part of its history that is unique to it alone and parts that are shared with other lineages.

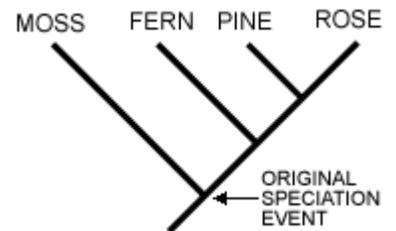


Similarly, each lineage has ancestors that are unique to that lineage and ancestors that are shared with other lineages—common ancestors.



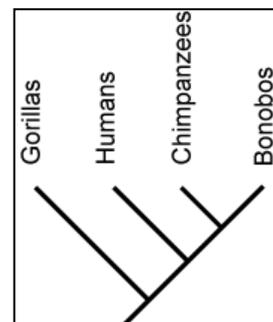
It's easy to misinterpret phylogenies as implying that some organisms are more "advanced" than others; however, phylogenies don't imply this at all.

In this highly simplified phylogeny, a speciation event occurred resulting in two lineages. One led to the mosses of today; the other led to the fern, pine, and rose. Since that speciation event, both lineages have had an equal amount of time to evolve. So, although mosses branch off early on the tree of life and share many features with the ancestor of all land plants, living moss species are not the ancestors to other land plants. Nor are they more primitive. Mosses are the cousins of other land plants.



The phylogeny of living species most closely related to us looks like this:

Question #1: Based on this phylogeny, humans are most closely related to which organism(s)? How do you know?

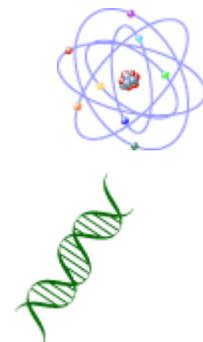
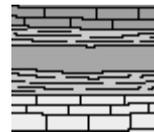


Evolutionary Time

If you wanted to squeeze the 3.5 billion years of the history of life on Earth into a single minute, you would have to wait about 50 seconds for multicellular life to evolve, another four seconds for vertebrates to invade the land, and another four seconds for flowers to evolve—and only in the last 0.002 seconds would “modern” humans arise.

Life began 3.5 billion years ago, and insects diversified 290 million years ago, but the human and chimpanzee lineages diverged only five million years ago. How have scientists figured out the dates of long past evolutionary events? Here are some of the methods and evidence that scientists use to put dates on events:

1. **Radiometric dating** relies on half-life decay of radioactive elements to allow scientists to date rocks and materials directly.
2. **Stratigraphy** provides a sequence of events from which relative dates can be extrapolated by looking at layers that have formed in the earth's crust.
3. **Molecular clocks** allow scientists to use the amount of genetic divergence between organisms to extrapolate backwards to estimate dates of a common ancestry.



Since we are studying DNA, we will focus on MOLECULAR CLOCKS.

For the past 40 years, evolutionary biologists have been investigating the possibility that some evolutionary changes occur in a clock-like fashion. The molecular clock hypothesis suggests that random mutations in the DNA sequence have a rate proportional to the passage of time. In other words, ticks of the clock correspond to the number of changes in the DNA sequence that occurs over time. An accurate molecular clock would make it possible to put a timepiece to evolutionary events. Instead of settling for relative relationships, a functional molecular clock could apply absolute dating to the development and divergence of life (phylogenetic history).

Over the course of millions of years, mutations may build up in any given stretch of DNA at a reliable rate. For example, the gene that codes for the protein alpha-globin (a component of hemoglobin) experiences base changes at a rate of 0.56 changes per base pair per billion years. If this rate is reliable, the gene could be used as an estimate for a molecular clock.

Using molecular clocks to estimate divergence dates depends on other methods of dating. In order to calculate the rate at which a stretch of DNA changes, biologists must use dates estimated from other relative and absolute dating techniques.

Biologists often represent time on phylogenies by drawing the branch lengths in proportion to the amount of time that has passed since that lineage arose. The following phylogeny represents vertebrate evolution. The lengths of the branches have been adjusted to show when lineages split and went extinct.

Question #2: Answer the following questions based on the phylogenetic tree shown above:

- Which group shares the most recent common ancestor with snakes? When did this ancestor live?
- Which group shares the most recent common ancestor with birds? When did this ancestor live?
- When did the non-avian dinosaurs go extinct?

Question #3: If there is a 22 nucleotide base sequence difference for a gene found in both humans and penguins, what is the estimated mutation rate for that gene (your answer should be in # of mutations per million years). Use the phylogenetic tree shown and SHOW YOUR WORK.

