

QUESTION 1. Suppose that the following sequences represent homologous introns (admittedly very short ones) from gene X in organisms 1, 2, 3 and 4, with the dashes denoting gaps.

1 G T C T T T C G T C A G G - T G G A C G T C C C C A G C C C A G

2 G T C T C G A G C C A G T C T G G G T G T T C T C A G C C C A G

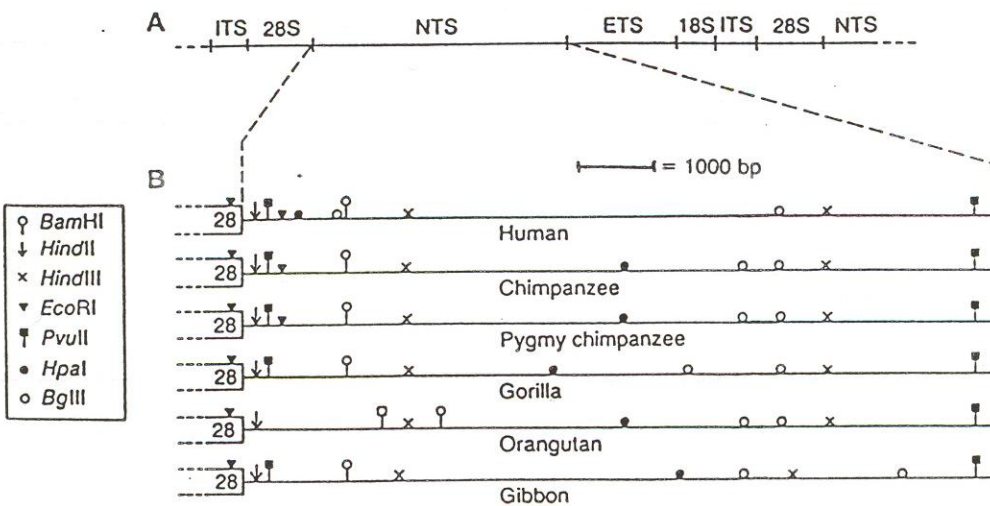
3 G T C T T T G A - C A A G A T G A T G A T C C T T A G C C C A G

4 G T C T C G T A A C A G T C T G G G - G T T C T C A G C C C A G

- Use the UPGMA method to reconstruct a phylogenetic tree from these data. Be sure to show your reasoning. What are limitations of the UPGMA method?
- With these same data, use the maximum parsimony method to infer potential relationships. Be sure to show your reasoning, and explain (with examples) how sites can differ in their informational content.
- What are advantages/disadvantages of using *intron* sequences in tree reconstruction?

QUESTION 2

Use the UPGMA method to reconstruct a phylogenetic tree from the data shown below.

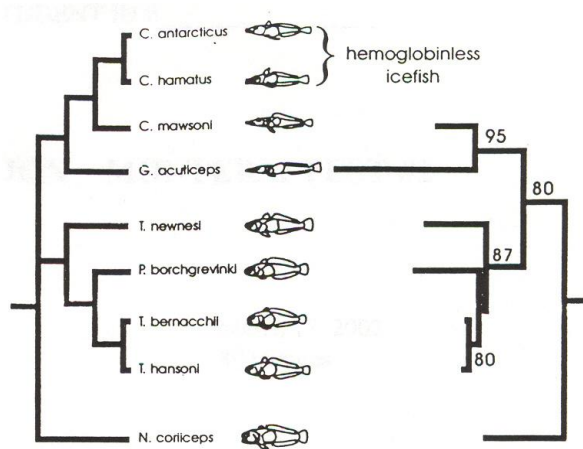


Restriction enzyme maps of the nontranscribed spacer regions in the rRNA genes of human and apes. (A) The organization of one of the repeated units, in which the transcribed region carries sequences for 18S and 28S rRNA. (B) The sites recognized by seven restriction enzymes are indicated for the nontranscribed region of each of several species.

QUESTION 3

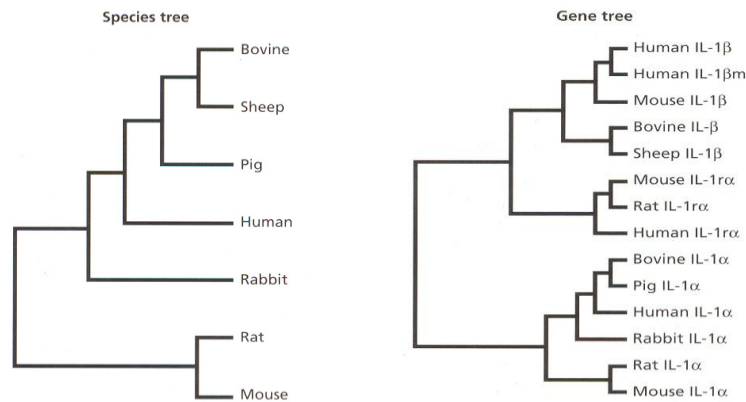
This figure is from a research paper on Antarctic fish hemoglobins (Bargelloni et al. *PNAS* 95:8670, 1998). Tree A (left side) is a species tree and tree B (right side) is based on β -globin

sequence data. How do you interpret these data? What questions arise from these observations, and what strategies could be used to address them?



QUESTION 4

Interleukin-1 (IL-1) sequences from various mammals were used to generate the tree shown on the right side below. [Page & Holmes "Molecular Evolution: A Phylogenetic Approach", 1998, p.289]. How do you interpret these data? Give possible evolutionary models and tests that you could perform to distinguish among them. Note that in 1998 the complete genome sequences were not available for any of these animals. In your answer, give possible reasons why a gene tree might differ from a species tree.



QUESTION 5

You have discovered, in an Arctic ice core sample, what you believe is an ancient microorganism. Instead of having two translation elongation factor genes (EF-G and EF-Tu), it has only one. What strategy would you use to determine its position on a "tree-of-life"? Give your rationale and include clearly-labelled trees with its possible position(s) in your answer.