

# Comparisons of Genes in Organisms

Use the GenBank database to find the base sequence of a gene in two or more species. Then use the Clustal Omega tool to align base sequences in order to determine the differences between species. You will then be able to use create a Phylogram to help determine evolutionary relationships.

Your task is to analyse the differences between three or more species (the skill asks for two species, but the online Clustal tool works better with a minimum of three).

In order to see how these tools will work, you will run through the procedure using the COX1 (cytochrome c oxidase) gene and the following four organisms to practice: *Drosophila melanogaster* (fruit fly), *Gallus gallus* (chicken); *Bos taurus* (cattle); *Pan troglodytes* (chimpanzee).

For each chosen species retrieve the base sequence:

- Go to GenBank website <http://www.ncbi.nlm.nih.gov/genbank>
- Select "Gene" from the search bar.
- Enter the name "COX1".
- Select the "Name/Gene ID" to get a detailed view
- Scroll down to the "Genomic regions, transcripts, and products" section and click on "FASTA"
- Copy the entire sequence from '>' onwards
  - ✓ Save the sequence to a word document or open up a new browser and follow the instructions on aligning the sequences.
  - ✓ You will need to align with all other species you are comparing.

To align the sequences:

- Go to the Clustal Omega website <http://www.ebi.ac.uk/Tools/msa/clustalo/>
- In STEP 1 Select "DNA"
- Paste the chosen sequences into the box (each sequence must start on a new line)
- In STEP 2 leave output on "Clustal w/o numbers"
- Press 'Submit' (and wait – depending on the size of the sequences you may have to wait for a couple of minutes)
- Click the "Results Summary" tab.
- Click the "Percent Identity Matrix" to quantify the overall similarity (0 = no similarity, 100 = identical)
- Print your results and key out your organisms (1= *Drosophila melanogaster* (fruit fly); 2= *Gallus gallus* (chicken); etc)
- Click your back button to return ththe "Results Summary" tab.
- Click on the to "Phylogenetic Tree" tab.
- The default Phylogram is the Cladogram view.
- Chose the "Real" option for the Phylogram to get a visual representation of how similar the species are (based on the chosen gene).
- Sketch your "Real" Phylogram on your "Percent Identity Matrix" printout using the organism names instead of the gi code.

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**Exploration:** Repeat the assignment using a gene of your choice and compare the sequence in three different organisms. Make sure you;

- turn in your practice work using COX1
- turn in your "Percent Identity Matrix" printout of your gene comparison.
- write the name of your gene on your printout with a brief explanation of it's function.
- don't forget to sketch your exploration "Real" Phylogram.