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## Level 1 NCEA Genomics workshop for CB1.3

### Background:

A cladogram is a simple 'phylogenetic tree' that shows the branching order of species without necessarily indicating the exact timing of evolutionary events. It shows the relative recency of common ancestors and the emergence of traits. It does not represent the actual time scale or the amount of evolutionary change.

**Aim:** to be able to draw a simple cladogram showing the relationships between a dog, a cat and a rabbit.

### Methods:

- Consider the table below showing the presence or absence of specific characteristics in the dog, rabbit and cat.
  - 1 - shows that a species has the characteristic under study
  - 0 - shows that the species does not have the characteristic under study

Derived characters	Species			
	Retractable claws	Dog	Rabbit	Cat
		0	0	1
		1	1	1
	Fur	1	1	1
	Canines	1	0	1

- Rearrange the table with the least common characteristic at the top row and the most common characteristic (oldest) at the bottom row. You may rearrange the species too.

Derived characteristics	Species			

- Start a tree with the most common characteristic near the root and each new branch is the evolution of a new characteristic. Write the characteristic across the red lines. On the left, place the species with the least shared characteristics.

