

Exploring Bioinformatics: A Project-Based Approach
Key for BioConcept Questions, Chapter 6

1. In your own words, what is a molecular clock?

“Molecular clock” is a term sometimes used for a gene that can be used to measure evolutionary change. Any gene that is clearly conserved among the species to be tested can potentially be used, as changes in its sequence among species represent mutations occurring over evolutionary time. However, some genes may be subject to more selective pressure in some species than others, so it’s important to select a “clock” gene that in fact changes at a constant rate as much as possible.

2. Measuring the rate of substitution between two species is not the same as measuring the rate of mutation. What is the difference between mutation and what an evolutionary biologist understands by substitution?

Any two individuals’ genomes could differ by a random mutation at any given nucleotide. But a tiny variation isn’t important evolutionarily if only one individual has it. Evolutionary biologists use the word “substitution” to mean a mutation that spreads through a population over time so that it becomes one of a few recognizable major variants in a particular gene or sequence.

3. What advantages does the use of gene comparisons have over traditional phylogenetic methods such as comparing the bone structure or other observable features of various species? Can you think of any potential disadvantages of these molecular methods?

Comparing genes can be a way to look beyond superficial similarities to find out what is really happening at the molecular level—since all the variation we see has its roots in genetic change, this is in a sense looking at variation at its most fundamental level. But, even molecular comparisons can be misleading: perhaps a gene used for comparison has not changed at a steady rate over time, for example. They are also much more computationally and labor intensive than comparing more accessible features of the organisms.

4. If you wanted to draw a phylogenetic tree for all living things (bacteria, fungi, plants, animals...), what sorts of genes might serve as reasonable molecular clocks? What would be examples of genes that would *not* be good clocks? How might your choice change if you wanted to look at evolutionary relationships only among primates?

You would need a “clock” gene that is conserved among *all* living things to draw such a tree. One such gene that is commonly used is the 16S ribosomal RNA gene, which is recognizably conserved in bacteria, archaea and eukaryotes. A tree that only looks at primates would have a lot more flexibility in terms of what “clock” genes might be used: something like the casein gene (unique to mammals) would work fine even though most living things lack this gene.

5. Suppose there are four differences in the sequence of a gene between species A and species B, and also four between the sequences for species B and species C. You would initially think that A is just as closely related to B as B is to C. But what might have happened that would make this conclusion false?

You can’t see just from the number of changes what the pathway of change was. Perhaps on the path between the ancestor of A and B and the modern species, a C changed to a T and then changed back: that’s two more changes (for a total of six, rather than four), but you can’t see any direct evidence of that just by comparing the sequences.