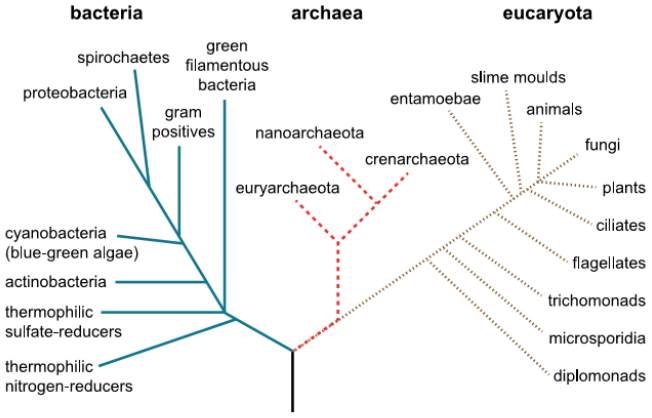
1.8 Genomic Sequencing

DNA sequencing is the process of determining the order of **nucleotides** in a section of DNA. It is now possible to determine the sequence of nucleotides in relatively small sections, i.e. a **gene**, or very large sections, i.e. a complete **genome**.

Once the DNA has been sequenced and the data has been collected, it must be analysed which is achieved through using techniques known as **bioinformatics**. These techniques include using **computer** and **statistical** analysis.

Phylogenetic trees

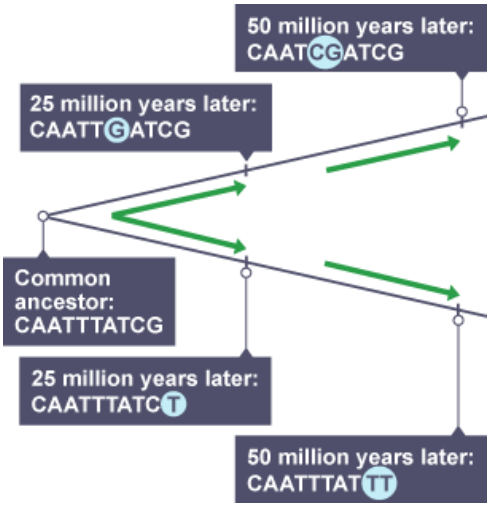
Phylogenetics is the study of the evolutionary **relatedness** between groups of organisms using genomic sequencing. Phylogenetic **trees** are diagrams that show evolutionary relationships, they are constructed by comparing genome **sequences**. The phylogenetic tree below shows the separation of living things into three key lineages – bacteria, archaea and eukaryotes.



Three domains in the tree of life

Molecular Clocks

Sequence **divergence** can be used along with **fossil** records in drawing molecular clock graphs. Molecular clocks measure the number of **mutations** that accumulate in a DNA sequence over **time** and we can use this information to work out when speciation occurred and when one lineage separated into two new lines. These molecular clock graphs are based on the assumption that the mutation rate of genes leading to amino acid differences in proteins is **constant** through time.



Currently, **sequence** data and **fossil** evidence are both used to determine the main sequence of events in the **evolution** of life.

Main sequence of events in evolution

Approximate time (million years BP)	Event in evolution
3600	Appearance of prokaryotic cells
3500	Existence of the last universal ancestor
3400	Photosynthesis
2000	Appearance of eukaryotic cells
1000	Appearance of multicellular organisms
600	Appearance of animals
540	Appearance of vertebrate animals
475	Appearance of land animals

Comparison of genomes from different species

Comparison of genomes reveals that many genes are highly **conserved** across different organisms. Many genomes have been sequenced, particularly of **disease**-causing organisms, **pest** species and species that are important **model** organisms for research.

Personalised genomics and health

Personal genomics is the sequencing and analysis of an individual's **genome**. Once an individual genotype (or part of it) is known it is compared to references in the published literature. From this, any mutations or sequences likely to give rise to **disease** can be identified. This is now referred to as predictive medicine, which in turn can lead to the use of an appropriate **drug** treatment if required, a process known as **pharmacogenetics**.

As a result of advances in this field, a question of **ethics** has also arisen. Insurance companies, banks and others may decline services or increase premiums as a result of finding less desirable traits, e.g. Alzheimer's or other degenerative diseases. This has been termed genetic **discrimination**. As yet, regulations in this and associated fields are not clearly laid out.

Personal genomics could bring about greater understanding of the varying effects of drugs between different individuals.