Exploring Bioinformatics: A Project-Based Approach

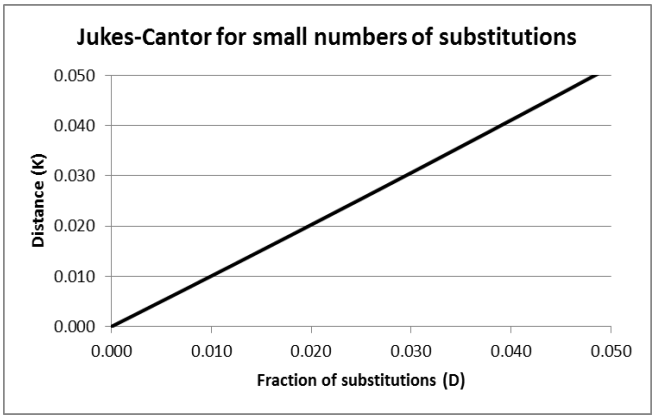
Key for Test Your Understanding Questions, Chapter 6

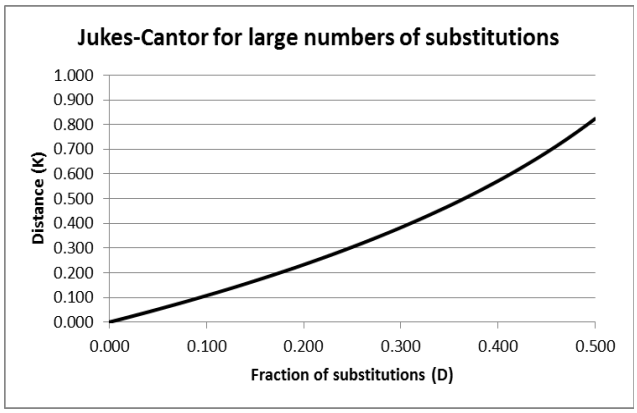
1. Two aligned sequences for the same gene differ by four substitutions, all transitions. Two more sequences for the same gene also differ by four substitutions, two transitions and two transversions. Which pair of sequences has probably been evolving independently longer, and why do you think so?

   Because transversions are rarer than transitions, it seems likely that more evolutionary time would have to have passed in order for two transversions to have occurred versus two transitions. So, there is probably more evolutionary distance between the second pair (at least, Kimura would have thought so).

2. Using the Jukes-Cantor equation and a spreadsheet, determine K for some values of D between 0 and 1. Then graph K vs. D. What happens to the rate of change of K as the number of observed substitutions increases? Why did Jukes and Cantor think this was a desirable result?

   For small numbers of substitutions, the increase in distance looks essentially linear as the number of substitutions increases. But, as more and more substitutions occur, the Jukes-Cantor model calculates an exponentially increasing distance, accounting for the increased likelihood of "hidden" substitutions.





3. Using the Kimura equation and a spreadsheet, determine K for some values of S and V. Keep the sum of S and V constant. Then graph K vs. V. What happens to K as V increases? Why did Kimura think this was a biologically relevant pattern?

   You might not have expected this, but the Kimura formula actually gives smaller evolutionary distances as transversions increase so long as the total number of substitutions is small. Since transversions are rare, the likelihood is that a small number of them represents the actual number of mutations that have occurred. But, as the number increases, the distance begins to increase exponentially, reflecting the long evolutionary time that would be required for many of these rare mutations to occur.