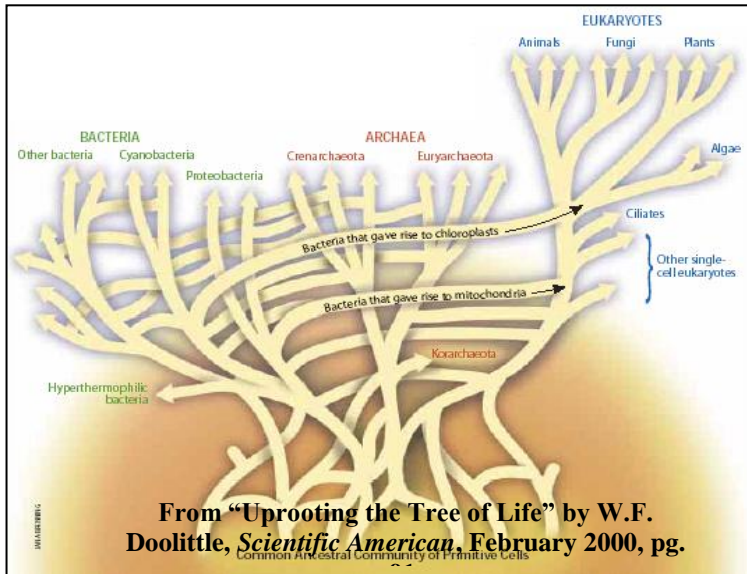
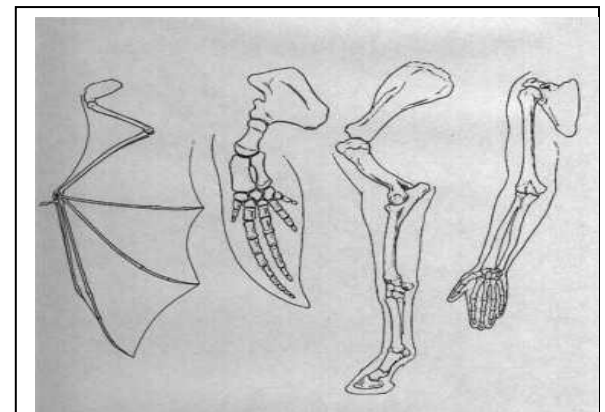


# Phylogenetic Evidence in a Nutshell



The hypothesis that all life forms are related through “common ancestry” can be tested by constructing hypothetical “family trees” (called “phylogenetic trees”). In the field of systematics, evolutionists construct phylogenetic trees by comparing the similarities of characteristics or DNA sequences of organisms. Since the DNA codes for the characteristics, one would expect phylogenetic trees constructed by both methods to be the same. In addition, if common descent is true, trees should show neat lines of ancestry and inheritance. But, such comparisons often do not form a “tree,” as is demonstrated in the “bush” at left. This phenomenon is well-known, as one evolutionist said,

*“competing ... proposals [of] the prevailing phylogenies of the mammalian orders would reduce [the mammalian tree] to an unresolved bush...”* This occurs because, when different characteristics of organisms are compared, they commonly predict different trees. Trees based upon one gene commonly conflict with trees based upon another gene. Similarly, how “related” two organisms are based on DNA sequence very much depends on which sequence is examined. This should not be the case if common ancestry were true. Furthermore, such analyses make a prior, and therefore scientifically invalid, assumption: similarities are the result of common descent rather than “common design” (compare the limbs at right as evidence for “common design”). These assumptions and discrepancies show that this type of evidence for common ancestry is weak.



Couldn't these limb similarities be the result of *common design* rather than common descent?