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EEOB563

Assignment #3

1a.

1b. The sequences are homologous but this is not necessarily the best alignment. There are a multitude of alignment programs and algorithms that serve certain projects and sequences better than others. Using the Blosum 62, aligning the two sequences base or base appears to be the best given the circumstances. There are no places where a gap will provide a better outcome.

2a.

2b.

2c. Theoretically, we found ONE of the best trees we could. It is impossible currently to find the single best tree for any sample due to the sheer number of possible tree and the impossibility of finding every single tree and comparing them. That is why certain processes such as TBR and NNI etc. are used. To try and find the best tree, then add to it and find a new best tree, and continue this process. In the end, it finds a tree that is pretty good.

3a. In order from left to right (ATG on the left and CTT on the right) the fourth and fifth are informative. That is because there are at least two character states present that are also in at least two sequences. Many of the sites have two character states but the base change is present in only one sequence making it uninformative.