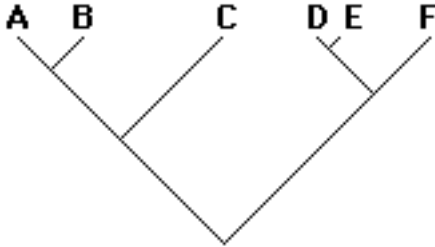


PRACTICE PROBLEMS 1

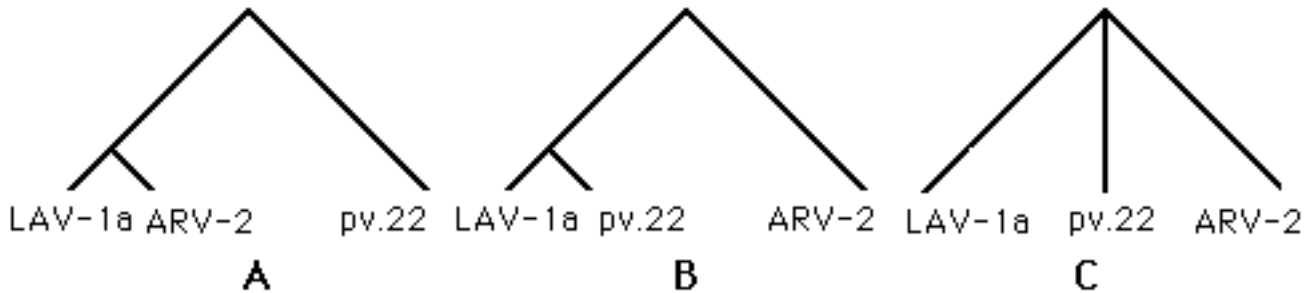
Problem 1. In the following tree, identify all possible clades. Why isn't A C a clade?



Problem 2. Two evolutionary geneticists compared the base sequences of the *gag* genes of three different viruses that cause AIDS. The results are as follows:

differences between	base pair differences per 1,500 base pairs
LAV-1a and pv.22	6
LAV-1a and ARV-2	42
pv.22 and ARV-2	45

Based on these data, which is the correct phylogenetic tree for these viruses (A, B, or C)?



Problem 3. Assume that the molecular clock ticks at a rate of 5×10^{-9} bp substitutions per bp per ye. On a volcanic island you find two species of *Drosophila*, descended from one species that colonized the island some time after it first rose out of the ocean. You sequence the *Adh* genes of the two species and find they show 5 synonymous substitutions in 1 kbp.

- What is the frequency of synonymous substitutions between the two species?
- How long ago did the two species diverge?
- How old is the island?

Problem 4. On the next page is a phylogenetic tree of the SSU rRNA gene from 13 species of spore-forming bacteria related to *Bacillus subtilis*, and an outgroup (*Lactobacillus casei*). At the top is *Bacillus permians*, obtained from a drop of salt water inside a bed of salt in a salt mine. The salt was deposited in the Permian period about 250 Mya. The scientists who isolated it argued that their *B. permians* clone must have come from a spore formed 250 Mya, which lay dormant in the salt bed since then. Sequence data show that its closest known relative is *Bacillus marismortui*, isolated from the highly saline Dead Sea. Both of these isolates are very salt-tolerant. What do the sequence data say about the age of *B. permians*?

