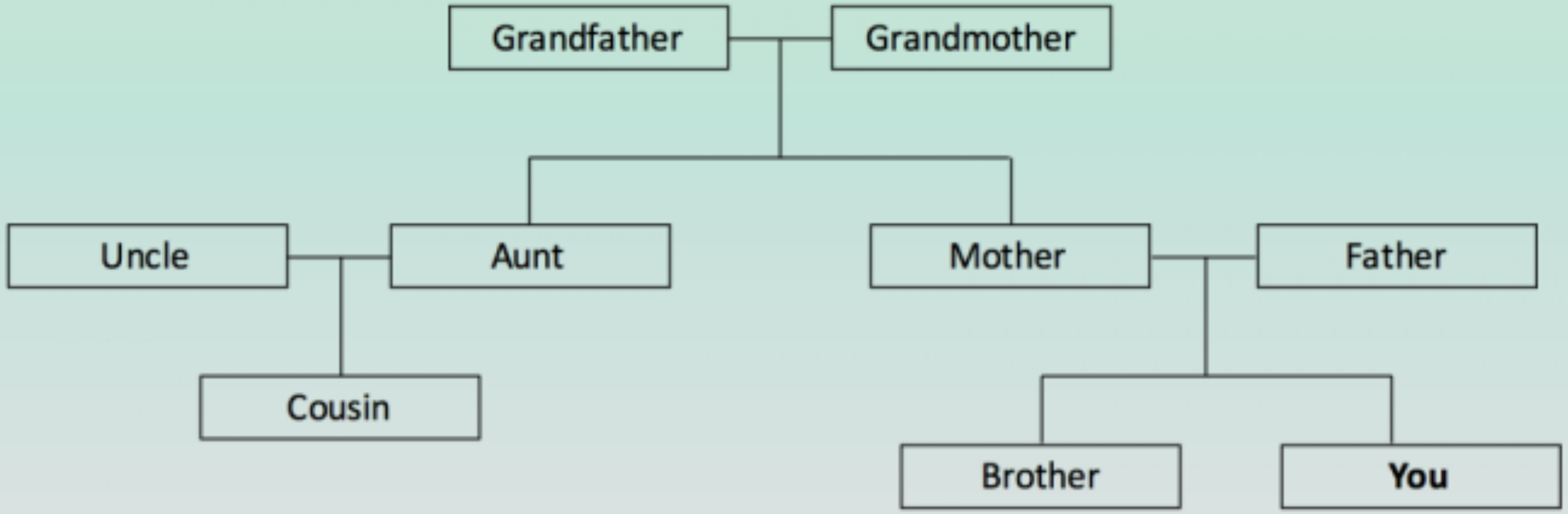
Phylogeny using bioinformatics

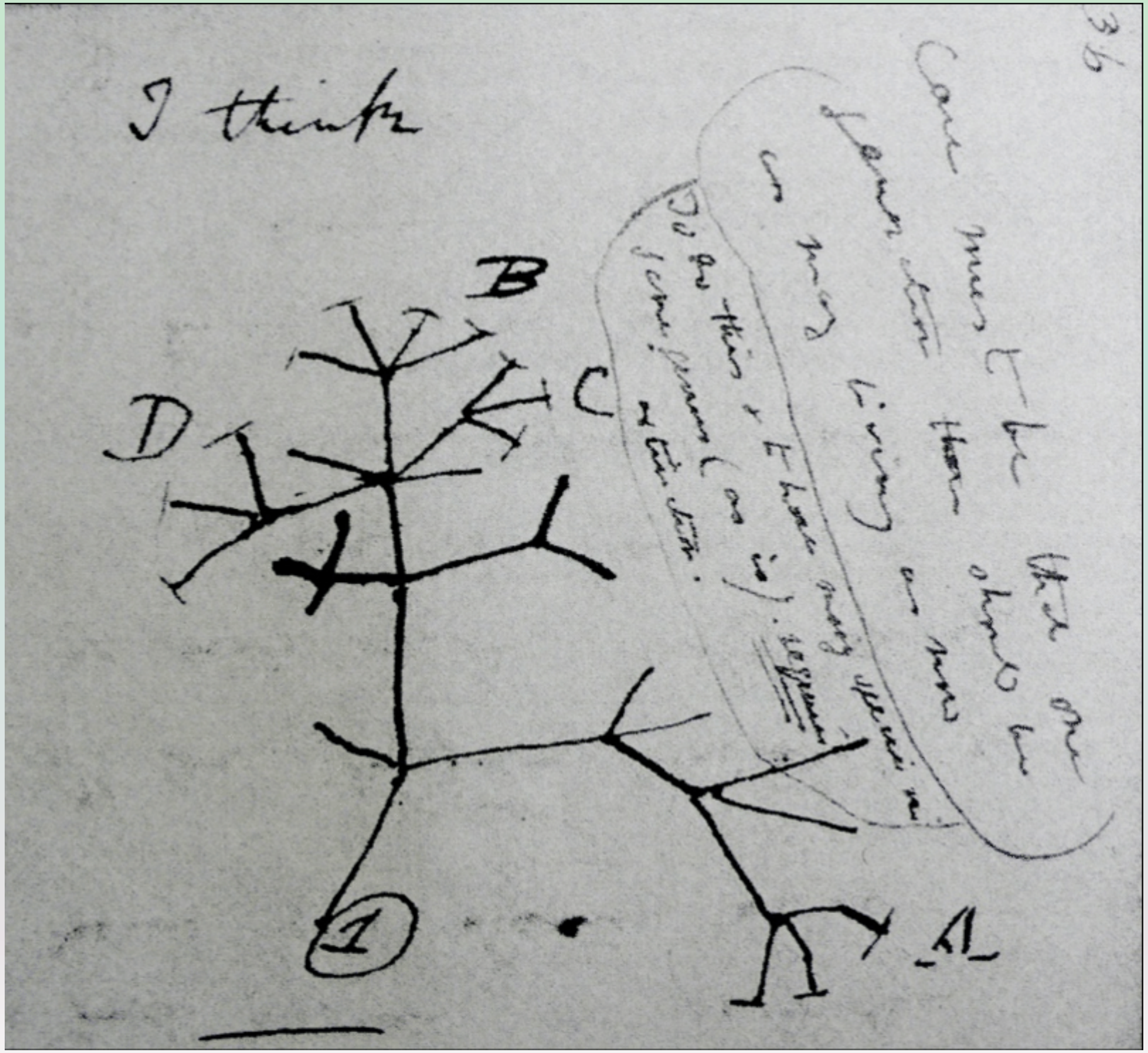
GROW
NEXT GEN

Taxonomy/phylogeny

Phylogeny using bioinformatics

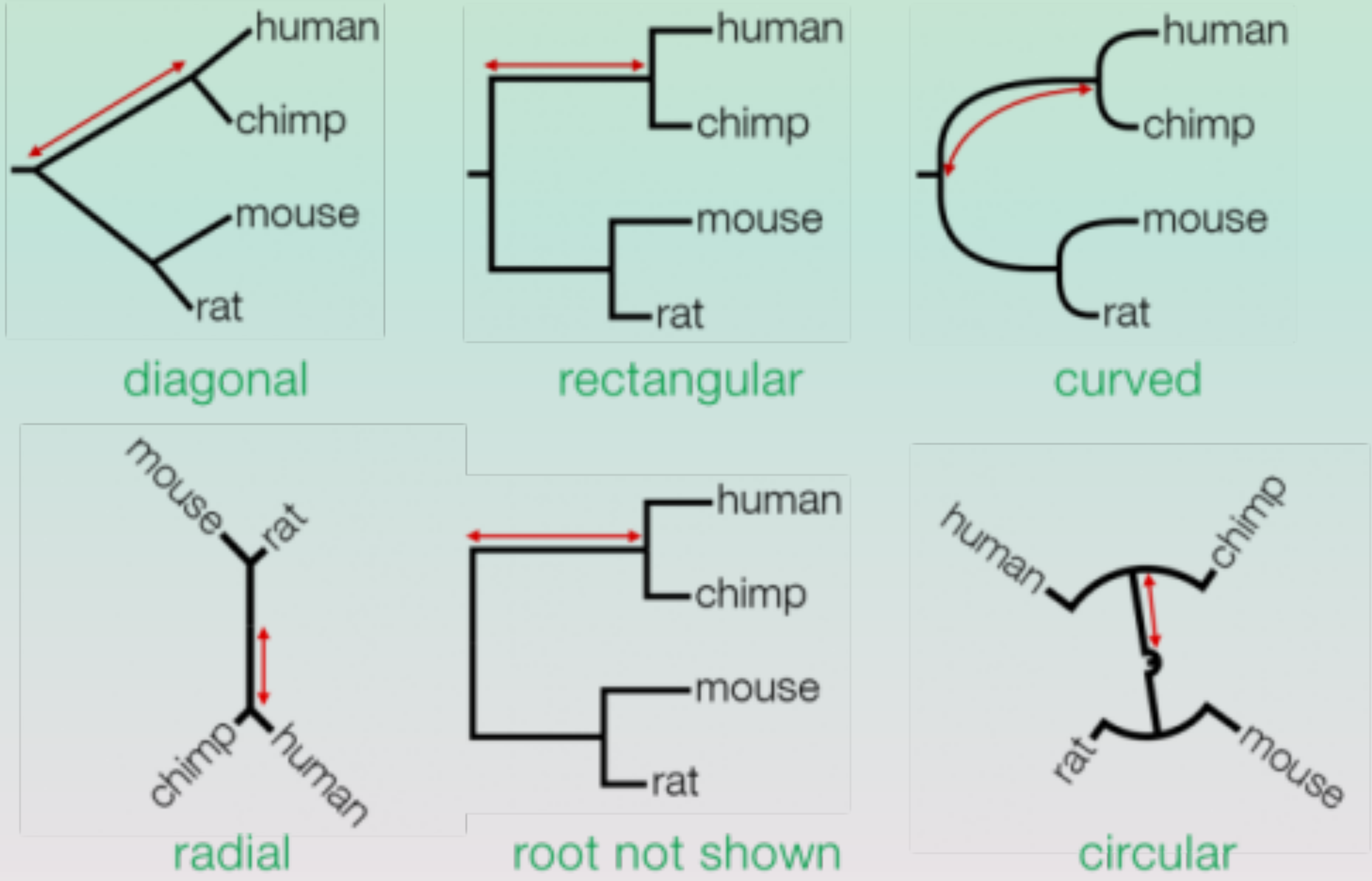


Interpreting a family tree is very similar to phylogenetic trees.
Both are used to explain relatedness.



Charles Darwin was the first to develop the idea of the tree of life and the branching relatedness among species. Each species splitting from a common ancestor.

There are multiple ways to display phylogenetic trees that show the same relationship among species.



diagonal

rectangular

curved

radial

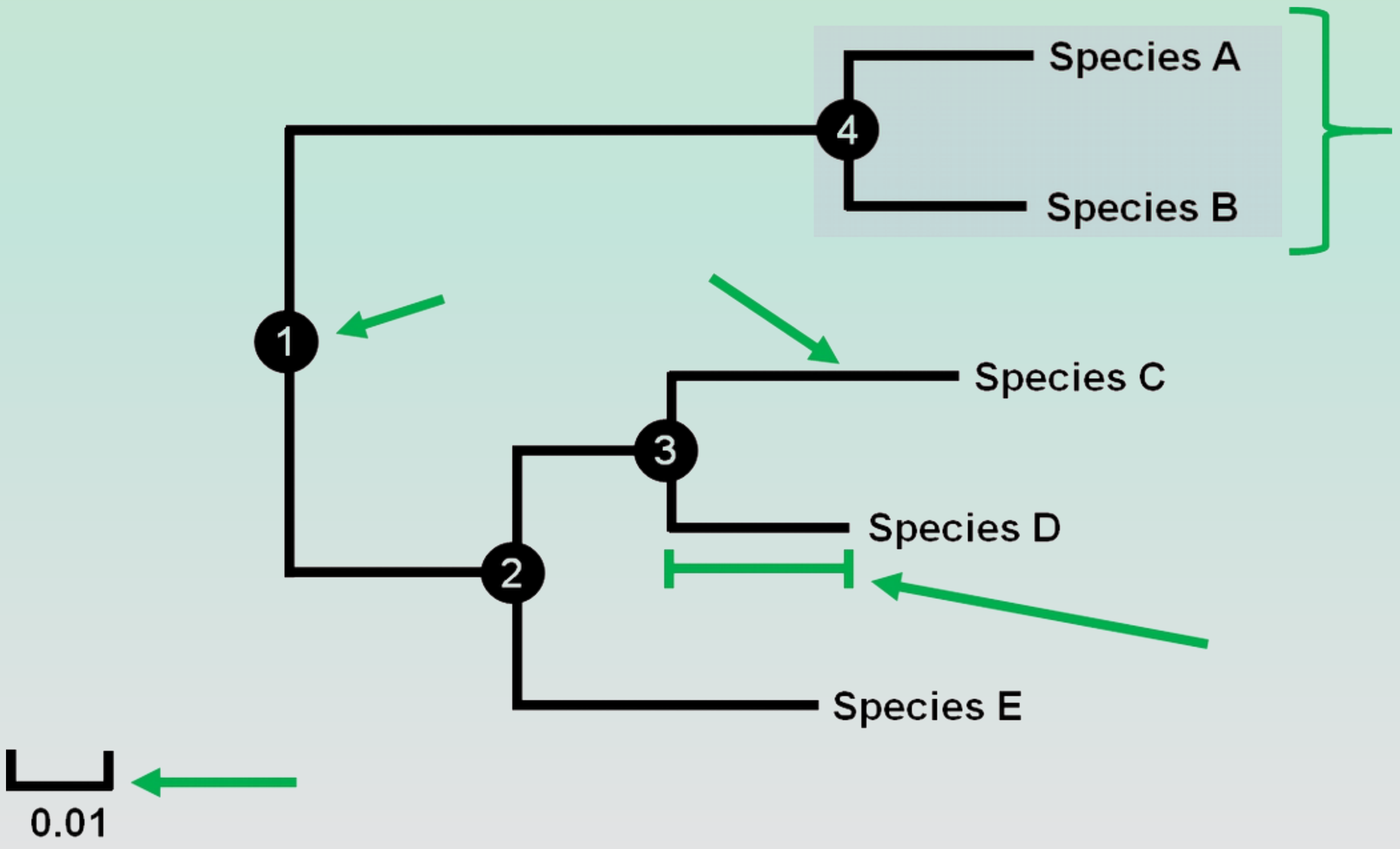
root not shown

circular

Topology: The branching structure of phylogenetic trees. Model trees with different and the same topology.

Basic terms and components to interpret phylogenetic trees

- Branch
- Node
- Clade
- Distance scale



Identifying relationships between modern species uses genetic data.

Barcoding regions within the genome show species-specific patterns in the DNA.

Barcodes

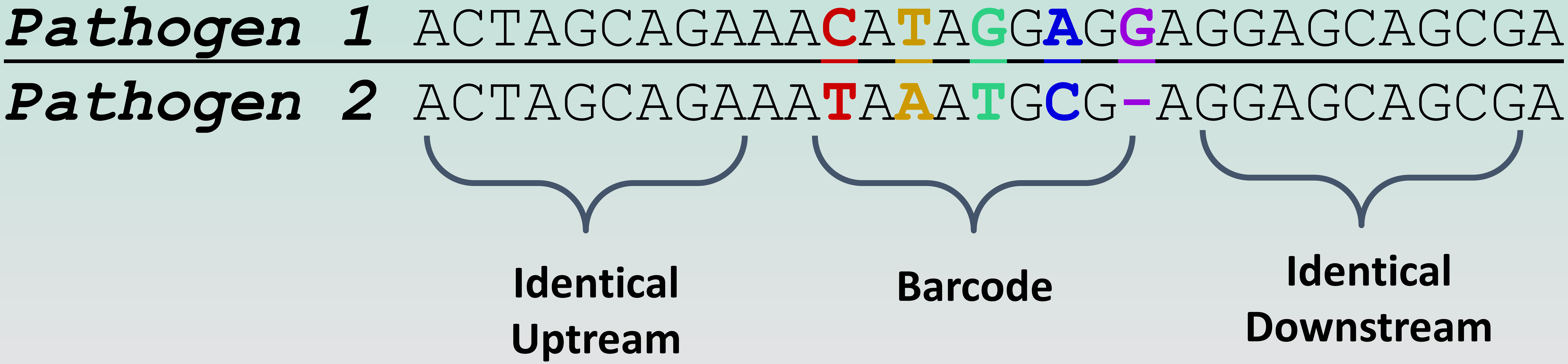
Linear lines that optical scanners (barcode readers) can determine a product based on lines of various widths.

Pasta 1

Pasta 2

Barcodes

Regions of DNA that differ between species.



Pathogen 1 ACTAGCAGAAA**C**A**T**A**G**G**A**G**G**AGGAGCAGCGA

Pathogen 2 ACTAGCAGAAA**T**A**A**A**T**G**C**G**-**AGGAGCAGCGA

Identical Uptream

Barcode

Identical Downstream

Barcodes

There are multiple barcoding regions or genes, which are used for different groups.

Organism	**Barcode**	**Function**	**Location**
Plants	RuBisCo (rbcL)	Carbon fixation from CO_2	Chloroplast
Plants	Maturase K (matK)	Protein that splices introns	Chloroplast
Plants and fungi	Ribosomal RNA including ITS1, ITS2	Essential for protein synthesis	Nucleus
Animals	Cytochrome C Oxidase Subunit I (COI)	Key enzyme in the electron transport chain	Mitochondria

The number of DNA sequence differences inform branch lengths and genetic distances.

Corn	**ATGTTGACTC**
Soybean	**ATGCTGACTC**

In this example, 1/10 = 0.1 substitutions per site.

This is the basis for genetic distances used in phylogenetic trees.

Resources

- Link to sequences:
  `grownextgen.org/go/crops`
- Link to simple phylogeny:
  `ebi.ac.uk/Tools/phylogeny/simple_phylogeny`