

Upon completion of *The HIV Clock (WB)*, students should be able to:

1. Describe mutation in the context of a DNA or RNA sequence.
2. Explain how random genetic drift can affect the frequency of a mutation in a population.
3. Predict that, on average, a new neutral mutation in one individual is unlikely to spread through a population over the long term.
4. Define a molecular clock.
5. Describe how the number of neutral sequence differences between two related populations correlates with the number of generations since the populations split.
6. Explain how mutations accumulate differently in a population over time depending on whether the mutations are neutral, beneficial, or deleterious.
7. Given data showing the number of neutral sequence differences between two populations over time, and the equation of a best-fit line for the data, estimate the number of generations since the populations diverged.
8. Understand that the number of neutral sequence differences between two populations increases linearly over time.
9. Describe the evolutionary relationships among the populations represented in a phylogenetic tree.
10. Given a hypothesis about when two related populations diverged, determine whether or not data on sequence differences over time support the hypothesis.
11. Given different rates of molecular evolution for different regions of a population's genome, make a reasonable prediction about whether mutations incurred in the regions are neutral, beneficial, or deleterious.