



WILDLIFE GENETICS

INTERDISCIPLINARY PROJECT: BIOLOGY,
COMPUTING AND SUSTAINABILITY

STEM education and training seeks not only to develop expertise and capability in each individual field but also to develop the ability and skills to work across disciplines through interdisciplinary learning.



GROUNDING IN THE BIOLOGY CURRICULUM

N5

Cell Biology, Key Area 3: DNA and the production of proteins

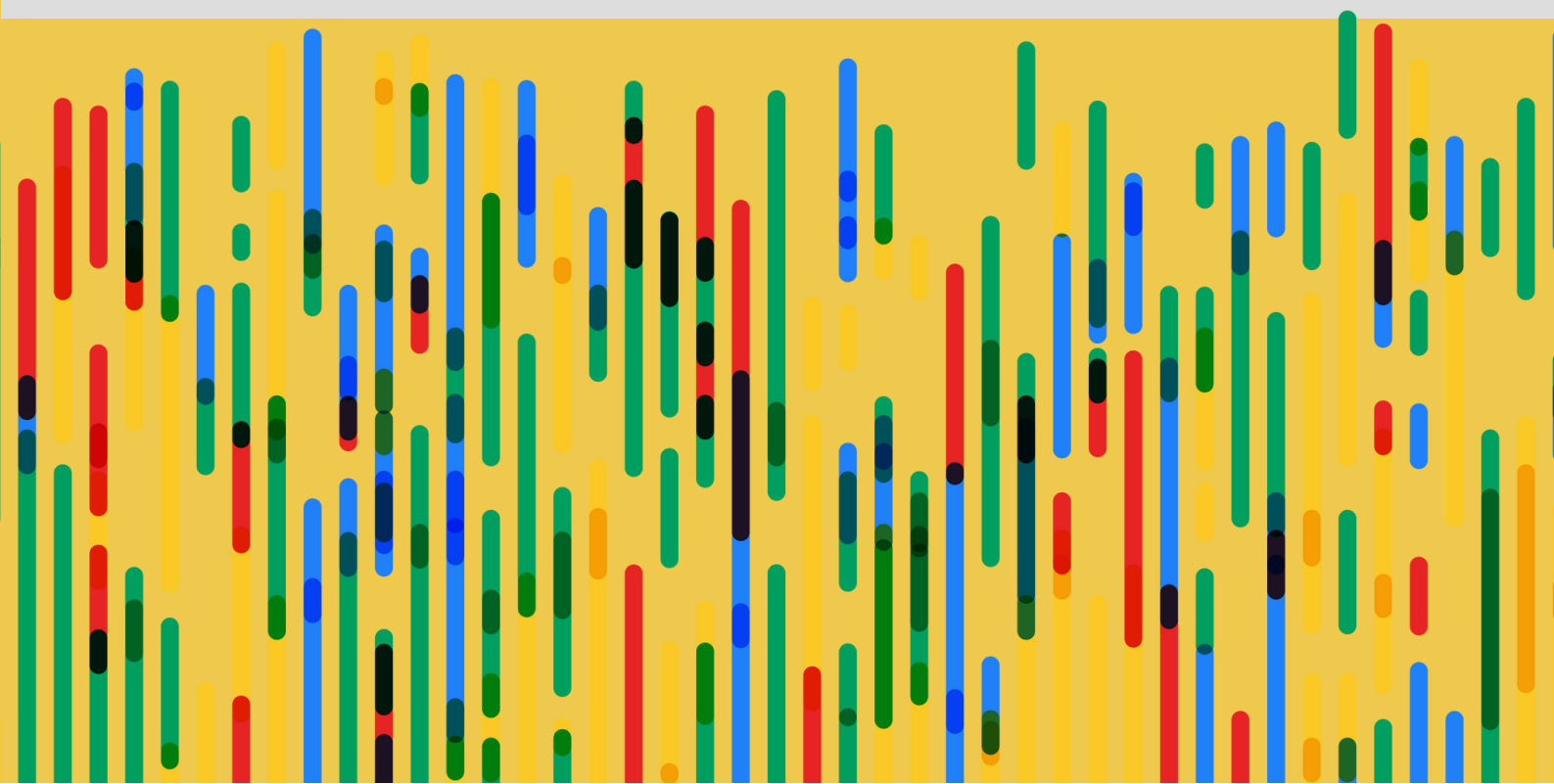
H

Higher Biology: DNA & the genome: Key Area 8: Genomic sequencing

Higher Human Biology: Human Cells, Key Area 5: Human genomics

AH

Organisms & Evolution, Key Area 2c: Identification & taxonomy



Your Project



Aim

As a wildlife conservation scientist, you have been working in Yangmingshan National Forest Park in Taiwan, collecting biological samples. Upon your return to the lab, you isolate DNA from a particular sample and send it to the sequencing department.

Two days later you receive your DNA sequence. Using bioinformatic platforms, identify the species from which the DNA sample was from. Was this a significant find?

Find out about the location

Before you start your bioinformatics journey, use Google Maps to remind yourself where this sample was found.

Jalview

Jalview is a free program for multiple sequence alignment editing, visualisation and analysis. Download the software OR use it within a web browser. Click here to launch.



JalviewJS

Launch JalviewJS

1

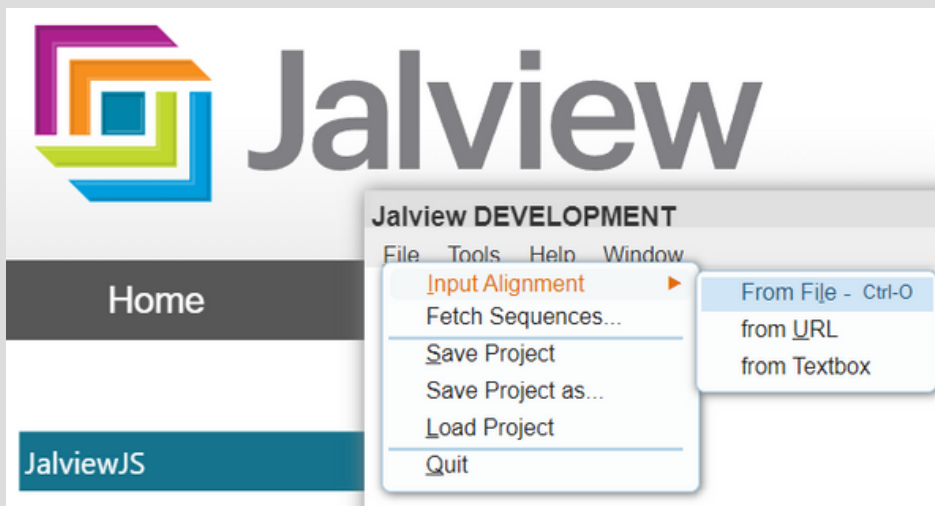
Download the multiple sequence alignment by clicking the box below.

Alignment
Mystery Sample

2

With Jalview installed as a desktop application, double-click on the downloaded **Alignment Mystery Sample**.

Alternatively, if using the browser version, click **File, Input Alignment** and then **From File** (as shown in the screenshot below). Select the downloaded **Alignment Mystery Sample**.



3

Jalview will launch its sequence alignment window. This will show five aligned DNA sequences, including the **Unknown Sequence** extracted from the biological sample from Yangmingshan National Forest Park.

4

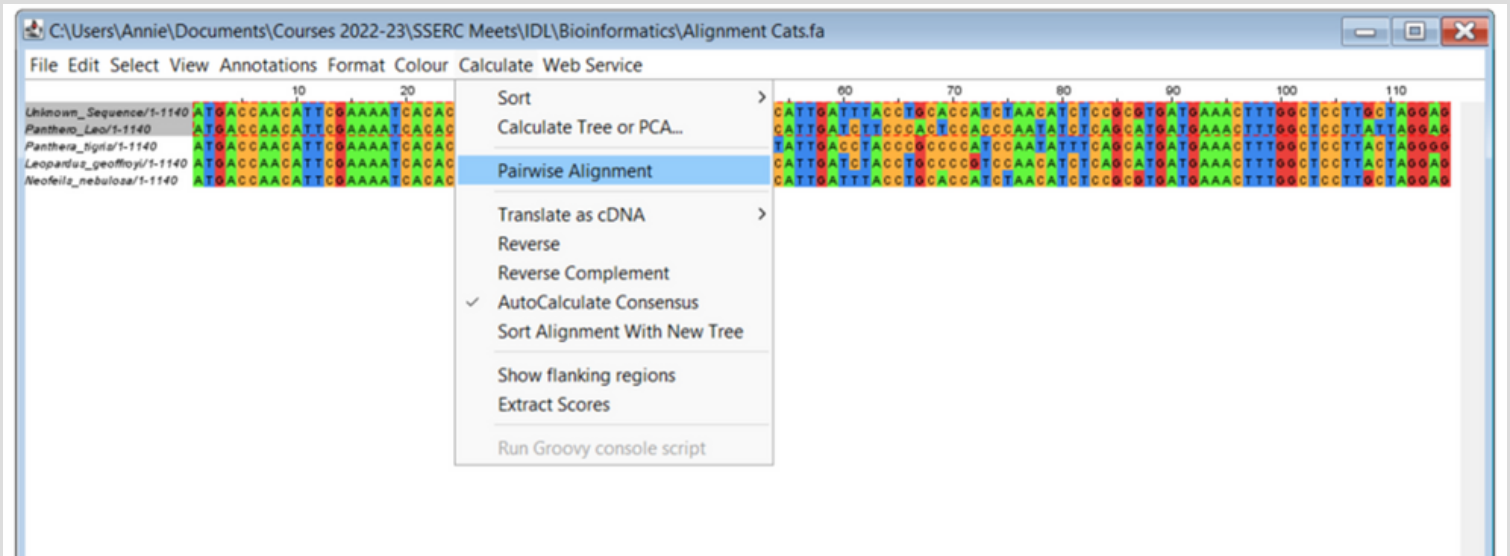
Using the menu bar, choose **Colour --> Nucleotides**. This will display the multiple sequence alignment with each nucleotide a different colour. Use the scroll bar at the bottom of the window to visually assess the differences between the sequences.

The *Consensus* bar, at the bottom of the Alignment window, indicates differences in the sequences. What do you notice about the sequences? How similar are they?

5

Comparing DNA sequences by eye is time-consuming and error-prone. Jalview provides a quick and simple way of comparing our sequences using *Pairwise Alignment*.

To determine the percentage identity between the "Unknown sequence" and each of the other DNA sequences, left-click on the **Unknown sequence**, hold the **CTRL** key, and then click on a **second sequence** for comparison. Click **Calculate** --> **Pairwise Alignment**.



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A window will be displayed on screen showing the pairwise alignment of the two selected DNA sequences. Scroll to the bottom of the screen to see the percentage identity/homology between the two sequences. Record the value in a table similar to the one below. Repeat the process until all DNA sequences have been compared to the Unknown Sequence.

Compared sequences	Pairwise identity (%)
Unknown : Panthera leo	
Unknown : Panthera tigris	
Unknown : Leopardus geoffroyi	
Unknown : Neofelis nebulosa	

7

Based on your pairwise alignments, from which species was the unknown DNA sequence from?

In the next section, you are going to carry out a **phylogenetic analysis** using the DNA sequences. Phylogenetics is one way that allows biologists to classify organisms. The wide availability of DNA sequences has enabled this - previously, classification of organisms was based on taxonomy, which involves the identification and naming of organisms and their classification into groups based on shared characteristics.

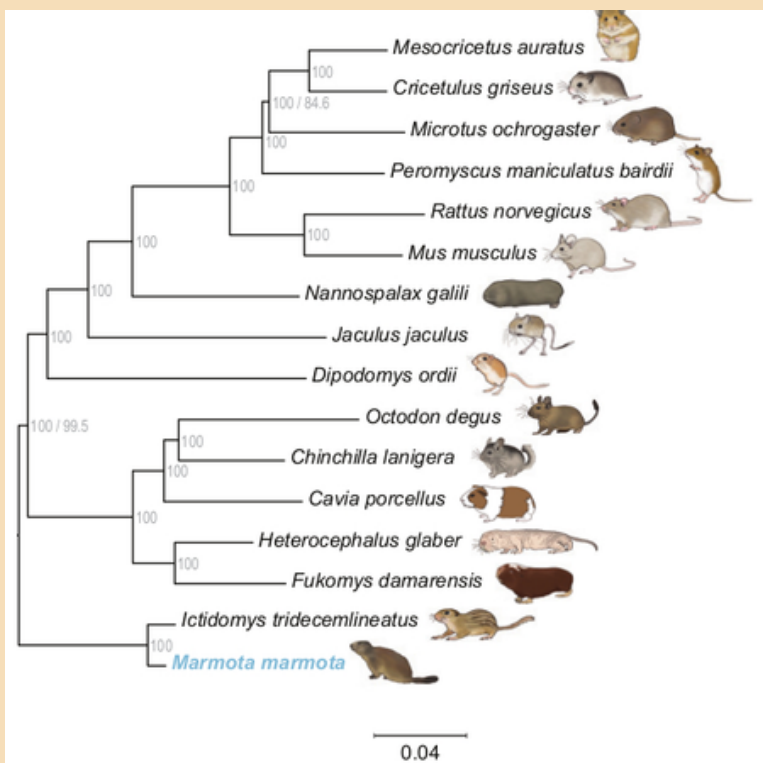


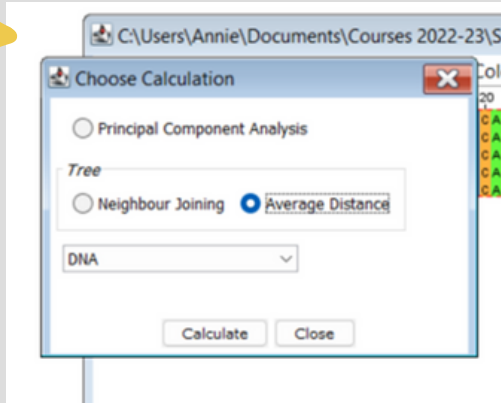
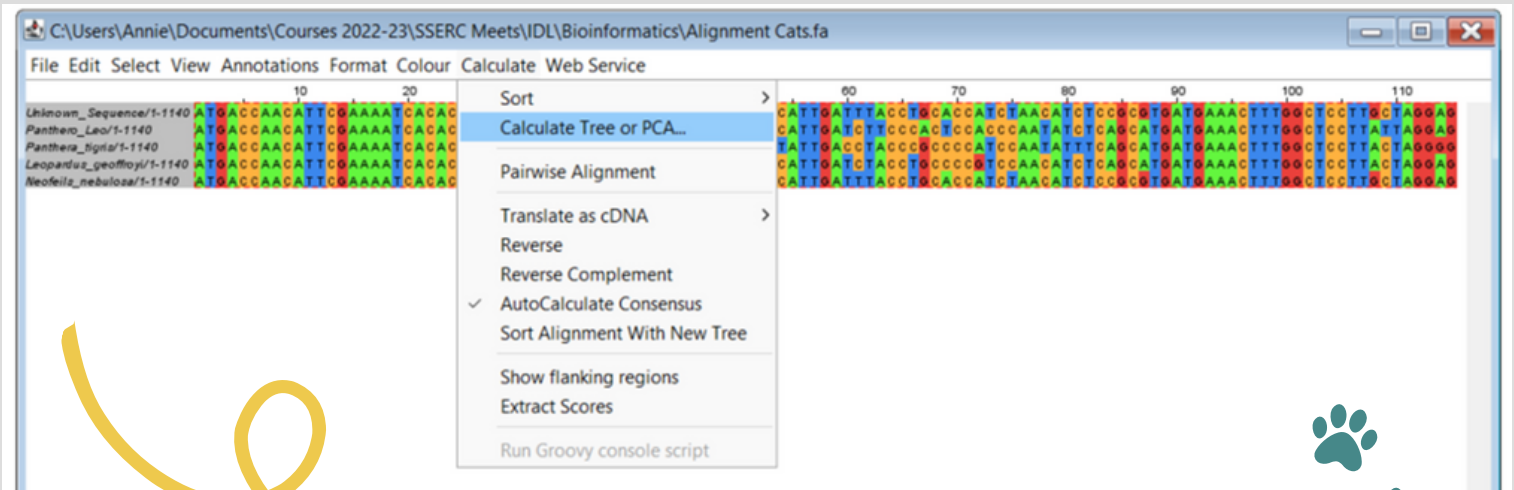
Figure 1: In the phylogenetic tree above, the relatedness between these different chordates is depicted (Wikimedia Commons).

Phylogenetics is the study of the evolutionary history and relationships among individuals or groups of organisms. It uses heritable traits, e.g. morphology, DNA sequences, and protein structure to make inferences about an organism's evolutionary history and create a phylogeny (or phylogenetic tree; example in Figure 1). This tree provides a diagrammatic hypothesis of the relationships between organisms. Genetic evidence can reveal relatedness that might be obscured by divergent or convergent evolution.

8

Perform a phylogenetic analysis using Jalview. To do this, return to the multiple sequence alignment window.

- Click on **Unknown Sequence**.
- Click and hold **SHIFT**.
- Click on the last sequence displayed in the alignment window. This should highlight all sequences.
- Select **Calculate --> Calculate Tree or PCA**.
- Select **Average Distance --> DNA --> Calculate**.



A new window will appear to display the phylogenetic tree.

Copy and paste the phylogenetic tree into your own notes. The phylogenetic tree generated will include numbers, which are the branch lengths. What do you think is the connection between the length of the line and similarity of the sequences?

Which species are the most closely related?

Which species is the **Unknown Species** most closely related to?



Neofelis nebulosa
(Wikimedia Commons).

Visit the [IUCN Red List of Threatened Species](#) website. Search for ***Neofelis nebulosa***. Read the information about this species. Reflect back on the project aim. The biological sample was originally taken from Yangmingshan National Forest Park in Taiwan. Was this a significant finding?



Taking it further

Get involved in citizen science by visiting [MammalWeb](#) - this project collates data from motion sensing "camera traps", set up to photograph and monitor wild mammals in the UK. You don't need to have your own camera trap - simply log on, view images collected from camera across the globe, and record what you can see.

References



The Jalview platform is an open source project. The development of Jalview is coordinated by James Procter and Geoff Barton in the School of Life Science's Division of Computational Biology at the University of Dundee, with support Wellcome Trust and UKRI's Biotechnology and Biological Science Research Council.