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-- OliverVoigt - 24 Feb 2013

Assignment 3- SeaView alignment editor

1. In the file [accasions_hydra.txt](#) you find accession number of a *Hydra* dataset, containing sequences of the mitochondrial cytochrome oxidase subunit 1 gene. Import these sequences into [SeaView](#) and save the file in nexus format to ensure that additional changes in the assignment are saved with the file. Attention: The Hydra sequences are in the wrong orientation, so you need to reverse-complement them. To do so, choose ONE sequence at a time, go to "Edit-Complement sequence". A reverse-complement sequence will occur in the alignment, delete the original sequence to continue. Align the sequences automatically or manually.
2. [SeaView](#) can translate DNA sequences to proteins (in the props menu). It will always assume that position 1 of the alignment is codon position 1. To change the reading frame, you will have to add gaps to all sequences, if necessary. The sequences are mitochondrial, the genetic code for cnidarian mitochondrial genes is 4. Mark all taxa and set the correct code in the edit menu. How can you recognise the correct reading frame? What is the correct reading frame (+1,+2 or +3)?
3. Create three different site sets: including all positions where sequence information is available for all taxa three datasets, where all taxa have information for: Codon positions 1+2 and 3, respectively. Save the file, open it in a text editor and check the file syntax.
4. Use the "tree" menu to calculate a distance tree for each set (codon position 1, codon position 2, codon position 3). Compare the trees- how do they differ??



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