IB Biology DP

5. Evolution and Biodiversity

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5.1 Evolution & Natural Selection
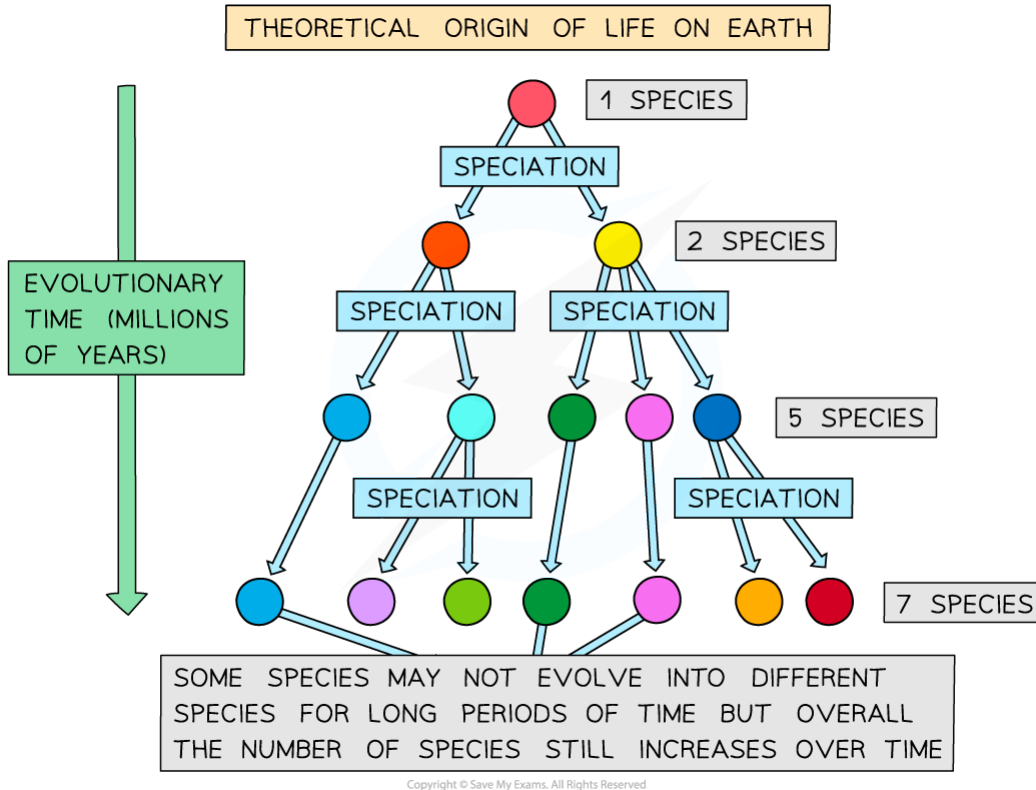
5.1.1 Evolution

Evolution Defined

- Species **do not stay the same over time**; the species that we see around us today have developed over millions of years
  - This process of species change is known as **evolution**
- Evolution can be defined as:
  - **Changes in the heritable characteristics of organisms over generations**
- **Heritable** characteristics are those that can be **inherited by,** or **passed on to, the next generation**
  - Changes in characteristics that are not inherited, e.g. a plant having its leaves eaten, do not lead to evolution
  - Heritable characteristics are determined by the alleles of genes that are present in an individual
  - Alleles may change as a result of **random** mutation, causing them to become more or less advantageous
- Heritable characteristics that are **advantageous** are **more likely to be passed on** to offspring, leading to a **gradual change** in a species over time
  - This is the process of **natural selection**
- Changes in the heritable characteristics of organisms can also lead to the development of completely **new species**
- The formation of new species via the process of evolution has resulted in a **great diversity of species** on Earth
  - Theoretically, at the origin of life on Earth, there would have been just **one** single species
  - This species evolved into **separate new species**
  - These species would then have **divided** again, each forming new species once again
  - Over millions of years, evolution has led to countless numbers of these **speciation** events, resulting in the millions of species now present on Earth

THEORETICAL ORIGIN OF LIFE ON EARTH

Evolutionary change over a long period of time has resulted in a great diversity of species
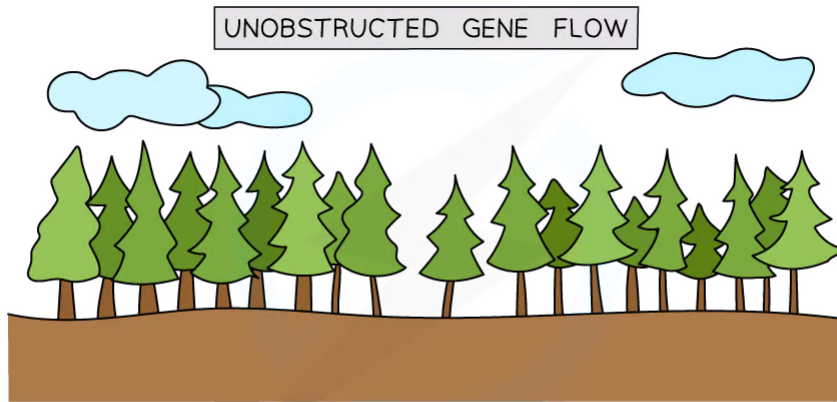
Speciation

- The **theory of evolution** states that species **do not stay the same**, but change over time; this can lead to the process of **speciation**
- Speciation can be defined as:
  - **The development of new species from pre-existing species over time**

- Speciation can result from **geographical isolation**
  - This means that a species is separated into two populations by e.g. being on different islands or different sides of a mountain range
    - The ocean and the mountains in these examples are **geographical barriers**

- This creates two populations of the same species who cannot interbreed due to being in different places; as a result, **no exchange of genes,** or **gene flow,** will occur between them
- The different environmental conditions for the two populations might mean that **different alleles are advantageous**, so different alleles are more likely to be passed on and become more frequent in each population; this is the process of **natural selection**
  - The allele frequencies in the two populations change over time
  - Genetic drift can also affect allele frequencies

- Over time, the two populations may begin to differ **physiologically**, **behaviourally** and morphologically to such an extent that they can no longer interbreed to produce **fertile offspring**; speciation has occurred

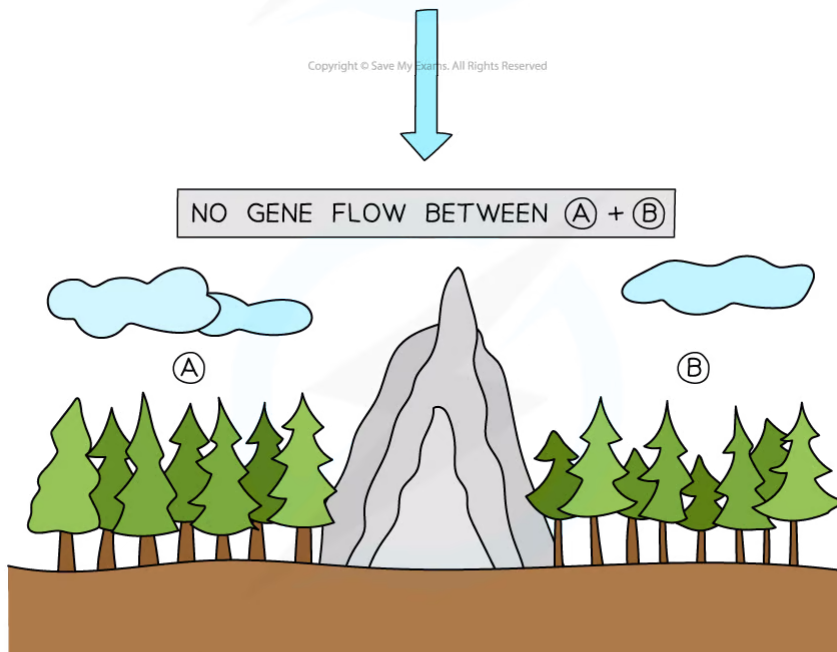## Example: speciation in trees

- A population of trees exists in a mountainous habitat
- A new mountain range forms that **divides the species** into **two populations**
- The geographical barrier prevents the two populations from **interbreeding**, so there is **no gene flow** between them
- The two populations experience **different environments**, so different **alleles** become **advantageous**
- Different alleles are therefore more likely to be **passed on** in each population
- Different alleles become **more frequent** in each population
- Over thousands of years, the divided populations **form two distinct species** that can no longer interbreed to produce fertile offspring
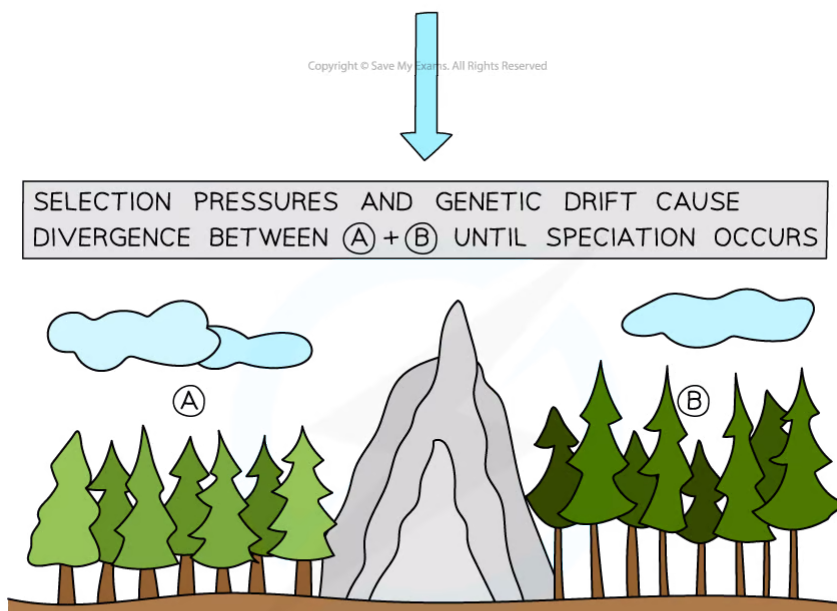
UNOBSTRUCTED GENE FLOW

NO GENE FLOW BETWEEN Ⓐ + Ⓑ

Ⓐ   Ⓑ

SELECTION PRESSURES AND GENETIC DRIFT CAUSE
DIVERGENCE BETWEEN Ⓐ + Ⓑ UNTIL SPECIATION OCCURS

Ⓐ   Ⓑ

POPULATION Ⓐ AND Ⓑ CAN NO LONGER INTERBREED: THEY ARE DIFFERENT SPECIES

The geographical barrier of a mountain range can lead to speciation in trees

💡 Exam Tip

Speciation commonly occurs after a species **expands its range** to new geographical areas. This phenomenon is evidenced by the large number of endemic species found on islands such as the Hawaiian honeycreepers; a group of more than 50 bird species found in the Hawaiian archipelago!

Evidence for Evolution: Fossils

- Fossils are the **preserved remains** of organisms, or the traces left by organisms, such as footprints, burrows and faeces
  - These remains can be **preserved,** e.g. in **rocks,** by the process of petrification, during which the tissues of organisms are replaced with minerals
  - The fossil record is small in relation to the number of organisms that have ever lived, due to the **conditions for fossilisation** being so **rare**

- We can tell from fossils that organisms have **changed significantly over millions of years**
  - Fossils, as well as the rocks they are found in, can be **dated**, allowing us to accurately put fossil organisms into a **sequence** from oldest to youngest, and therefore see how organisms have changed through **evolutionary time**
  - The fossil record shows the kind of **progression** that the theory of evolution would lead us to expect, with older fossils showing **simpler life forms** and **complexity increasing with time**
  - The sequence of fossils aligns with **ecology groups**:
    - Plant fossils appear earlier in the fossil record than animals
    - Plants with the ability to be pollinated by insects appear before insect pollinators

  - Fossils can show evidence for **transitional species**, showing how one species could evolve into another e.g. *Ambulocetus* is a fossil that links amphibians with early whale-like organisms, and *Archaeopteryx* appears to link reptiles with birds

Evidence for Evolution: Selective Breeding

- **Selective breeding** is a process in which **humans choose** organisms with **desirable characteristics** and **breed them together** to increase the expression of these characteristics over **many generations**
  - The process of selective breeding has enabled humans to produce **desirable crop varieties** and **livestock with exaggerated characteristics** from **wild varieties and species,** e.g.
    - Desirable crop varieties include those with a high yield and disease resistance
    - Exaggerated characteristics in livestock include thick, heavy wool in sheep, and large volumes of milk produced in dairy cattle

- Selective breeding involves **changes to** heritable **characteristics over many generations**, and so it is an example of **evolution in action**
- This practice is also known as **artificial selection**
  - It makes use of the **principles of** natural selection, but is carried out by humans
    - In natural selection, **advantageous** alleles are more likely to be passed on because they increase an organism's chances of survival
    - In artificial selection, or selective breeding, **desirable alleles** are more likely to be passed on because humans decide which individuals will be used for breeding

- Humans have been selectively breeding organisms for thousands of years, long before scientists understood genes and alleles

The process of selective breeding

1. The population shows **variation;** there are individuals with different characteristics
2. Breeders select **individuals with the desired characteristics;** selected individuals should not be closely related to each other
3. Two selected individuals are **bred** together
4. The offspring produced reach maturity and are then **tested for the desirable characteristics;** those that display the desired characteristics to the greatest extent are selected for further breeding
5. The process is repeated over **many generations**; the best individuals from the offspring are continually chosen for breeding until all offspring display the desirable characteristics
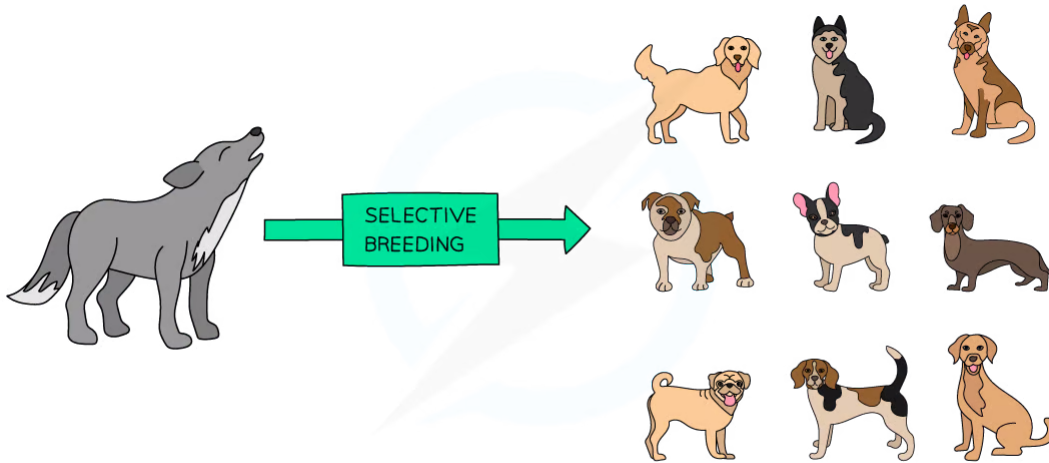
The wolf was bred selectively over thousands of years to produce a wide variety of domesticated dog breeds.

Evidence for Evolution: Homologous Structures

- **Homologous structures** are body parts that may **look and function very differently** but share **structural similarities**
- The limbs of animals are a good example of this; animals have many different mechanisms of motion and limb use, but the **basic arrangement of bones** in many different types of limbs is **very similar**
  - E.g. The limbs of birds, bats, crocodiles, whales, horses, and monkeys are used very differently and are visually very different, but are structurally **very similar** to each other

- One explanation for the surprising similarities of these different limbs is that of **adaptive radiation;** the idea that organisms with homologous structures have all **evolved from a shared, common ancestor** but have **adapted to different environments** in the process
  - Note that adaptive radiation does not provide **proof** that these organisms have evolved from a common ancestor, but it is a good explanation for the existence of homologous structures

A homologous structure: the pentadactyl limb

- A **pentadactyl limb** is any limb that has **five digits** i.e. five fingers or toes
- Pentadactyl limbs are present in **many species** from **many groups of organisms**, including mammals, birds, amphibians, and reptiles
- In different species, the pentadactyl limb has a **similar bone structure** but can enable an animal to move in a very different way
  - The **human foot** evolved for **upright walking** and **running**
  - **Whale flippers** enable them to **propel** themselves through a **marine environment**
  - **Bird wings** are usually highly adapted for **flight**
  - The **limbs of frogs** allow them to **walk, jump** and **swim**
  - **Alligator limbs** enable them to **walk** and **swim**

- Although the **individual bones** of the pentadactyl limb in these example animals are **very different shapes and sizes** due to their different mechanisms of **locomotion**, their **layout** is almost **exactly the same**
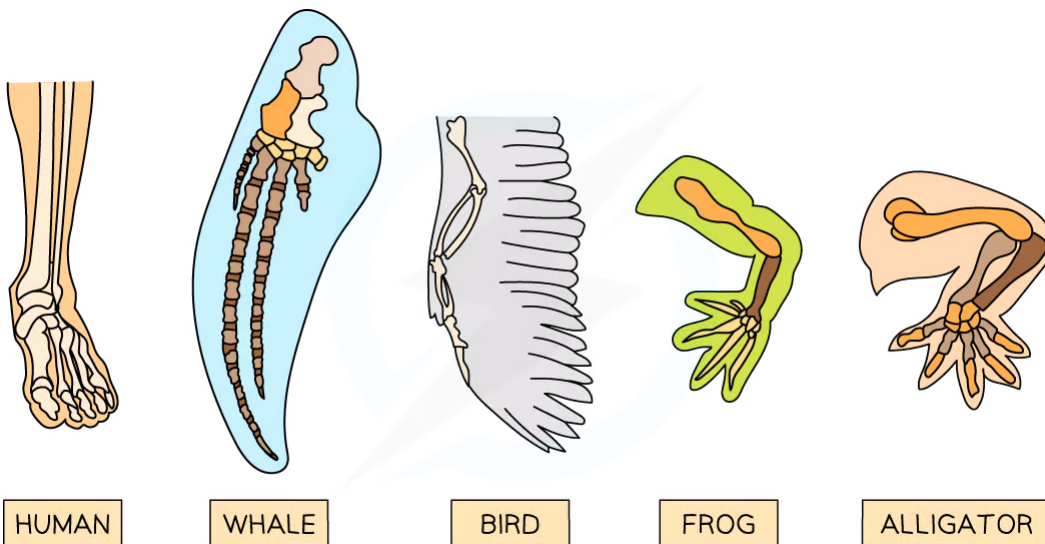
| HUMAN | WHALE | BIRD | FROG | ALLIGATOR |

The bone structure of the pentadactyl limb of a human, whale, bird, frog, and alligator; they all have the same basic layout despite having evolved for different functions

Vestigial structures

- Note that **vestigial structures**, while different in nature from homologous structures, **can also be explained by common ancestry**
  - Vestigial structures are those that **no longer have a function** in an organism
    - E.g. pelvis bones in snakes and whales and wings in flightless birds

- These structures tend to be **homologous to structures that perform a function** in other species
- The presence of vestigial structures suggests a **shared ancestry** with those species that possess a **fully functioning equivalent** of the same structure
- Vestigial structures are considered to be 'evolutionary leftovers'; they **would have had a function in an ancestral organism**, but a change in the environment led to **loss of use** e.g. a group of fish trapped in a dark cave would have no use for eyes
  - The presence of vestigial structures **does not harm** the species in which they are found, so there is no advantage to be gained by losing them completely; hence their persistence

NOS: Looking for patterns, trends and discrepancies; there are common features in the bone structure of vertebrate limbs despite their varied use

- When **patterns** and **trends** are observed in nature, scientists seek to find **explanations** that fit with these observations
  - Here, scientists have observed a **pattern** in the limb structure of animals; despite **differences in appearance and function**, the **general structure** of the pentadactyl limb is **repeated** throughout the animal kingdom
  - The **explanation** that best fits this **observation** is that all animals evolved from a **common ancestor** that itself had a pentadactyl limb, in the process of **adaptive radiation**
    - This is the only explanation so far that makes sense of the **pattern of homologous structures** seen in nature, and it supports the theory that **organisms evolve over time**
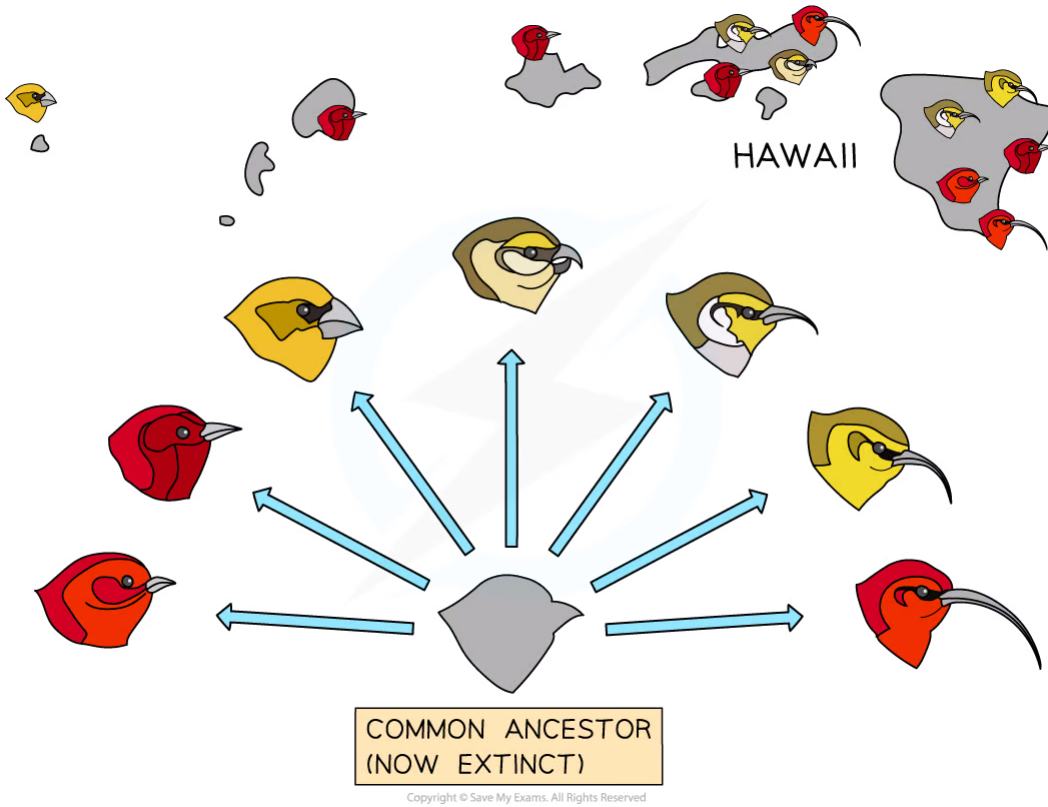
Evidence for Evolution: Continuous Variation Between Populations

- Different populations of a species may show small amounts of variation between each population e.g. a few mm in beak length between bird populations
  - Beak length is an example of continuous variation

- The presence of **continuous variation** between populations **across their geographical range** can lead to **gradual divergence**
  - The term **divergence** refers to the species becoming **separate;** this is the process of speciation

- It can sometimes be difficult to make decisions about the point at which populations showing **continuous variation** have **diverged into different species**, and biologists sometimes **disagree** over whether separate populations are the same species, different subspecies, or separate species
  - E.g. Orca, or killer whale, populations can show different body shapes and markings, and there is debate among scientists around whether there is only one species of orca, several subspecies, or several species

Evidence for gradual divergence

- There are several examples around the world of groups of species found in a **particular geographical location** where the **differences between those species are small**, e.g.
  - Darwin's finches; many species of small bird observed by Darwin in the Galapagos islands
  - Hawaiian honeycreepers; a group of more than 50 bird species found in the Hawaiian archipelago

- The presence of **continuous variation** like this, between species, and **across their geographical range,** suggests that these species evolved by **gradual divergence** as a result of continuous variation between historical populations
- For example, Hawaiian honeycreepers show **continuous variation across their geographical range**; because of this, they are thought to have **evolved** from a **series of ancestral populations,** from which **gradual divergence** gave rise to many different species

The Hawaiian honeycreepers show continuous variation across their geographical range, suggesting that they diverged gradually from a common ancestor

Evidence for Evolution: Melanistic Insects in Polluted Areas

- Because evolution generally happens over **millions of years,** it is difficult to see it taking place, and we often have to rely on evidence from the **fossil record,** and evidence of **common ancestry** such as **homologous structures** and **continuous variation** between species
- There are, however, some examples of evolution, on a small scale, that show changes in heritable characteristics in a short time frame
    - E.g. in insects and bacteria
    - Examples like this rely on **short generation times**

- A famous example of evolution taking place in insects is that of the **peppered moth** and **industrial melanism**
    - **Melanin** is a dark pigment produced in the cells; the more melanin is produced, the more **melanistic** an individual is said to be, and the darker it will be in colour

- It has been noted that **melanistic peppered moths** have become **more common** than non-melanistic individuals in industrialised parts of the UK where **air pollution has increased**
    - Air pollution kills organisms called **lichens** that grow on the **bark of trees**
    - In areas with clean air, lichens grow on tree bark, causing tree trunks and branches to appear **paler in colour**
        - In these areas, **non-melanistic moths** are **well camouflaged** against the trees, and therefore **more likely to survive** and **pass on the alleles** for non-melanism

    - In polluted areas, lichens are killed, causing tree trunks and branches to appear **darker in colour**
        - Here, **melanistic moths** are well camouflaged, increasing their chances of surviving and passing on the alleles for melanism

    - The frequency of **non-melanistic individuals therefore increases in non-polluted areas**, and the frequency of **melanistic individuals increases in polluted areas**

- This **change in the heritable characteristic** of melanin production **over generations** of moths shows **evolution taking place**
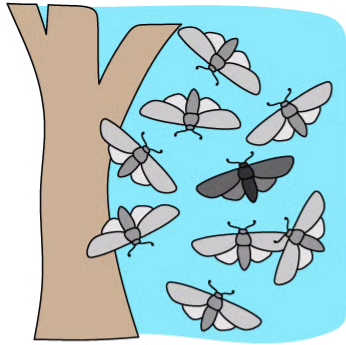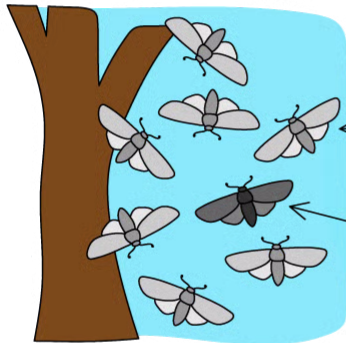
| 1 | THERE IS VARIATION WITHIN THE PEPPERED MOTH POPULATION – SOME HAVE ALLELES FOR MELANISM, AND SOME DO NOT |

| 2 | IN INDUSTRIALISED AREAS WHERE AIR POLLUTION IS HIGHER, LICHENS ARE KILLED, CAUSING TREE BARK TO APPEAR DARKER IN COLOUR |

| 3 | NON–MELANISTIC MOTHS ARE NOW MORE LIKELY TO BE EATEN BY BIRDS, AND LESS LIKELY TO REPRODUCE |

| 4 | MELANISTIC MOTHS ARE NOW MORE LIKELY TO SURVIVE AND REPRODUCE, PASSING ON THEIR ALLELES FOR MELANISM TO THEIR OFFSPRING |

| 5 | OVER TIME, THERE IS A GRADUAL INCREASE IN THE FREQUENCY OF MELANISTIC MOTHS IN INDUSTRIALISED AREAS |
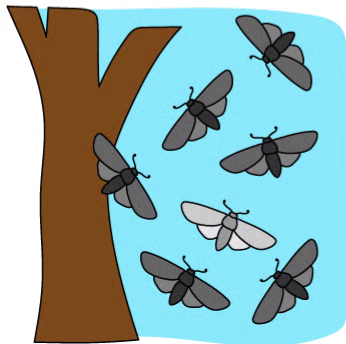
In areas with higher levels of air pollution the frequency of melanistic moths increases

YOUR NOTES
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Variation

- **Differences** exist between organisms of the same species
  - These differences are known as **variation**
  - Examples of variation include:
    - Coat colour in mammals
    - Body length in fish
    - Flower colour in flowering plants

- The process of natural selection can **only take place** when there is **variation in a population**
  - If every organism in a population is identical then no individual will be favoured over another
  - There will be no **advantageous characteristics** leading to **increased survival** and **chances of reproduction**, and so there would be no increased likelihood of passing on those **advantageous** alleles
  - In this situation, a population's characteristics would remain **the same over time** and it would be **unable to adapt** to any environmental changes

Causes of Variation

- **Variation** results from small differences in **DNA base sequences** between individual organisms within a population
- There are several sources of these differences in DNA base sequences:
  - Mutation
  - Meiosis
 - Random fertilisation during sexual reproduction

Mutation

- The original source of genetic variation is **mutation**
  - A mutation is a change in the **DNA base sequence** that results from a copying error during DNA replication

- Mutation results in the **generation of new** alleles
- Mutations that take place in the **dividing cells of the sex organs** lead to changes in the alleles of the gametes that are passed on to the next generation
  - A new allele may be **advantageous, disadvantageous** or have **no apparent effect**
  - An advantageous allele is **more likely to be passed on** to the next generation because it increases the chance that an organism will survive and reproduce
  - A disadvantageous mutation is **more likely to die out** because an organism with such a mutation is less likely to survive and reproduce

- Note that a mutation taking place in a body, or somatic, cell will **not be passed on to successive generations**, and so will have no impact on natural selection
- Mutation is the only source of variation in asexually reproducing species

Meiosis

- There are two main events during the process of **meiosis** that **generate variation**
  - Crossing over
  - Random orientation

- **Crossing over** is the process by which **homologous chromosomes** exchange alleles
  - During meiosis I homologous chromosomes pair up
  - The **non-sister** chromatids **can cross over** and get entangled
  - As a result of this, a section of chromatid from one homologous chromosome may **break and rejoin** with the chromatid from the other chromosome

- This swapping of alleles is significant as it can result in a **new combination of alleles** on the two homologous chromosomes
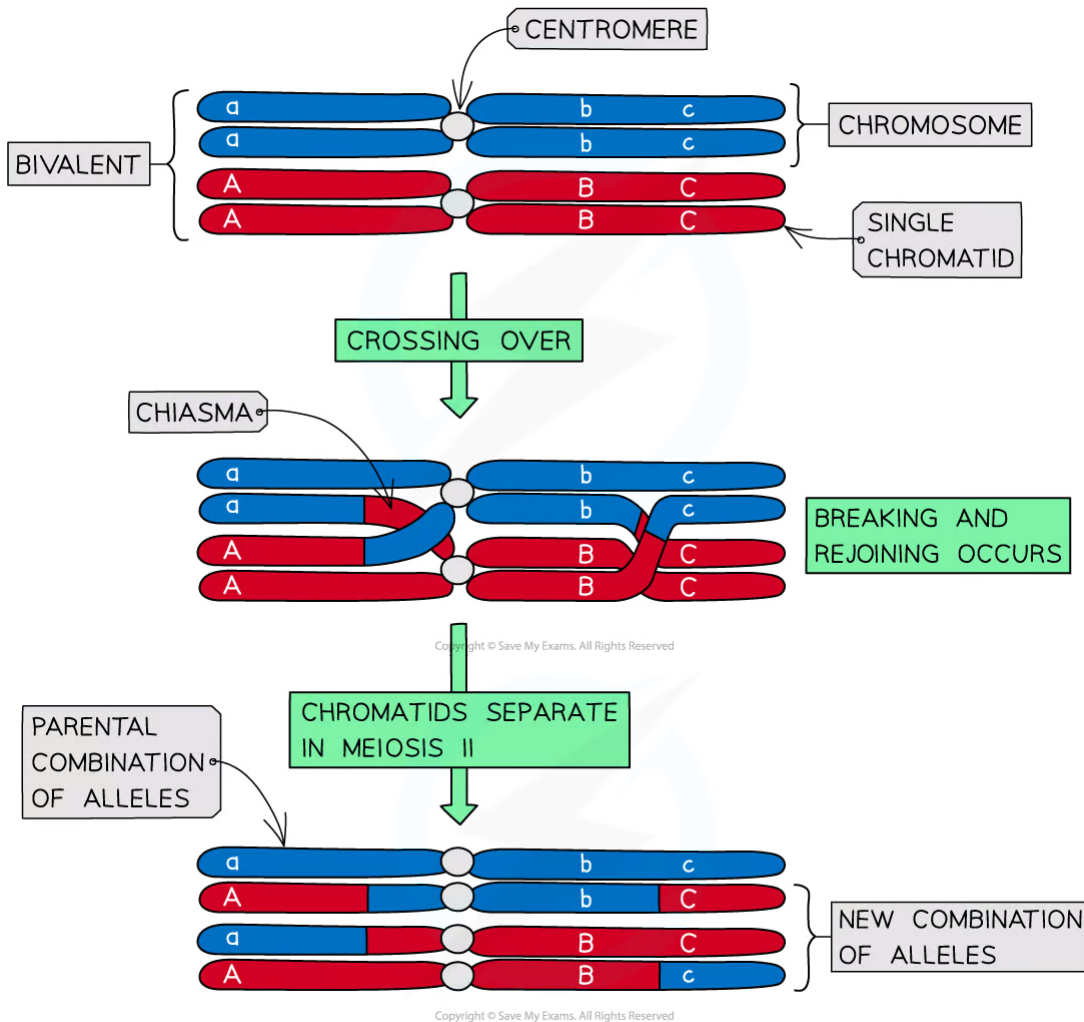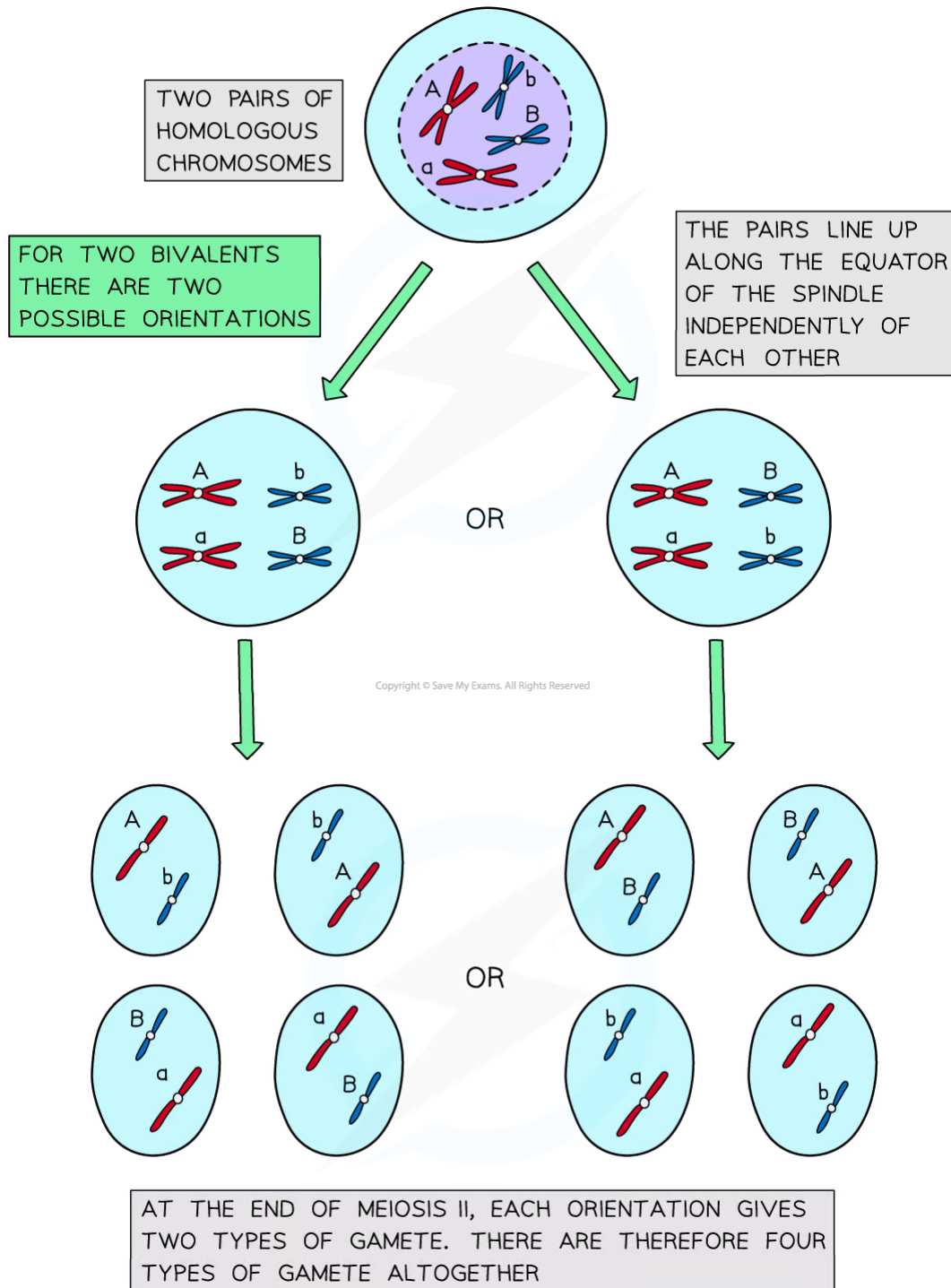
The process of crossing over can result in new combinations of alleles

- **Random orientation** occurs due to the **independent arrangement** of homologous pairs along the equator of the cell during metaphase I
  - **Each pair can be arranged with either chromosome on either side of the cell;** this is completely random
  - The **orientation of one homologous pair is independent,** or unaffected by the orientation of any other pair
  - This is sometimes described as **independent assortment**

- The homologous chromosomes on the equator of the cell are **pulled apart** to different poles, and will each end up in a separate daughter cell
- The combination of alleles that end up in each daughter cell depends on **how the pairs of homologous chromosomes were lined up**
- To work out the number of different possible chromosome combinations the formula 2^n can be used, where n corresponds to the number of chromosomes in a haploid cell
  - E.g. for humans this is 2^{23} which calculates as 8,324,608 different combinations

TWO PAIRS OF HOMOLOGOUS CHROMOSOMES

THE PAIRS LINE UP ALONG THE EQUATOR OF THE SPINDLE INDEPENDENTLY OF EACH OTHER

FOR TWO BIVALENTS THERE ARE TWO POSSIBLE ORIENTATIONS

OR

OR

AT THE END OF MEIOSIS II, EACH ORIENTATION GIVES TWO TYPES OF GAMETE. THERE ARE THEREFORE FOUR TYPES OF GAMETE ALTOGETHER

Random orientation of chromosomes

Random fertilisation during sexual reproduction

- **Meiosis** creates genetic variation between the gametes through **crossing over** and **independent assortment**
- This means each gamete carries substantially **different alleles**

- During fertilisation any male gamete can fuse with any female gamete to form a zygote
- This **random fusion of gametes** at fertilisation creates genetic variation **between zygotes** as each will have a unique combination of alleles
- There is an almost zero chance of individual organisms resulting from successive sexual reproduction being genetically identical
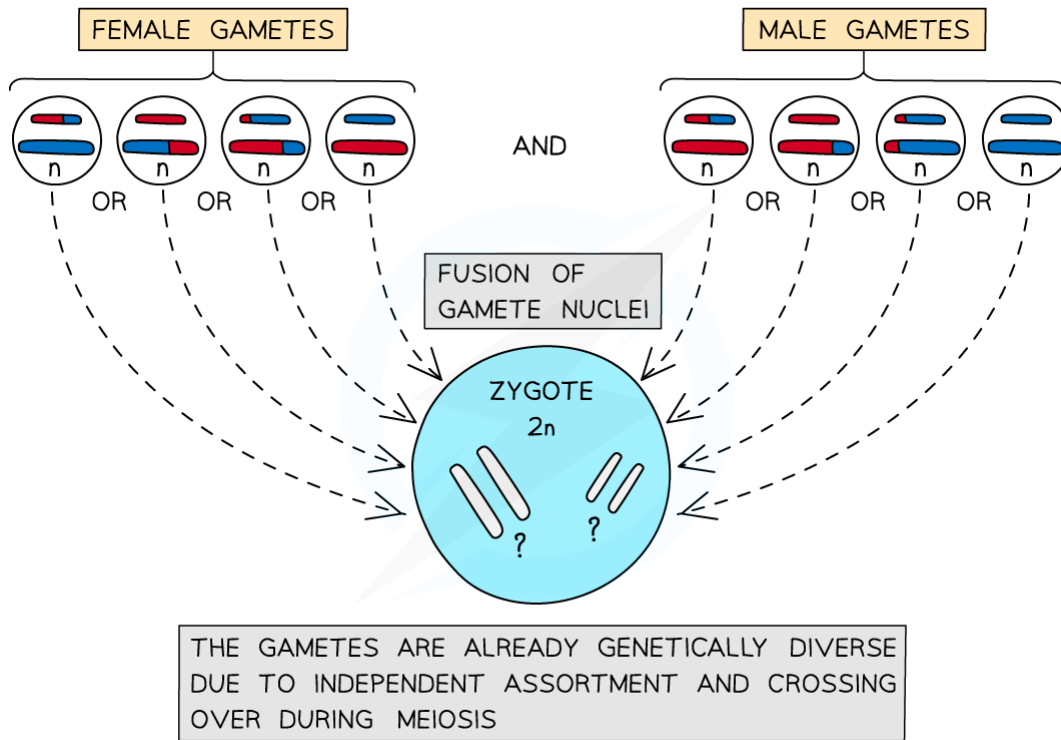
The random fusion of gametes during fertilisation

Sources of Genetic Variation Table

Process	Mechanism	Consequences
Independent assortment of homologous chromosomes during metaphase I	Random alignment of chromosomes results in different combinations of chromosomes and different allele combinations in each gamete	Genetic variation between gametes produced by an individual
Crossing over of non−sister chromatids during prophase I	Exchange of genetic material between non−sister chromatids leads to new combinations of alleles on chromosomes. It can also break linkage between genes	Genetic variation between gametes produced by an individual
Random fusion of gametes during fertilization	Any male gamete is able to fuse with any female gamete (Random mating in a species population)	Genetic variation between zygotes and resulting individuals
Mutation	Random change in the DNA base sequence results in the generation of a new allele. Mutation must exist within gam−etes for it to passed onto future generations	Genetic variation between individuals within a species population

Adaptations

- Adaptations can be defined as:
  - **Characteristics that cause individuals to be well suited to their environment and methods of living**

- When describing an adaptation it is always a good idea to relate the **structure** of a characteristic to its **function**, e.g.
  - Fish gills are an adaptation for survival underwater; they have a very **large surface area**, enabling them to **maximise oxygen absorption** from water
  - The thick fur of a polar bear is an adaptation for survival in a cold environment; it is **thick**, trapping a layer of warm air next to the polar bear's body and **providing insulation**
  - Different beak shapes in birds enable the consumption of different types of food; some species of finch have **short, cone-shaped beaks** that enable them to **crack nuts and seeds**

- Adaptations arise in species gradually by **evolution** through the **process of natural selection**
  - In a **slowly changing environment**, populations are able to **adapt** by natural selection and survival continues
  - If an **environment changes quickly**, the process of **natural selection is too slow** and adaptation cannot occur fast enough; in this situation, a population must **migrate** to a different environment or it will go **extinct**

> 💡 Exam Tip
>
> Remember that adaptation occurs as a result of **natural selection**; a process that acts on **randomly occurring variation**, and does not occur as a direct, purposeful response to an environment; avoid any statements that imply that adaptations occur 'so that' an organism can survive in its environment. Instead, it is correct to say that adaptations occur by **natural selection** as a result of **random variation** in populations.

YOUR NOTES
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Overproduction of Offspring

- The **number of offspring**, or young, produced in each breeding event **differs between species**
  - Some species produce **small numbers** of young, e.g. elephants usually give birth to just one baby per pregnancy
  - Some species produce **many offspring** e.g. some species of ant can lay 3–4 million eggs in one go

- It is more usual for organisms to produce **multiple offspring**, to the extent that there are **more offspring produced than can be supported** by the surrounding environment
  - Darwin noticed this, and named the phenomenon '**overproduction of offspring**'

- Overproduction of offspring means that there is **always competition** for resources

Survival of the Fittest

- In any habitat there are **environmental factors** that **affect survival chances**
  - E.g. predation, competition for food, and disease
  - Environmental factors that influence survival chances are said to act as **selection pressures**

- In any population, due to the variation present, some individuals will have **characteristics** that make them **better adapted** for survival
  - For example, lions that are stronger and faster are more likely to be able to catch prey and therefore more likely to survive
  - This is sometimes described as '**survival of the fittest**'

- Individuals that are well adapted and **survive into adulthood** are **more likely to find a mate** and **reproduce**, producing **many offspring**
- Individuals that are less well adapted **do not survive long** into adulthood are likely to **reproduce less often** than those that survive for longer, so producing **fewer offspring**
  - These individuals may not reach adulthood and so do **not get the chance to reproduce** at all

> 💡 **Exam Tip**
>
> When answering exam questions, be careful not to imply that organisms better adapted to their environments are guaranteed to survive. Instead, you should say that they are **more likely** to survive. Organisms that are less suited to an environment are still able to survive and potentially reproduce within it, but their chance of survival and reproduction is lower than their better-adapted peers.

Inheritance

- Many of the **characteristics** that affect an individual's chances of survival are determined by the alleles of genes present in their DNA
- Characteristics that are **determined by alleles** are heritable
  - Heritable characteristics can be **physical** e.g. the length of a giraffe's neck, or **behavioural** e.g. the innate behaviour of a woodlouse moving towards a dark hiding place

- Individuals with characteristics that **increase their chances of survival** are likely to produce **more offspring**
- This means that they are more likely to **pass on the alleles** that code for these **advantageous characteristics** to their offspring
- Note that **non-heritable characteristics are not passed on to offspring**
  - Non-heritable characteristics are those **acquired during the lifetime** of an organism e.g. gaining weight after eating lots of nuts and berries in autumn, or being injured by a predator

Change in Frequency of Characteristics

- **Natural selection** can be defined as
  - **The process by which organisms that are better adapted to their environment survive, reproduce, and pass on their advantageous alleles, causing advantageous characteristics to increase in frequency within a population**

- The **increased survival chances** of individuals with **advantageous alleles** mean that advantageous characteristics are **more likely to be passed down** through the generations
- The number of individuals in a population with a particular favourable characteristic will increase over time; the characteristic is said to **increase in frequency**
- Eventually this favourable characteristic will become the **most common** of its kind in the population; the population can be said to have **adapted** to its environment by the process of **natural selection**
- While favourable characteristics increase in frequency by natural selection, **unfavourable characteristics decrease in frequency** by the same process
  - Individuals with unfavourable characteristics are less likely to survive, reproduce, and pass on the alleles for their characteristics, so unfavourable characteristics are eventually lost from the population

An example of natural selection in rabbits

- **Variation** in fur colour exists within a rabbit population
  - One allele codes for **brown fur** and another for **white fur**

- Rabbits have natural predators such as foxes which act as a **selection pressure**
- The brown rabbits are **more likely to survive** and **reproduce** due to having more effective camouflage
- When the brown rabbits reproduce they **pass on their alleles** to their offspring
- The frequency of brown fur alleles in the population will increase
- **Over many generations,** the **frequency** of **brown** fur will **increase** and the frequency of white fur will decrease
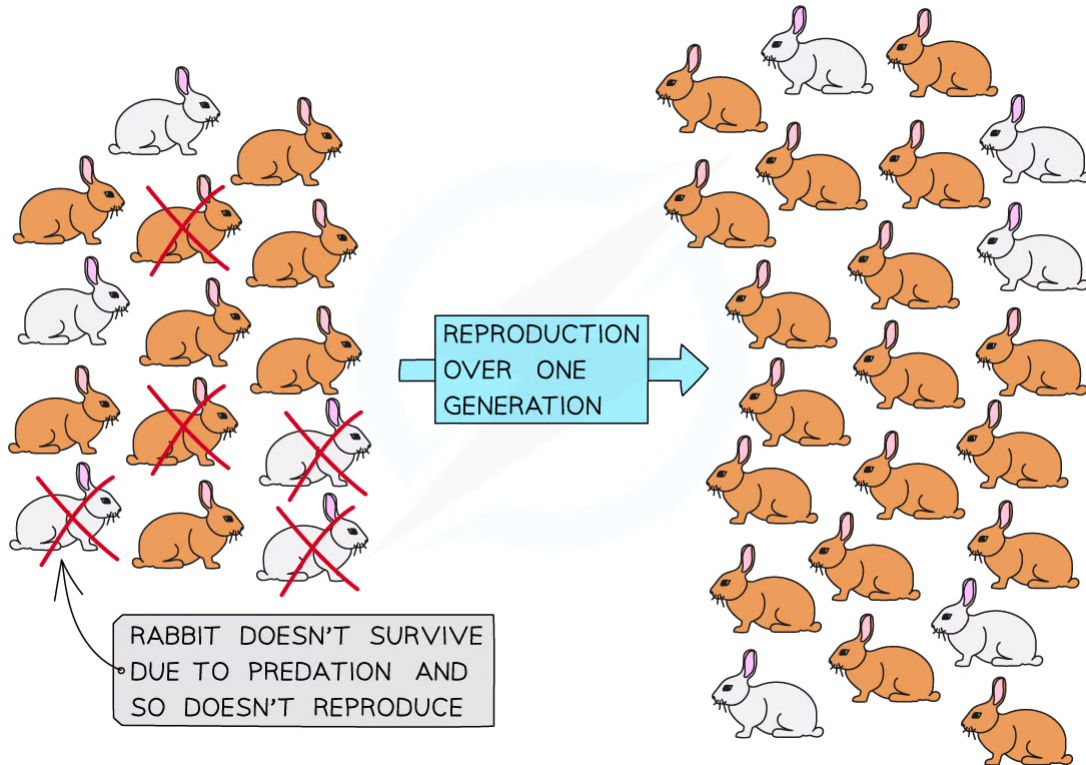
Selection pressures acting on a rabbit population for one generation; predation by foxes causes the frequency of brown fur in rabbits to increase and the frequency of white fur in rabbits to decrease

5.1.5 Natural Selection Examples

Examples of Natural Selection

- Because evolution by natural selection generally happens over **millions of years,** it is difficult to see it taking place, and we often have to rely on evidence from the **fossil record,** and evidence of **common ancestry** such as homologous structures and continuous variation between species
- There are, however, some examples of evolution, on a small scale, that show changes in heritable characteristics in a **short time frame**, e.g.
  - Finches on Daphne Major
  - Antibiotic resistance in bacteria

Finches on Daphne Major

- **Daphne major** is an island in the Galapagos, the wildlife of which inspired **Charles Darwin** to come up with his **theory of evolution by natural selection**
- He noticed that some of the birds of the Galapagos, identified as **finches**, bore a strong resemblance to each other, but that they also showed **differences that were specific to each island**
  - Scientists now know that Darwin's famous finches are not technically finches at all, but they are usually still referred to as 'Darwin's finches'

- In particular, finch **beak shape** and **size** corresponded to the **diet available** to them on **each island**

Geospiza magnirostris

Geospiza fortis

Geospiza parvula

Geospiza olivasea

Darwin noticed that Galapagos finches had beaks that were perfectly adapted to the food sources available on the island on which they lived

- Since Darwin, many **evolutionary biologists** have studied the wildlife of the Galapagos
- Scientists **Peter** and **Rosemary Grant** carried out a long-term study on the finch species *Geospiza fortis* on the island of **Daphne Major**
- *G. fortis'* diet consists of seeds, which when **weather conditions are normal** are **plentiful, small,** and **soft,** but which become **fewer, larger,** and **tougher** during **times of drought**
- The Grants observed a **wide range of beak sizes** in *G. fortis* when weather conditions were normal, but found that during periods of drought **beak size increased**
  - When seeds were plentiful, small, and soft, there was **no advantage** for individuals with larger beaks, and so alleles for different beak sizes were **passed on** to *G. fortis* offspring **in equal proportions**
  - When seeds were fewer, larger, and tougher, finches with larger beaks had an **advantage** when competing for food, and were therefore more likely to **survive** and **pass on the alleles** for large beak size, leading to an **increase in frequency of large beaks** in the population

- The observation that finches with larger beaks produce large-beaked offspring while finches with smaller beaks produce smaller-beaked offspring suggests that beak size is **largely determined by genes**, and so is heritable
- The heritable nature of beak size means that *G. fortis* can **adapt to a changing environment** by the process of **natural selection**
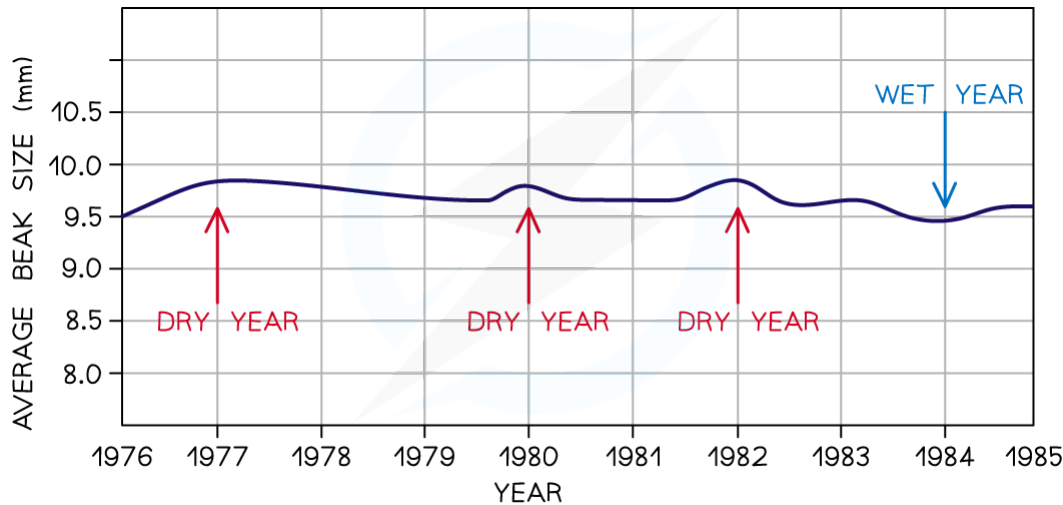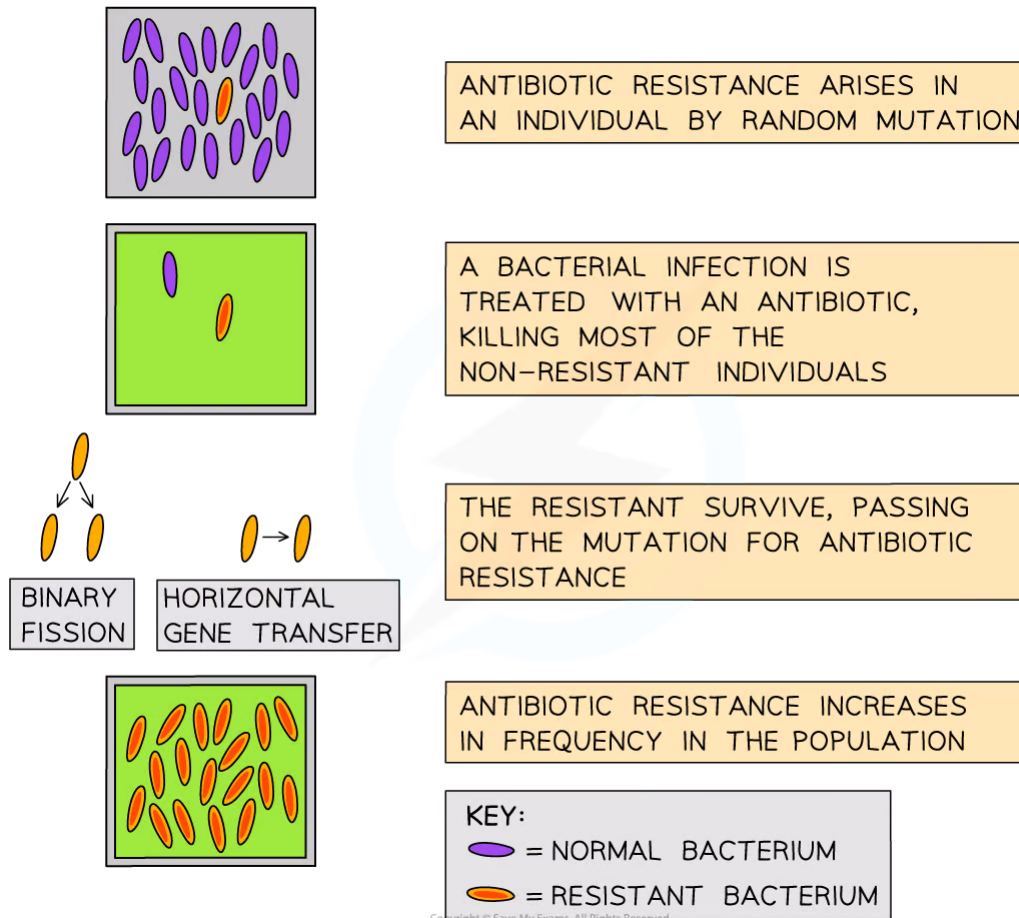
Peter and Rosemary Grant found that average beak size in G. fortis on Daphne Major increased in drought years when seeds became larger and tougher, and decreased in wet years when seeds became smaller and softer

Antibiotic resistance in bacteria

- **Antibiotics** are chemical substances made by some **fungi** or **bacteria** as a defence mechanism
- They **kill bacteria** by targeting processes and structures that are specific to bacterial cells
    - Antibiotics are **effective against bacteria** but **not against viruses**, and usually have **no effect on animal cells**

- The use of antibiotics has **increased significantly** since they were first introduced in the 1930s, **saving millions of lives**
- Since their discovery and widespread use **antibiotic resistance** has developed in many different types of bacteria
    - Antibiotic resistant bacteria are not killed by antibiotics

- Antibiotic resistance is a **heritable** characteristic and so develops in bacterial populations by the process of **natural selection**
    - Bacteria, like all organisms, have mutations in their DNA that give rise to **variation**
    - A mutation may give rise to **resistance to a particular antibiotic** in an individual bacterial cell
    - If a bacterial infection is treated with that antibiotic, a bacterial individual with the mutation for resistance is likely to **survive**
        - The antibiotic in this situation acts as a **selection pressure** in the same way that a predator would in a rabbit population

    - The bacterial cell with the resistance mutation will **reproduce** by binary fission, **passing on the mutation** and causing antibiotic resistance to **increase in frequency** in the population
        - Bacterial cells are also able to transfer genes to each other by a process called horizontal gene transfer, further increasing the number of individuals with the resistance mutation

- Note that if antibiotic use stops, an **antibiotic resistance mutation will no longer be advantageous**, and it will not be passed on to offspring **any more often than the original non-resistant form of the gene**
  - Antibiotics should not be used any more often than necessary so that a **selection pressure** is not provided; this will reduce the likelihood of an antibiotic resistant population developing

	ANTIBIOTIC RESISTANCE ARISES IN AN INDIVIDUAL BY RANDOM MUTATION
	A BACTERIAL INFECTION IS TREATED WITH AN ANTIBIOTIC, KILLING MOST OF THE NON-RESISTANT INDIVIDUALS
BINARY FISSION / HORIZONTAL GENE TRANSFER	THE RESISTANT SURVIVE, PASSING ON THE MUTATION FOR ANTIBIOTIC RESISTANCE
	ANTIBIOTIC RESISTANCE INCREASES IN FREQUENCY IN THE POPULATION

KEY:
⬮ = NORMAL BACTERIUM
⬮ = RESISTANT BACTERIUM

Antibiotic-resistant bacterial populations can evolve by natural selection

- Natural selection takes place very quickly in bacterial populations because
  - Bacterial populations contain **many individuals**, so the **chances of an advantageous mutation appearing are higher** than in other types of organisms
  - They can **reproduce very quickly**, meaning that generation times are short and any mutations that do arise can be **passed on to many offspring in a very short time**
    - Bacteria can reproduce as often as every 20 minutes

  - Bacteria can **transfer genes horizontally**, further increasing the rate at which advantageous mutations can spread

- Antibiotic resistance is a huge problem; antibiotics have been revolutionary in the treatment of disease, and losing them as a medical tool would be devastating

- Scientists are looking for ways to **reduce the rate at which resistance evolves** e.g. by reducing the use of antibiotics and the spread of infection, as well as seeking out **alternatives to current antibiotics** e.g. new antibiotics and other types of antibacterial agent

NOS: Use theories to explain natural phenomena; the theory of evolution by natural selection can explain the development of antibiotic resistance in bacteria.

- Scientists can gather information about the world by **observing events**, or **phenomena**
- They **formulate theories** that seek to explain observed events
- In the case of antibiotics, it has been **observed** that antibiotic resistance in bacteria is on the increase
  - In particular it has been noticed that once an antibiotic starts to be used to treat a particular infection, resistance rates begin to rise

- Scientists use the **theory** of natural selection to **explain this observation**
  - Antibiotics act as a selection pressure
  - Resistant individuals are 'selected' when non-resistant bacteria are killed by treatment
  - Resistant individuals survive, reproduce, and pass on the resistance characteristic
  - Resistant individuals increase in frequency

- **Understanding the mechanism** by which resistance evolves means that scientists have a better chance of **solving** or **reducing the problem**
  - E.g. by reducing the selection pressure, i.e. the use of antibiotics, natural selection can be slowed down

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💡 Exam Tip

While you are expected to know the examples of natural selection described above, you could also be given an unfamiliar example, so make sure that you can describe the **process of natural selection**:

- Within a species, there is always **variation** in **heritable** characteristics due to chance mutation
- Populations will have **selection pressures** acting on them
- Individuals with advantageous characteristics are more likely to **survive** and **reproduce**
- Heritable advantageous characteristics are **passed on** to offspring
- The advantageous characteristic **increases in frequency**

5.2 Classification & Cladistics

5.2.1 Classification System

Binomial System

- The **diversity of life** on Earth is vast, and is known as **global biodiversity**
- The extent of global biodiversity is such that scientists can only **estimate** the total number of species present on Earth, and it is likely that there are **many species yet to be discovered**
- For biologists to make sense of the huge array of species, **organising them into logical groups** is essential
  - This process of putting organisms into groups is known as **classification**
  - The science of classification is known as **taxonomy,** and scientists working in the field of taxonomy are **taxonomists**

- Classifying an organism involves deciding which **biological group**, or **taxon** (plural **taxa**), it fits into best, and then **naming it** according to its taxon
- Historically an organism's biological group was determined on the basis of its **observable characteristics**, and today this information is combined with **DNA sequence data** for more accurate classification

A Universal Naming System

- The biological system of naming used to **name species according to their taxa** is known as the **binomial system**
- This system is **universal**, ensuring that scientists around the world all use the **same method** of naming species
  - In the past, individual scientists decided on species names; names could be very **long**, and often one species could have **different names** in different parts of the world

- To ensure that all biologists know, and agree on, the criteria for naming species, regular meetings called **congresses** are held to discuss naming conventions
  - The first **International Zoological Congress** was held in 1889, during which taxonomists **agreed on the rules** that should be used for classifying and naming species
  - Congresses have since been held at regular intervals, with separate meetings for scientists who study different groups of organisms e.g. animals, plants, and fungi

The Binomial System

- The **binomial naming system,** or system of nomenclature, was introduced by the Swedish taxonomist **Carl Linnaeus** in his 1758 book, *Systema Naturae*
- The system involves giving a species a **two-part name,** hence binomial
- Both parts of the name are in **Latin**, or a **latinised version** of a non-Latin word
  - e.g. *Eriovixia gryffindori* is a species of orb spider named after a famous school house

- The first part of the name is an organism's **genus**, and the second is its **species** name
  - E.g. the binomial name of a wolf is *Canis lupus*; wolves belong to the genus *Canis*, and the species *lupus*

- There are several **conventions**, or rules, that should be used when writing binomial names
  - The **genus should begin with a capital letter**, and the **species with a lower-case letter**, e.g. the honey bee is *Apis mellifera*
  - When typed, binomial names should appear in **italics**, and when written by hand, they should be **underlined** e.g. a limpet is *Patella vulgata* when typed, or <u>Patella</u> <u>vulgata</u> by hand
  - The first time a binomial name is used in a text it should appear **in full**, e.g. wheat is *Triticum aestivum*, but the **genus name can from then on be abbreviated** to *T. aestivum*

NOS: Cooperation and collaboration between groups of scientists; scientists use the binomial system to identify a species rather than the many different local names

- The work of scientists does not take place within the **confines of a laboratory**, or even a **country**, but can have implications for the work of other scientists around the world
- Because of the **international nature of scientific research**, it is essential that scientists are able to **communicate with each other clearly** about their work
- For scientific communication to be **effective** and **allow collaboration**, it is essential that scientific language enables scientists to be sure that they are **talking about the same thing**
- The **binomial naming system** is a good example of a system that enables scientists to communicate clearly with each other about living organisms
- The binomial system is essential because it ensures that scientists are all **talking about the same species**
  - **Different countries** may have **different common names** for the same species e.g. In English, *Felis domesticus* is known as a cat, but around the world it is also known as kitte, maow, chat, kissa, bili, and gato
  - **Different local** or **cultural names** may arise even within a country e.g. in the UK alone the woodlouse, *Onescus asellus,* has more than 50 different local names that include woodpigs, cheesy bobs, woodywigs, chuggy pigs, and crunchy bats, and another country may have an equally long list of local, or cultural names for the same species
  - There are also examples of species where **one name might be used for different species** in different parts of the world, e.g. the robin in the US is a completely different species of bird to the robin in Europe

- There is nothing wrong with maintaining the use of different common names around the world, but when scientists discuss their work, the binomial system ensures that they are **communicating effectively** with each other

Taxonomy

- **Biological classification** involves putting organisms into groups, or **taxa** (singular **taxon**)
- The taxa form a **hierarchy**
  - A hierarchical system is one in which **larger groups contain smaller groups** with no overlap between groups

- The smallest taxon in the taxonomic hierarchy is **species**
- The species taxa are grouped within the next biggest taxon in the hierarchy, **genus** (plural **genera**)
- The genera are grouped within the next taxon, **family**, and so on until the biggest taxon, **domain**

Domains

- **Taxonomy** is the practice of **biological classification**
  - Organisms are **grouped into taxa**, with the smallest taxon being species

- The science of taxonomy has **frequently changed** to match the latest discoveries about the features of organisms
  - Historically, the largest taxonomic groups were the **plant** and **animal kingdoms**, then **fungi** were discovered and added (incorrectly) to the plant kingdom
  - **Microscopes** led to the discovery of **prokaryotes** and **eukaryotes**, and the taxa were later divided into five kingdoms; **plants, animals, fungi, protoctists**, and **prokaryotes**
    - The protoctists are eukaryotic, primarily single-celled, organisms

  - **RNA analysis** has recently shown that there are **two distinct groups of prokaryotes**, leading to a **shift in taxonomic thinking** and the beginnings of the **three domain system**

- The **largest taxonomic group** is now known as a domain
- There are three domains, which are:
  - Archaea (prokaryotes)
  - Eubacteria (prokaryotes)
  - Eukaryotes (eukaryotes)
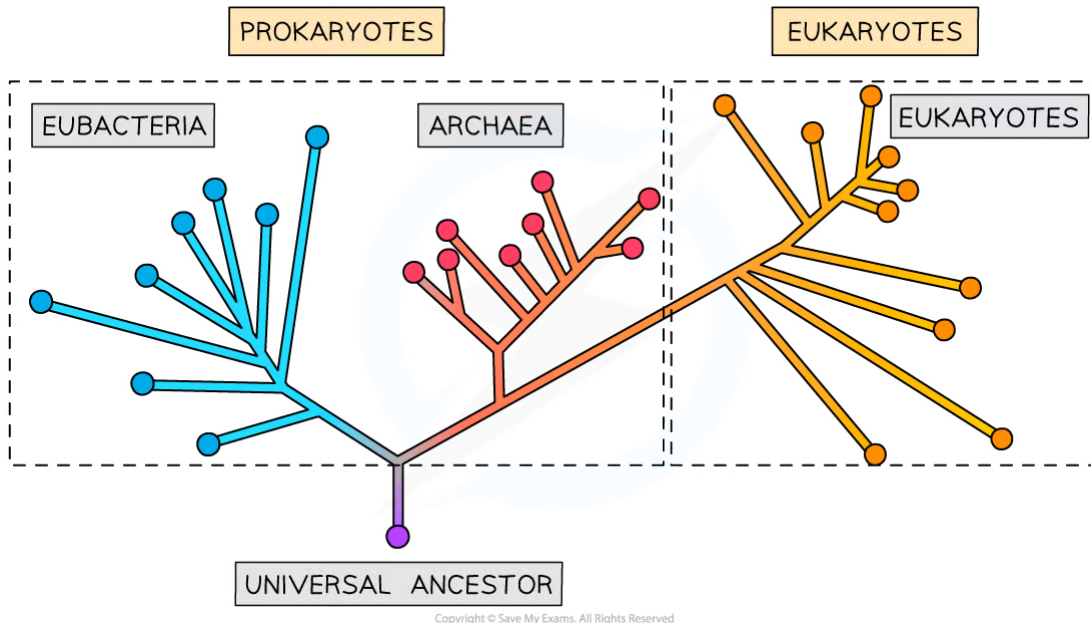
The three domains

Classifying the Archaea

- The archaea were originally classified with the rest of the bacteria in one taxon due to **sharing several features** with them
  - Prokaryotic cell structure
  - Circular chromosome
  - Presence of a cell wall

- 70S ribosomes
- Closer analysis of the archaea however showed that **some of their features were distinct** from the rest of the prokaryotes
  - Their **cell walls are made of a different material** from the cell walls of the rest of the bacteria
  - Their **cell membranes are made of a distinct type of lipid**
  - The **small subunit** of their **ribosomes** is **more similar to eukaryotic ribosomes** than to the ribosomes of the rest of the prokaryotes
- These discoveries led to a **change in the classification of the archaea**, which became their own domain

The Features of the Three Domains Comparison Table

| Feature	Archaea	Eubacteria	Eukaryotes
Cell type	Prokaryotic	Prokaryotic	Eukaryotic
Chromosome	Circular	Circular	Linear chromosomes + circular mtDNA and cpDNA
Cell membrane lipids	Glycerol−ether lipids	Glycerol−ester lipids	Glycerol−ester lipids
Ribosomes	70S ribosomes but small subunit is more similar to eukaryotic ribosomes	70S ribosomes	Larger 80S ribosomes in cytosol and 70S ribosomes in mitochondria and chloroplasts
Cell walls	Always present (without peptidoglycan)	Always present (with peptidoglycan)	Sometimes present (without peptidoglycan)
Histones	Yes	No	Yes
Introns	Sometimes	Rarely	Yes

Hierarchy of Taxa for Eukaryotes

- Eukaryote is the domain of **all eukaryotes**, distinguishable from the Bacteria and the Archaea which are **both prokaryotic** domains
- Just like the other domains, the Eukaryote domain contains a **hierarchy of taxa**
- The taxonomic hierarchy contains the following taxonomic groups in descending order of size:
  - Domain
  - Kingdom
  - Phylum
  - Class
  - Order
  - Family
  - Genus
  - Species

- It can be good to use a **mnemonic,** or memory aid, to help you remember the different ranks in the taxonomic classification system
  - There are lots out there, or you can make up your own, but here's an example that you might find helpful:
    - **D**o **K**eep **P**onds **C**lean **O**r **F**ish **G**et **S**ick
    - **D**omain, **K**ingdom, **P**hylum, **C**lass, **O**rder, **F**amily, **G**enus, **S**pecies
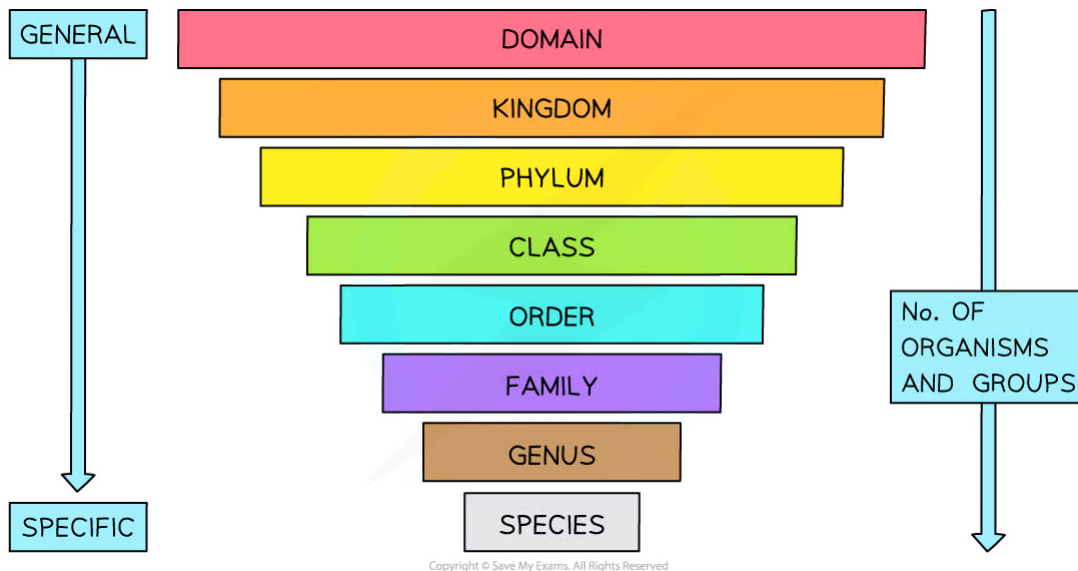
The hierarchy of taxa

- The wolf, *Canis lupus*, is an example of an organism in the **eukaryote domain**
  - A wolf belongs to the following **taxonomic groups**:
    - Domain: Eukaryote
    - Kingdom: Animalia
    - Phylum: Chordata
    - Class: Mammalia
    - Order: Carnivora

- Family: Canidae
- Genus: *Canis*
- Species: *lupus*

- The flowering plant *Hibiscus rosa-sinensis* is another example of an organism in the eukaryote domain
  - It belongs to the following **taxonomic groups**:
    - Domain: Eukaryote
    - Kingdom: Plantae
    - Phylum: Angiospermae
    - Class: Dicotyledonae
    - Order: Malvales
    - Family: Malvaceae
    - Genus: *Hibiscus*
    - Species: *rosa-sinensis*

The Classification of the Wolf and the Hibiscus Plant Table

Taxonomic Rank	Wolf	Hibiscus
Domain	Eukaryote	Eukaryote
Kingdom	Animalia	Plantae
Phylum	Chordata	Angiospermae
Class	Mammalia	Dicotyledonae
Order	Carnivora	Malvales
Family	Candidae	Malvaceae
Genus	Canis	Hibiscus
Species	lupus	rosa-sinensis

5.2.2 Classifying Organisms

Examples of Classification

- Biological classification involves putting organisms into **groups**, or **taxa** (singular **taxon**)
- The taxa form a **hierarchy**
  - A **hierarchical system** is one in which **larger groups contain smaller groups** with no overlap between groups

- The taxonomic hierarchy contains the following taxonomic groups in descending order of size:
  - Domain
  - Kingdom
  - Phylum
  - Class
  - Order
  - Family
  - Genus
  - Species

Examples of classification

- The wolf, *Canis lupus*, is an example of an organism in the **animal kingdom**
  - A wolf belongs to the following **taxa**
    - Domain: Eukaryote
    - Kingdom: Animalia
    - Phylum: Chordata
    - Class: Mammalia
    - Order: Carnivora
    - Family: Canidae
    - Genus: *Canis*
    - Species: *lupus*

- The flowering plant *Hibiscus rosa-sinensis* is an example of an organism in the **plant kingdom**
  - It belongs to the following taxa
    - Domain: Eukaryote
    - Kingdom: Plantae
    - Phylum: Angiospermae
    - Class: Dicotyledonae
    - Order: Malvales
    - Family: Malvaceae
    - Genus: *Hibiscus*
    - Species: *rosa-sinensis*

The Classification of the Wolf and the Hibiscus Plant Table

| Taxonomic Rank	Wolf	Hibiscus
Domain	Eukaryote	Eukaryote
Kingdom	Animalia	Plantae
Phylum	Chordata	Angiospermae
Class	Mammalia	Dicotyledonae
Order	Carnivora	Malvales
Family	Canidae	Malvaceae
Genus	Canis	Hibiscus
Species	lupus	rosa-sinensis

Natural Classification

- The taxonomic classification system organises species into groups based on their **evolutionary origins** and **relationships**
- This means that all members of a taxonomic group **share a common ancestor**
  - A **common ancestor** is one individual, or pair of individuals, from whom **all individuals in a group have descended**, e.g.
    - For a group of full siblings, the common ancestors will be their parents
    - For a group of cousins, the common ancestors will be their grandparents

- Grouping organisms into **taxa that share a common ancestor** is known as **natural classification** and a group of organisms classified in this way is known as a **natural group**
  - E.g. eukaryotic cells appear to have **only evolved once**, meaning that **one eukaryotic cell was the ancestor of all other eukaryotes**; the eukaryote domain is therefore a natural group

- It is possible to carry out **artificial classification**, grouping together **organisms from different ancestors**, e.g.
  - Dolphins and sharks could in theory be grouped together as they are both groups of aquatic animals that share a similar body shape, but they in fact **belong to different classes**
    - Dolphins are **mammals** and sharks are **fish**
    - Their streamlined body shapes **evolved separately** rather than originating in one common ancestor

  - Cacti and euphorbia are two groups of desert plant recognisable by their spiny leaves and branching, succulent stems, and it would be reasonable to assume from their appearance that they are closely related to each other, but they **belong to different orders** of plant
    - Cacti are found in the deserts of the Americas, while euphorbia are found in Africa
    - They evolved separately, but **adapted to similar environments**, hence they have similar characteristics; this kind of evolution is known as **convergent evolution**

- It can be difficult to carry out accurate natural classification from observation alone, but the development of **DNA sequencing technology** means that **natural classification on the basis of DNA sequence data has become possible**
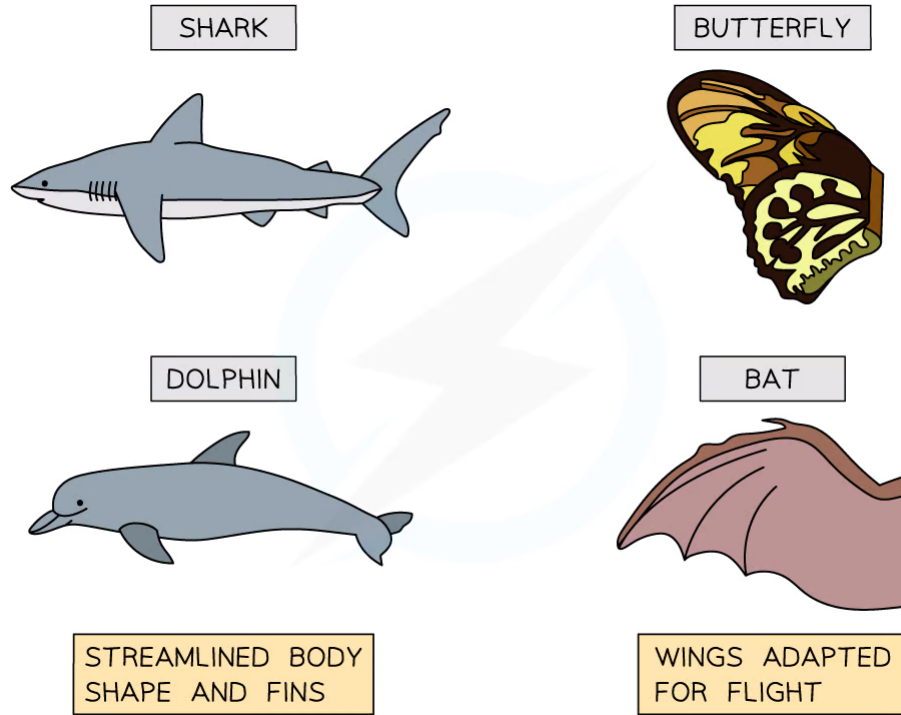
It would be possible to group both sharks and dolphins, and butterflies and bats, together on the basis of their shared characteristics, but this would not be a natural classification as they do not share recent common ancestors

The advantages of natural classification

- Natural classification enables **identification** of unknown species
    - E.g. when a sample of insects is collected and the researcher doesn't recognise all of the species collected
    - Using the natural classification system an unknown species can be identified by **logically working through the taxa**
        - This means first identifying the domain, then the kingdom, then phylum etc., **narrowing down the options** until a species is identified
        - An identification method known as a **dichotomous key** works using this principle

- Natural classification enables **predictions to be made** about the **characteristics** of a species
    - If all of the members of a taxon descend from a **common ancestor** means that it is likely that the members will **share common characteristics**
    - This can be useful when e.g. searching for new drugs; if researchers know that one member of a plant genus produces a chemical that is useful in treating a disease, then it is likely that other members of that genus may produce the same chemical
        - This allows researchers looking for new drugs to focus their search rather than testing every single plant species

Reclassification

- There can be **difficulties** when trying to determine the **ancestry** of species based on observation of shared characteristics
  - This can lead to **artificial** rather than **natural classification**
    - Convergent evolution can lead to groups of organisms **sharing similar characteristics** when they did not evolve from a shared common ancestor

- Advances in **DNA, RNA** and **protein sequencing** has allowed scientists to further investigate the relationships between species
  - This has revealed the true **ancestry** of taxa

- This sometimes leads to **reclassification** of taxa
  - Taxa may be **split** if taxonomists decide that they **do not descend from a common ancestor**
  - Taxa previously classified as separate may be **grouped together** if it is discovered that they **do descend from a common ancestor**

- An example of a taxon in which there has been a great deal of reclassification since the introduction of sequencing data is the Hominidea group to which humans belong
  - Humans were **originally thought to have their own taxon** separate from the rest of the great apes, but are **now known to be part of the same family**
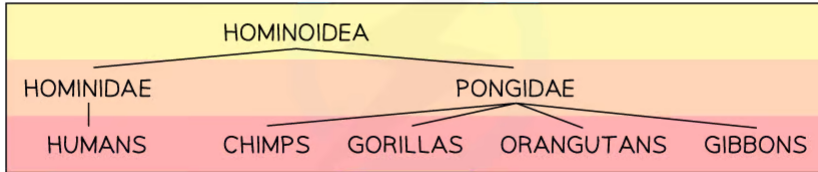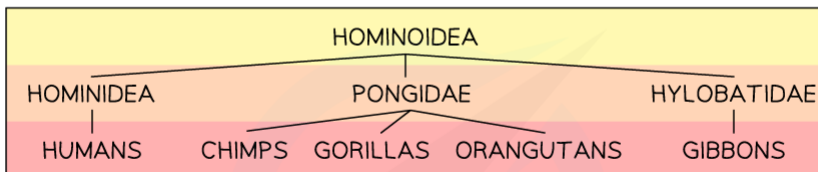
UNTIL THE 1960s, HUMANS WERE CLASSIFIED AS A SEPARATE GROUP FROM THE APES

HOMINOIDEA

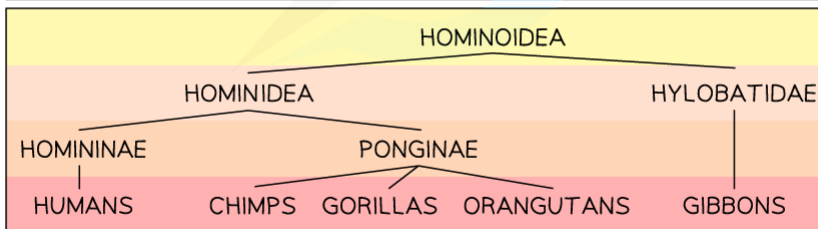HOMINIDAE — PONGIDAE

HUMANS   CHIMPS   GORILLAS   ORANGUTANS   GIBBONS

↓

EARLY PROTEIN ANALYSIS LED TO SEPARATION OF THE 'GREAT APES' (CHIMPS, GORILLAS, AND ORANGUTANS FROM THE 'LESSER APES' (GIBBONS))
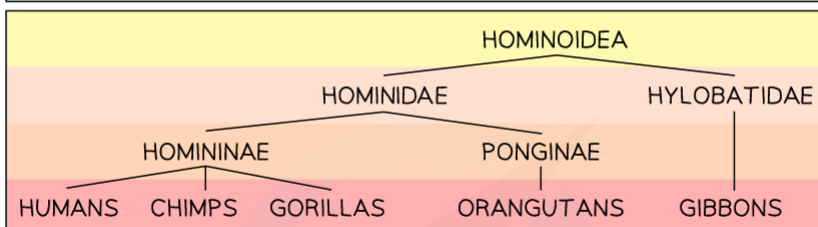
HOMINOIDEA

HOMINIDEA   PONGIDAE   HYLOBATIDAE

HUMANS   CHIMPS   GORILLAS   ORANGUTANS   GIBBONS

↓

THE GREAT APES ARE RECLASSIFIED IN THE SAME FAMILY AS HUMANS

HOMINOIDEA

HOMINIDEA   HYLOBATIDAE

HOMININAE   PONGINAE

HUMANS   CHIMPS   GORILLAS   ORANGUTANS   GIBBONS

↓

CHIMPS AND GORILLAS ARE CLASSIFIED IN THE SAME SUBFAMILY AS HUMANS

HOMINOIDEA

HOMINIDAE   HYLOBATIDAE

HOMININAE   PONGINAE

HUMANS   CHIMPS   GORILLAS   ORANGUTANS   GIBBONS

↓

DNA ANALYSIS SHOWS THAT HUMANS AND CHIMPS ARE MORE CLOSELY RELATED TO EACH OTHER THAN

TO GORILLAS
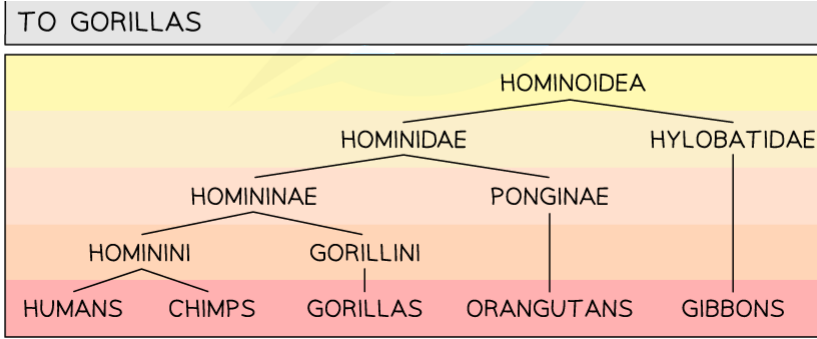
The taxon containing humans has been frequently reclassified

YOUR NOTES
↓

Plant Phyla Features

- All plants belong to the **plant kingdom**
- Within the plant kingdom are several **phyla** (singular **phylum**)
- Some plant phyla are small
  - E.g. the Glaucophytes contain only 70 species and the Gingkophytes contains only 1 living species

- There are **four major plant phyla**
  - Bryophytes (20 000 species)
  - Filicinophytes (10 000 species)
  - Coniferophytes (600 species)
  - Angiospermophytes (352 000 species)

- Each of the four main phyla can be identified by their characteristics

Bryophytes

- The **bryophytes** include **mosses, liverworts**, and **hornworts**
- They are **small, terrestrial** plants
- They have no vascular tissue
- **Cambium** tissue is also **absent**
  - Cambium is a tissue containing stem cells that differentiate into xylem and phloem cells

- Reproduction takes place via **spores**
  - Spores are produced in and dispersed from **spore capsules**

- Bryophytes do not produce flowers, pollen, ovules, seeds, or fruits
- No true roots are present, but hair-like structures called **rhizoids anchor plants in the soil**
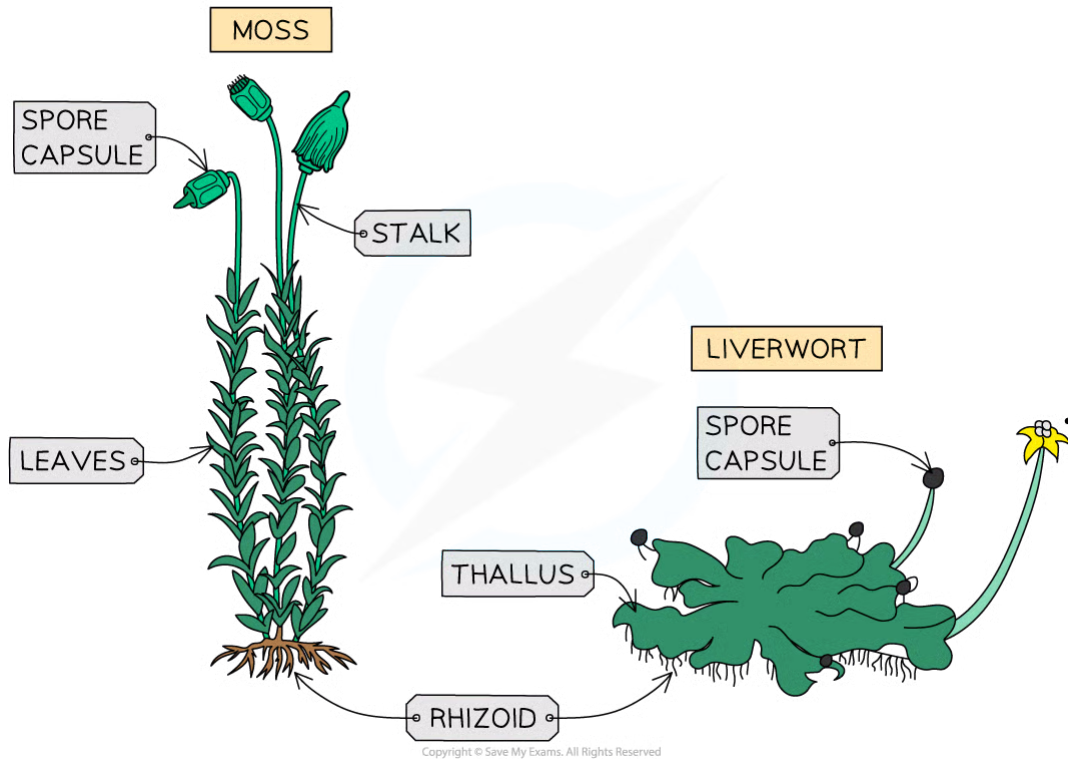
The bryophytes include mosses and liverworts

Filicinophytes

- Filiconophytes are the **ferns**
- Ferns are **mainly terrestrial** and have **vascular tissue**
- **Roots, stems**, and **leaves** are present
  - Fern leaves are divided structures known as fronds

- **Cambium** tissue is **absent**
- Reproduction takes place via **spores**
  - Spores are produced in and dispersed from structures on the underside of fronds called **sporangia**

- Filicinophytes do not produce flowers, pollen, ovules, seeds, or fruits
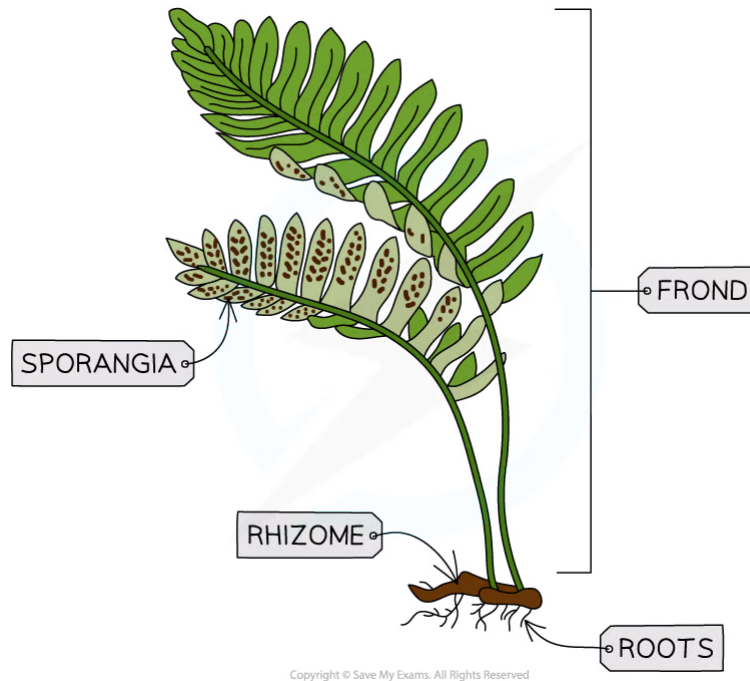
The filicinophytes are the ferns

Coniferophytes

- More commonly referred to as the **conifers**, the coniferophytes are usually **tall, straight, trees**
- **Roots, stems**, and **leaves** are present
- **Vascular tissue is present**, as well as **cambium tissue**
- **Reproduction** is carried out via pollen and **ovules**
    - **Pollen** is produced in male cones and **ovules** are produced in female cones
        - Pollen is the male gamete and ovules are the female gamete

    - **No flowers** are present
    - **Both male and female** cones are present on each tree
    - Pollen is carried from one cone to another by the **wind** in order for fertilisation to take place

- **Seeds** develop after fertilisation inside cones and are dispersed by falling to the ground or by animals
- Most coniferophytes are **evergreen** (i.e. they retain their leaves all year round)
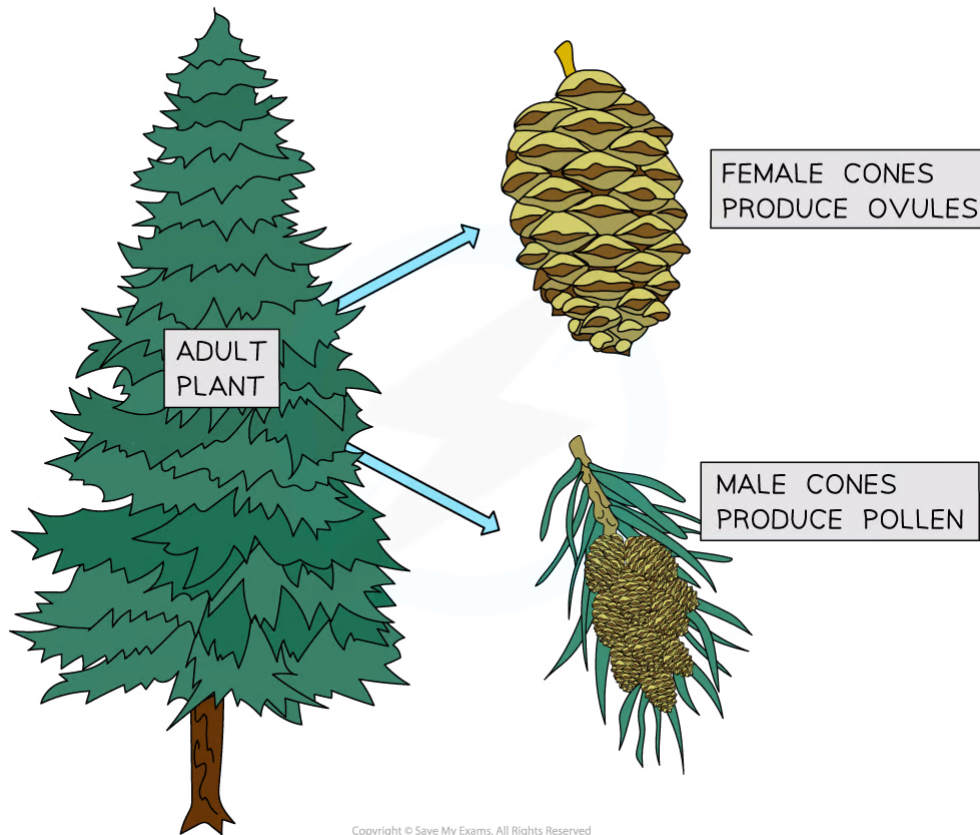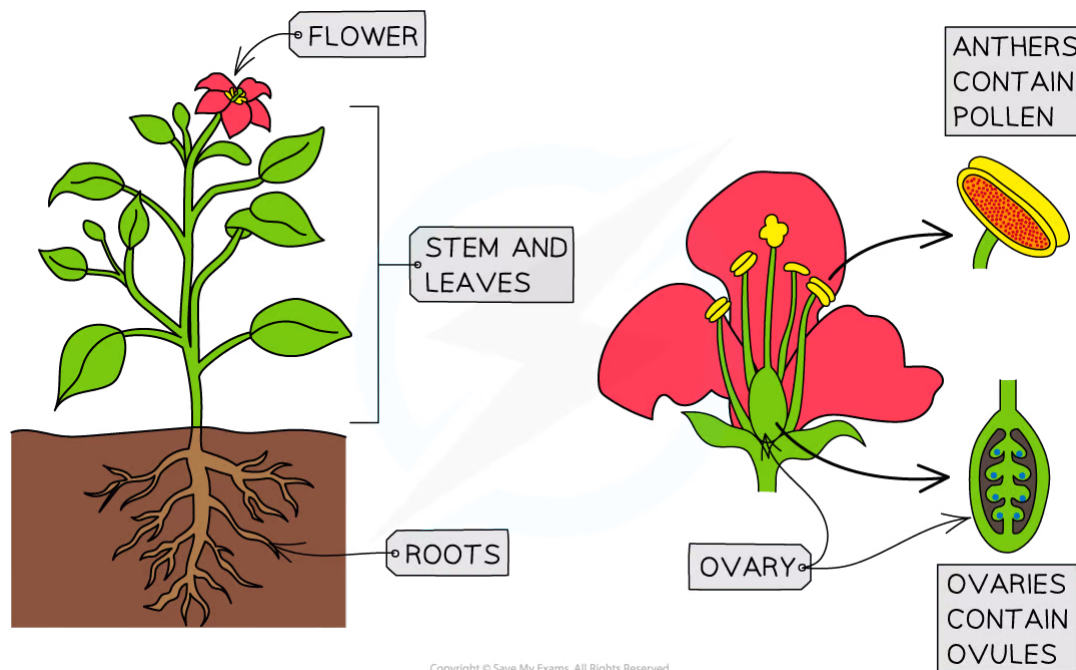
Coniferophytes reproduce via pollen and ovules that are produced inside cones

Angiospermophytes

- Often referred to as **angiosperms**, these are **flowering plants**
- This is an incredibly **diverse phylum**, with examples including **grasses, shrubs**, and non-coniferous **trees**
- **Roots, stems**, and **leaves** are present
- **Vascular** and **cambium tissues** are **present**
- Reproduction is carried out via **pollen** and **ovules**
  - **Flowers** produce pollen and also contain ovules within an **ovary**
  - Fertilisation occurs when pollen is transferred from one flower to another by e.g.
    - Insects
    - Animals
    - Wind

  - **Seeds** form and are **dispersed via fruits** which develop from the ovaries of flowers

FLOWER

STEM AND LEAVES

ROOTS

ANTHERS CONTAIN POLLEN

OVARY

OVARIES CONTAIN OVULES

Angiospermophytes reproduce via pollen and ovules produced in flowers

Plant Phyla Features Table

| Phylum	Plant structure under ground	Plant structure above ground	Vascular tissue	Mechanism of reproduction	Seeds	Fruits
Bryophyte	Rhizoid	Leaves or thallus	Absent	Spores in spore capsules	Absent	Absent
Filicinophyte	Roots	Leaves in the form of fronds	Present	Spores in sporangia	Absent	Absent
Coniferophyte	Roots	Stem and needle−like leaves	Present	Pollen and ovules in cones	Present in cones	Absent
Angiospermophyte	Roots	Stem and leaves	Present	Pollen and ovules in flowers	Present in ovary	Present

5.2.4 Animal Phyla Features

Animal Phyla Features

- Animals are **multicellular**, **eukaryotic** organisms
- They are heterotrophs and most have a **nervous system** that enables responses to the surrounding environment
- There are over **30 animal phyla**, some of which are **vertebrates** and some of which are **invertebrates**
  - Vertebrates have a backbone, or spinal column, while invertebrates do not

- Some of the major animal phyla include:
  - Porifera
  - Cnidaria
  - Platyhelminthes
  - Annelida
  - Mollusca
 - Arthropoda
  - Chordata

Porifera

- Simple **aquatic organisms** consisting of a **colony of cells**
  - Commonly known as the **sponges**
  - Once thought to be plants

- Two **layers of cells surround an internal cavity**
  - They **do not have a mouth** for taking in food, **or an anus** for egestion

- Water is drawn in through **pores** in the outer layer of cells, before **suspended particles from the water** are filtered out and t**aken up by surrounding cells** for food
  - Porifera are **filter feeders**

- There is **no symmetry** in the body plan of the porifera
- The **structure** of poriferans is supported by calcium or silica formations known as **spicules**
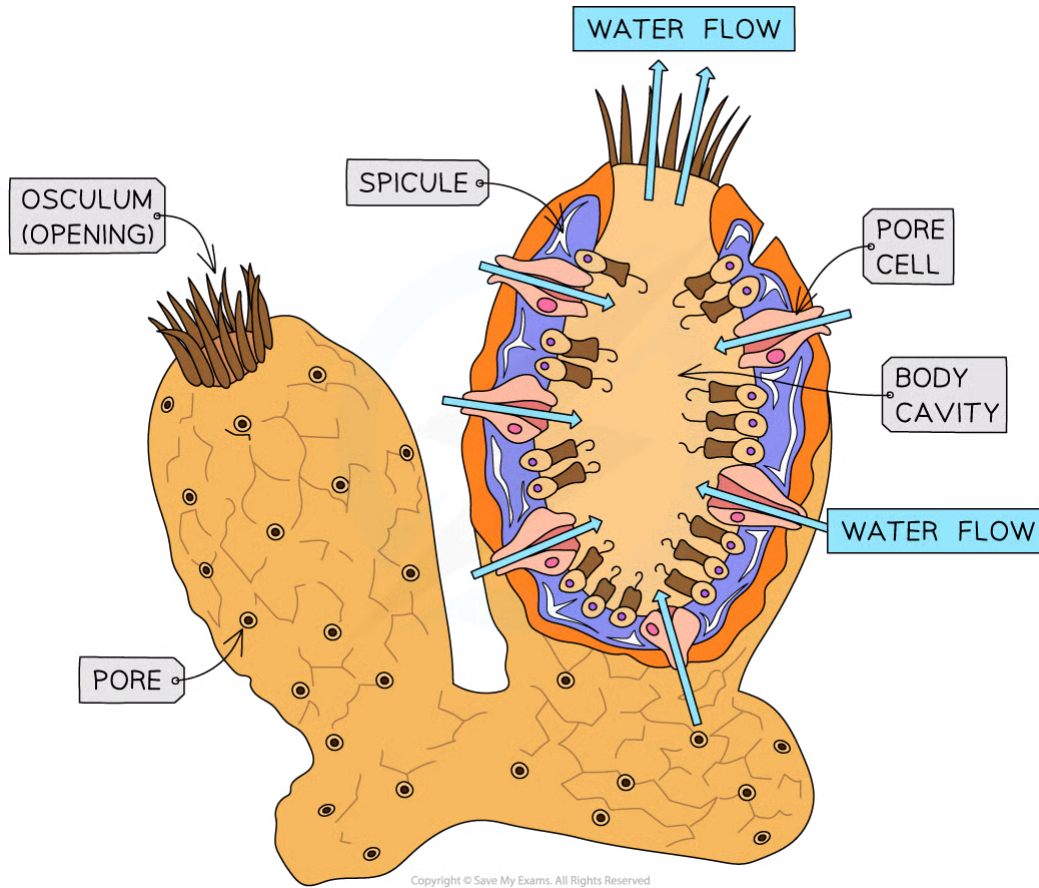
*Porifera take in water through pores for filter feeding*

Cnidaria

- **Aquatic organisms** also known as the coelenterates
- Their body cavity is surrounded by **two layers of cells** and has a **single opening for both ingestion and egestion**
- There are **two distinct body forms** present in the cnidaria phylum
    - **Polyps**, or hydroids are sessile e.g. coral and anemones
    - **Medusae** (singular **medusa**) float in the water e.g. jellyfish
    - Some cnidaria go through **both the polyp and medusa** body form during their **life cycle**

- Polyps are **filter feeders**, while medusae **catch prey** using **stinging cells** on their tentacles
- There is **radial symmetry** in the body plan of the cnidaria
- Most cnidaria have **soft bodies** that rely on the surrounding water for support, but **corals secrete an exoskeleton** made of calcium carbonate
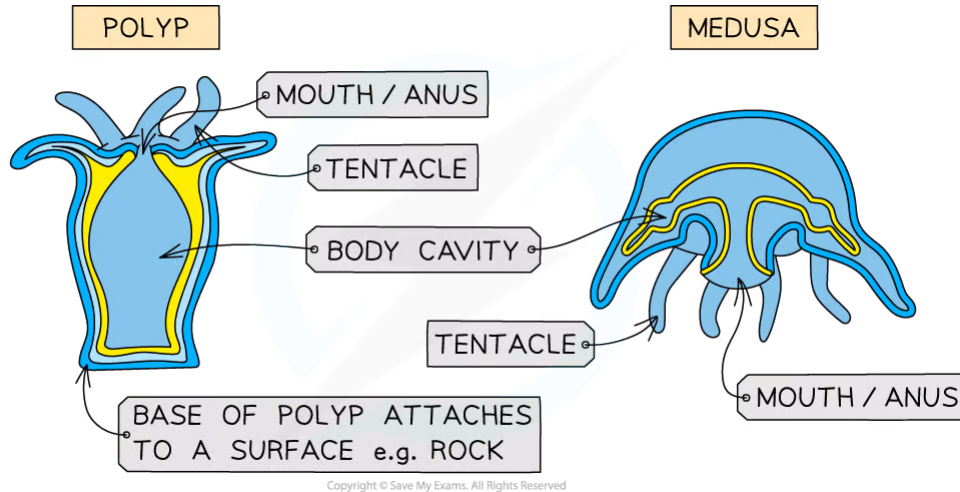
Cnidaria have two distinct body forms; polyps and medusae

Platyhelminthes

- **Flat-bodied, unsegmented** worms that include the **flatworms, tapeworms,** and **flukes**
- **Three layers of cells** surround a branched gut with **one opening for both ingestion and egestion**
- Platyhelminthes can be **free-living predators** or **scavengers**, or **parasites** that feed on their hosts
- The flat body shape of platyhelminthes means that the **diffusion distance** to all cells is **short**, and **no circulatory system** is present
- There is **bilateral symmetry** in the body plan of the **platyhelminthes**
- Platyhelminthes have **soft bodies** with **no skeletal support**
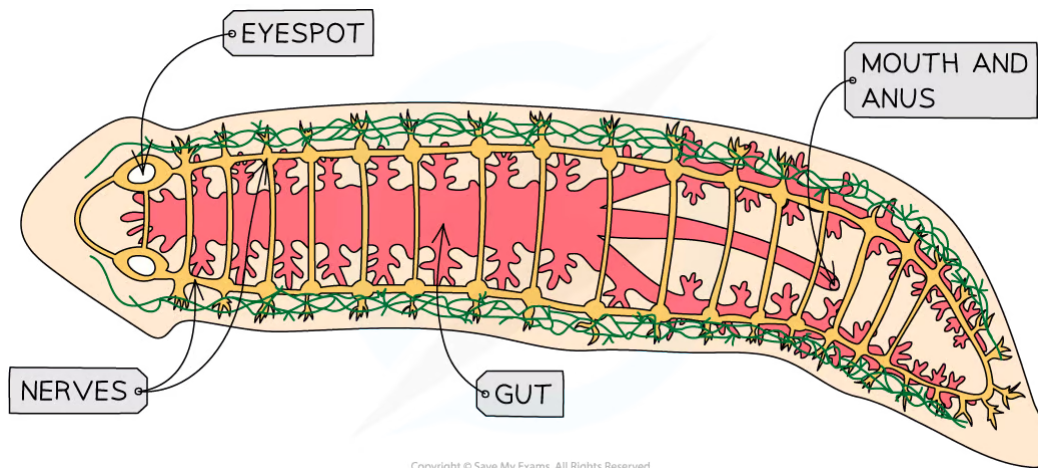
The body structure of a member of the phylum Platyhelminthes

Annelida

- **Round-bodied, segmented** worms that include the **earthworms** and the **leeches**
- Each **ring-shaped body segment** contains a repetition of the structures of blood vessels and nerves
- The **gut** has separate openings for the **mouth** and **anus**

- Annelida can be **free-living predators** or **scavengers**, or **parasites** that feed on their hosts
- Annelida have a **closed circulatory system**
- There is **bilateral symmetry** in the body plan of the **annelida**
- Annelida have **soft bodies** which are supported by a **hydroskeleton**
  - The hydroskeleton is an internal fluid-filled cavity called the coelom, against which the muscles of the body wall exert pressure
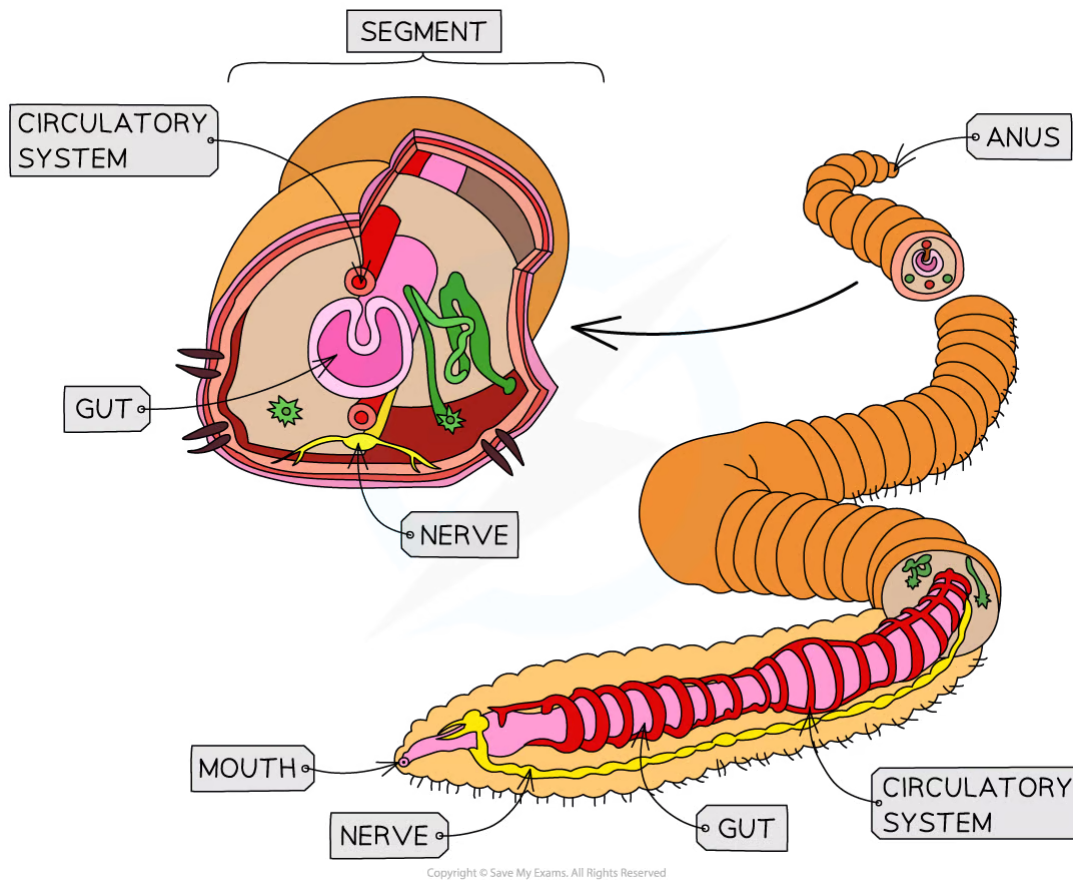

The annelida have a segmented body structure

Mollusca

- A diverse group of animals that includes the **snails, slugs, mussels**, **limpets**, and **octopuses**
  - It is the second-largest phylum (i.e. it contains a higher number of recorded species than any other phylum, except for Arthropoda)

- Most molluscs are **aquatic**, with **some terrestrial species**
- The body structure contains a **muscular foot** and a **visceral mass**
  - The foot is used for **motion** and/or **anchorage** e.g. as in limpets
  - The visceral mass is located above the foot and **contains the internal organs** (i.e. it is the soft, metabolic region that contains the digestive, excretory and reproductive organs)

- The **gut** has separate openings for the **mouth** and **anus**

- Mollusca have several feeding methods, including:
  - **Filter feeding** e.g. in bivalves such as mussels
  - Scraping at food sources such as leaves or algae on rocks using a rough, tongue-like organ called a **radula** e.g. snails and limpets
  - Active **predation** e.g. sea slugs

- Most mollusca have an **open circulatory system** in which the transport fluid bathes the internal organs
  - The cephalopods, which include squid and octopuses have a closed circulatory system

- There is **bilateral symmetry** in the body plan of the **mollusca**
- Mollusca have **soft bodies** that sometimes secrete a **calcium carbonate shell** from a mantle e.g. snails
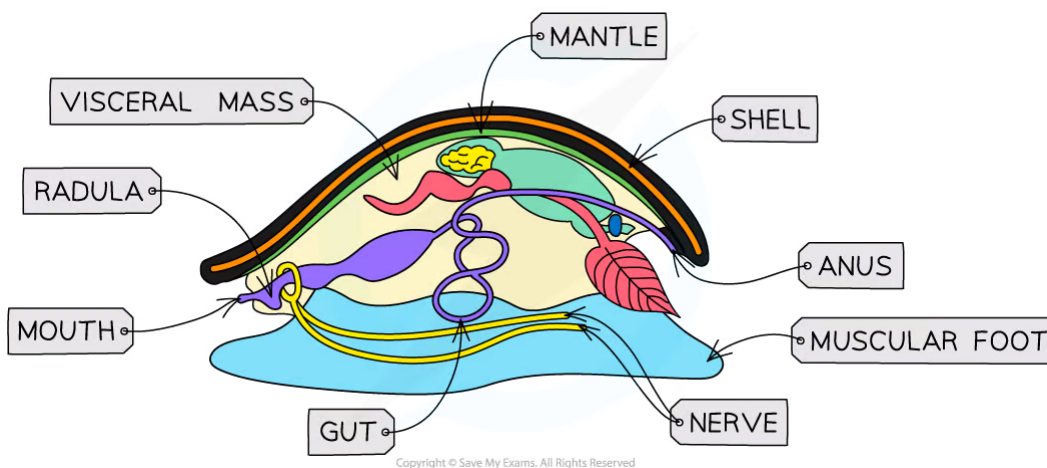
The body structure of snails; members of phylum Mollusca

Arthropoda

- Animals with **segmented bodies**, a **hard exoskeleton**, and **jointed limbs**
  - It is the **largest phylum** (i.e. it contains a higher number of recorded species than any other phylum)
  - It includes **insects, arachnids, crustaceans, centipedes**, and **millipedes**

- There is usually **one pair of jointed limbs per body segment**, though this is not always the case
- The **gut** has separate openings for the **mouth** and **anus**
- Arthropoda have an **open circulatory system**
- There is **bilateral symmetry** in the body plan of the **arthropoda**
- Arthropoda have a **hard exoskeleton** made of **chitin**
 - The exoskeleton is shed as the animal grows
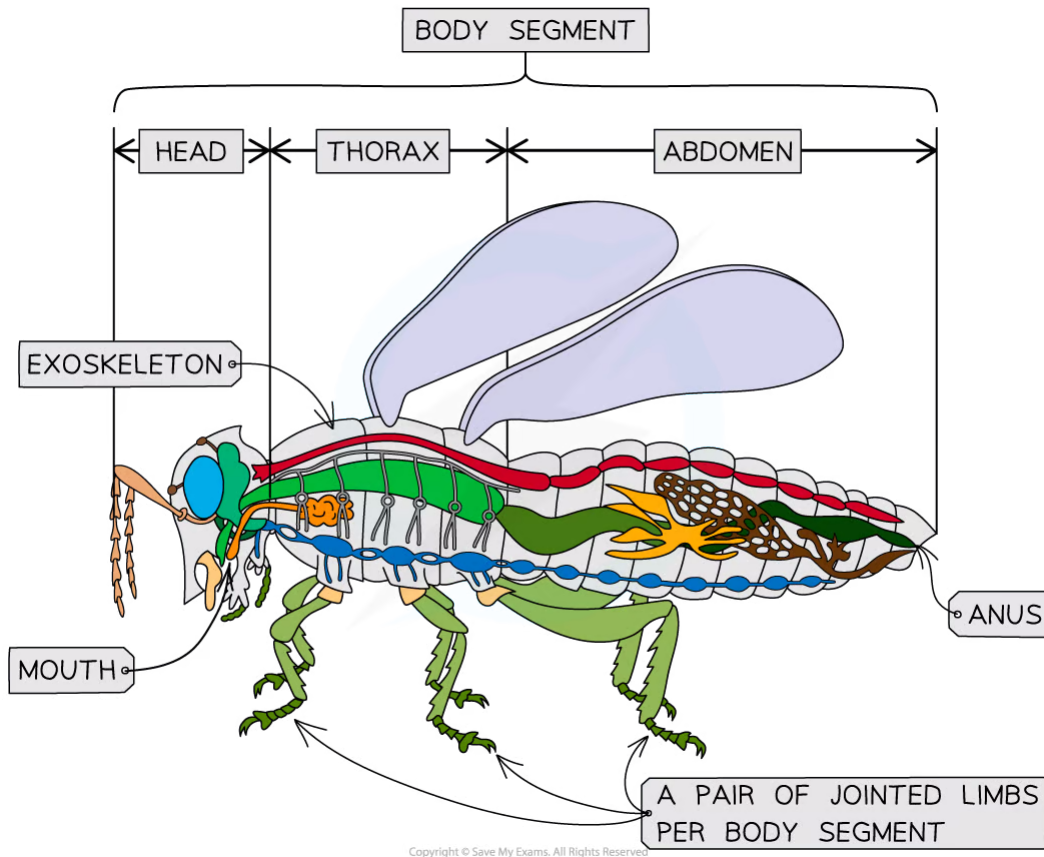
Insects are members of the phylum Arthropoda; they have three body segments, each with a pair of jointed limbs

Chordata

- The phylum **chordata** includes **all of the vertebrates**, as well as **some invertebrates** such as the tunicates; commonly known as sea squirts
- To be classified as a chordate, an organism must have the following features **at some stage during its development**:
    - A rod-like structure along the **dorsal** length of the body known as a **notochord**
        - Dorsal refers to the **back** of an organism

    - A **hollow nerve cord** located in the **dorsal** region
    - A series of slits behind the mouth known as **pharyngeal slits**
    - A **tail** that extends **beyond the anus**, known as a **post-anal tail**

- Some chordates only have these features during the **embryonic stages** of development, e.g.
    - In vertebrates, the notochord is replaced with the spinal column in fully developed individuals
    - The dorsal hollow nerve cord develops into the brain and spinal cord in most species of chordate
    - The pharyngeal slits are only retained into adulthood in some types of chordate e.g. in the gills of fish

- The post-anal tail has become a vestigial structure in the great apes
  - Vestigial structures are those that have lost their function, and are sometimes known as 'evolutionary leftovers'
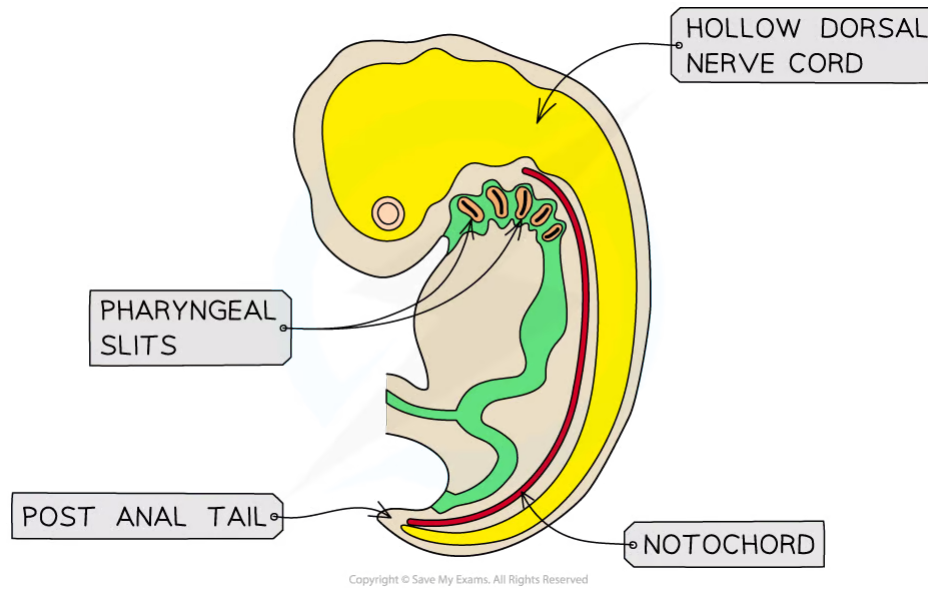
Human embryos have all of the features of phylum chordata

Phyla Features Table

YOUR NOTES
↓

| Phylum	Symmetry	Gut structure	Structural support	Other distinctive features
Porifera	None	None	Mineral structures called spicules	Filter water through pores on outer surface of body
Cnidaria	Radial	One opening for mouth and anus	Soft-bodied	Two distinct body forms; the polyp and the medusa
Platyhelminthes	Bilateral	One opening for mouth and anus	Soft-bodied	Unsegmented worms
Annelida	Bilateral	Separate openings for mouth and anus	Hydroskeleton	Segmented worms
Mollusca	Bilateral	Separate openings for mouth and anus	Soft bodied, but some also secrete a calcium carbonate shell	A muscular foot, and many have a radula
Arthropoda	Bilateral	Separate openings for mouth and anus	Hard exoskeleton	Segmented bodies and jointed legs
Chordata	Bilateral	Separate openings for mouth and anus	Internal skeleton	Must have a notochord, dorsal hollow nerve cord, pharyngeal slits, and a post-anal tail at some point during development

💡 Exam Tip

You do not need to be able to describe each of the above phyla in great detail, but be sure that you can state **how each phylum is distinct from the other phyla**, e.g. annelids are segmented worms while platyhelminthes are unsegmented worms, mollusca is the only phylum with a muscular foot, etc.

Vertebrate Features

- The vertebrates are organisms that have a **spinal column** made up of **vertebrae**
- There are 5 **major classes** of vertebrate
  - Bony ray-finned fish (27 000 species)
    - There are other classes of fish, e.g. the bony lobe-finned fish (6 species), and the cartilaginous fish, whose skeletons are made of cartilage rather than bone (around 900 species)

  - Amphibians (6000 species)
  - Reptiles (9000 species)
  - Birds (10 000 species)
  - Mammals (5 700 species)

- The 5 classes can be recognised by their features

Bony ray-finned fish

- The **ray-finned fish**, also known as class Actinopterygii, have **skeletons made of bone**, and **fins supported by rays**, or spines, of **bone**
- The **scales** covering the bodies of the ray-finned fish vary in shape and composition
- Oxygen is gained via **diffusion from the water into the gills**, which are covered by a gill flap called the **operculum**
- During reproduction, eggs and sperm are released into the water and fertilisation takes place outside the body; this is **external fertilisation**
- Their entire **life cycle** is **aquatic**
- **Body temperature is not regulated** but changes with the surrounding environmental temperatures
- Buoyancy is regulated by inflating and deflating an internal air sac called a **swim bladder**
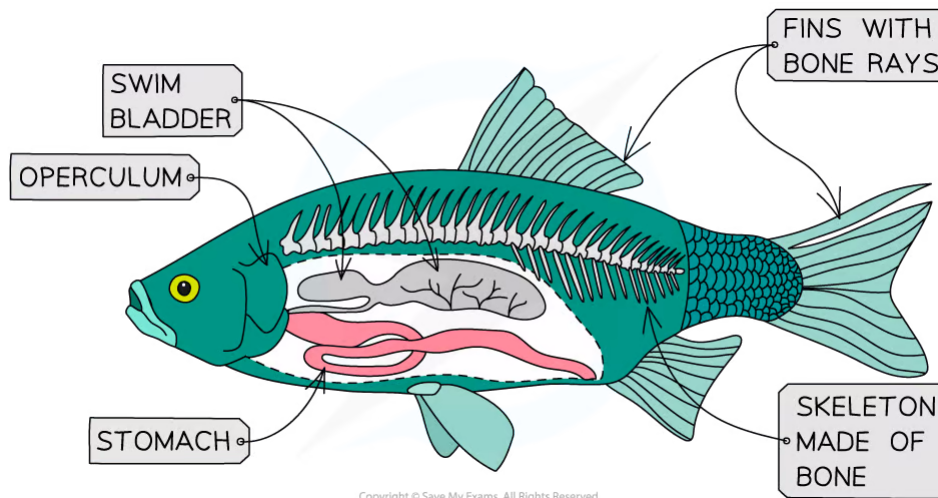
Ray-finned fish have a skeleton of bone, fins with bone rays, a swim bladder, and a gill operculum
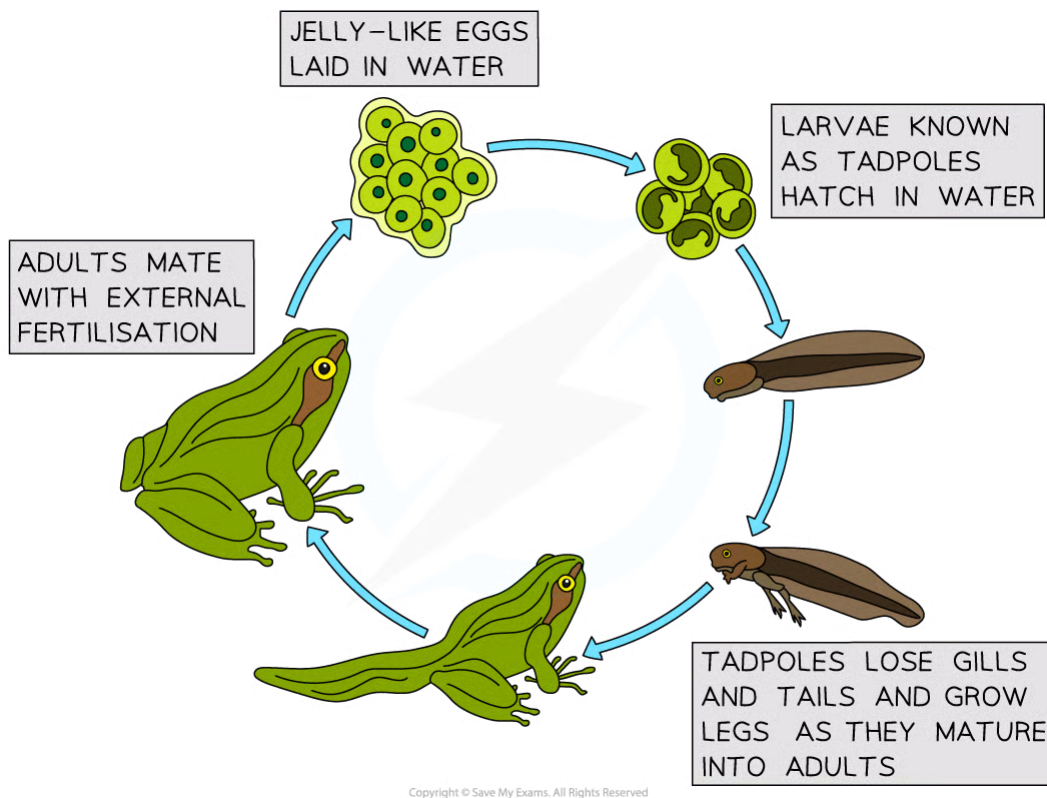
Amphibians

- This class includes animals such as **frogs, toads**, and **salamanders**

- Amphibians have **soft, moist skin**
- Amphibian skin is **permeable**, enabling exchange of gases while under the water
  - Simple lungs are also present for gas exchange on land

- During reproduction, fertilisation is **external**
- **Jelly-like eggs** must be laid in water, and the **larval stage of the life-cycle is aquatic** e.g. frog tadpoles
  - Larvae such as tadpoles mature into an adult body form
  - Adult amphibians often leave the water and spend most of their time on land
  - There are a few exceptions to this; some frog and toad species can lay eggs on land which hatch into tiny adults rather than tadpoles

- Body temperature is **not regulated**

The amphibian life-cycle includes an aquatic larval stage, and a terrestrial adult stage

Reptiles

- This class includes animals such as **lizards, snakes**, and **turtles**
- Reptiles have **impermeable, scaly skin** made of keratin protein
- Reptiles are mainly **terrestrial**, gaining their oxygen through highly folded surfaces in their **lungs**
- During reproduction, male sperm is deposited inside the female's body, so fertilisation is **internal**
- The eggs of reptiles are **soft-shelled**
- Reptile body temperature is **not regulated**
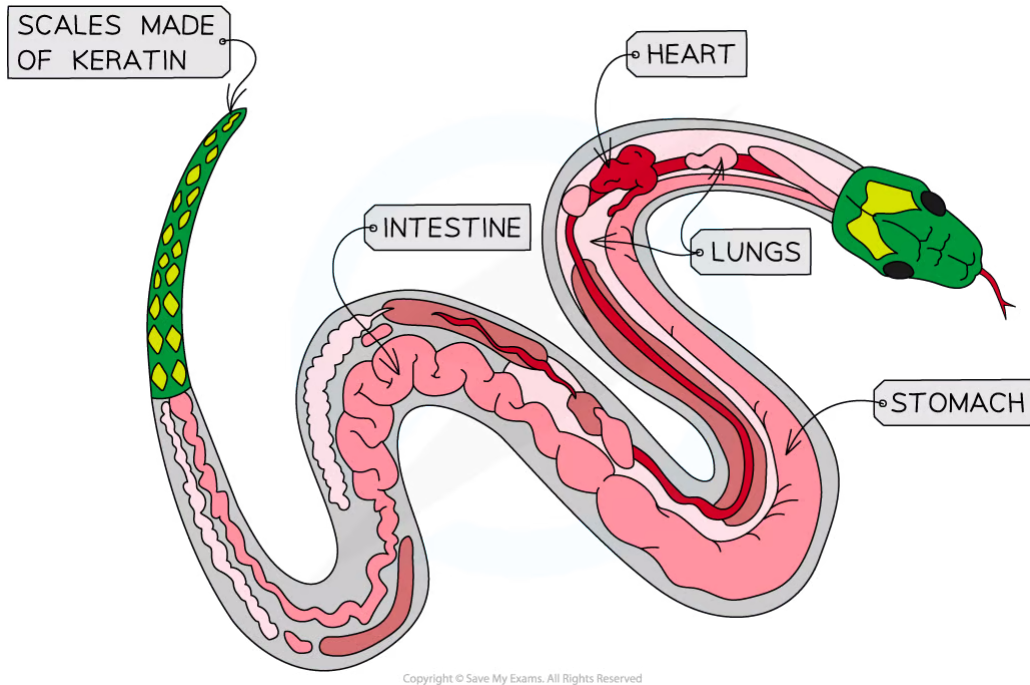
Reptiles have a body covering of scales, and breathe using highly folded lungs

Birds

- This class includes animals such as **chickens** and **ostriches**
- Skin is covered with **feathers** made of keratin
- The front limbs of birds are modified into **wings**, and **skeletons are lightweight**, both adaptations for **flight**
- Birds gain oxygen via a pair of **lungs** and connected **air sacs**
- Fertilisation is **internal**
- The eggs of birds are **hard-shelled**
  - Shells contain calcium carbonate

- Bird **body temperature is regulated**, so is often warmer than the surrounding environment

LIGHTWEIGHT BONES

LIMBS ADAPTED TO WINGS FOR FLIGHT

FEATHERS MADE OF KERATIN

CLOACA FOR INTERNAL FERTILISATION

LUNGS AND AIR SACS
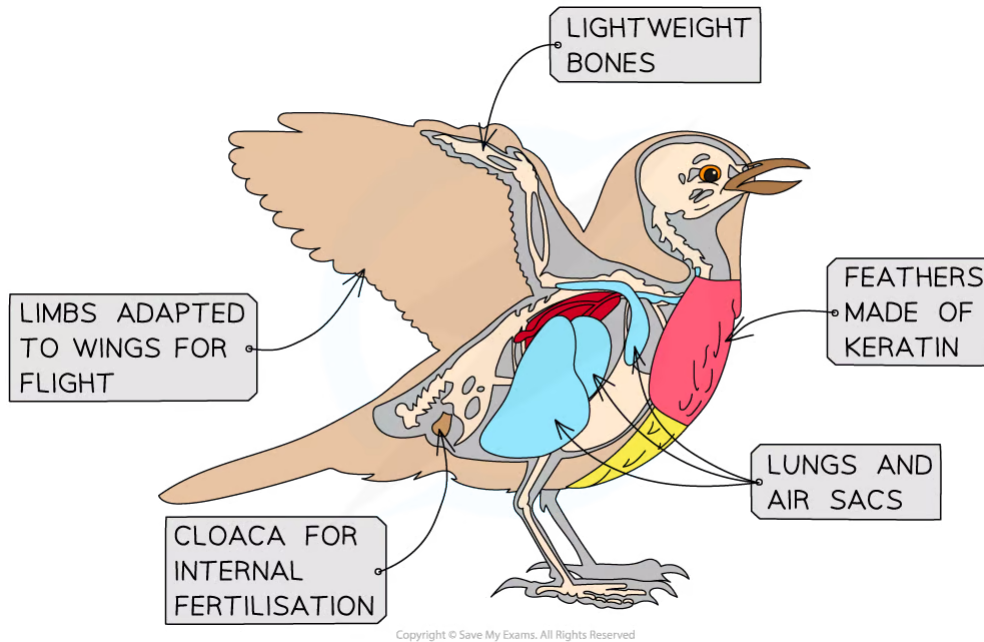
Birds are usually highly adapted for flight and reproduce using internal fertilisation

Mammals

- This class includes animals such as **elephants, humans,** and **whales**
- Skin is covered with **hair** made of keratin
  - In some mammals body hair is lost in adulthood, e.g. in aquatic mammals

- Mammals gain oxygen via a pair of **lungs**
- Fertilisation is **internal**
- The young of mammals develops **inside the body** of the mother, and **live young** are born
  - There are some unusual exceptions to this e.g. the duck-billed platypus and the echidna

- Young mammals are fed on **milk** produced in **mammary glands**
- Mammal **body temperature is regulated**

Vertebrate Features Table

YOUR NOTES
↓

Class	Skin covering	Gaining oxygen	Fertilisation	Reproduction	Body Temperature
Ray-finned fish	A variety of scale types	Gills	External	Eggs are laid and hatch in water. Hatchlings are fully developed	Unregulated
Amphibian	Soft, moist skin	Gills in larvae, then skin and lungs in adults	External	Jelly-like eggs are usually laid and hatch in water. Young are in the for of larvae which mature into adults	Unregulated
Reptile	Scaly skin of keratin	Lungs	Internal	Soft eggs are laid on land	Unregulated
Bird	Feathers of keratin	Lungs and air sacs	Internal	Hard eggs are laid on land	Regulated
Mammal	Hair of keratin	Lungs	Internal	Live young are born	Regulated

5.2.5 Cladistics

Clades

- The term **clade** can be defined as
  - **A group of organisms that have all descended from a common ancestor**

- **Cladistics** is the branch of science in which scientists put organisms into clades
  - It involves classification that is based on homologous characteristics rather than analogous characteristics

- Clades are formed on the basis of **evolutionary relationships** i.e. who is descended from which ancestor
- Note that while **taxonomy** is about classifying and then **naming organisms**, cladistics is about **identifying evolutionary relationships** between organisms
  - A **taxon** is a group of organisms that have been given a group name by taxonomists **on the basis on their shared features**
  - A **clade** is a group of organisms classified together **on the basis of their shared descent** from a common ancestor

- If taxonomy is carried out correctly then **all of the members of a taxon should form a clade**, but due to historical errors and the difficulties in distinguishing between **true homologous characteristics** and those that have come about by convergent evolution, this is not always the case
- Clades can include both **living** and **extinct** species
  - Some of the descendants of a common ancestor may have gone extinct
  - The common ancestor species itself may have gone extinct

- Clades can be **large** or **small** depending on the common ancestor being studied

Identifying Members of a Clade

- In the past, scientists encountered many **difficulties** when trying to determine the **evolutionary relationships** between species
  - Using the physical features of species has **limitations** and can often lead to organisms being put into **groups that are not true clades**
  - This would mean that all of the organisms in a group are **not descended from a common ancestor**
    - Some descendants might be missing
    - Some organisms might have been included that descend from a different ancestor

- Advances in **sequencing technology** have allowed scientists to further investigate the **evolutionary relationships between species**
- **Sequence data** that can be used to investigate evolutionary relationships can come from
  - DNA
  - mRNA
  - Amino acids in polypeptides

- Sequencing technology can determine the **order** of **DNA bases, mRNA bases** and **amino acids**
- For all types of sequence data, it can be said that the **more similar** the sequences, the **more closely related** the species are
  - Two groups of organisms with very similar sequences have **separated into separate species more recently** than two groups with less similarity in their sequences
  - Species that have been separated for longer have had a greater amount of **time to accumulate mutations and changes** to their DNA, mRNA and amino acid sequences

- Sequence analysis and comparison can be used to create family trees that show the **evolutionary relationships** between species

> 💡 **Exam Tip**
>
> You may be wondering why you would use amino acids when you could look at DNA or mRNA; it is often easier to find and isolate proteins from cells than it is to isolate DNA or mRNA. However, DNA or mRNA analysis is often more powerful because genes for the same protein may have slightly different base sequences in different species.

Divergence from a Common Ancestor

- The **evolutionary relationships** between species can be determined by analysing **sequence data** from e.g. **DNA, mRNA**, or **amino acids in polypeptides**
- The **number of differences** between sets of sequence data provides information on **how closely related** two species are
  - The **more differences** there are between the sequences, the **longer ago the species diverged**, and vice versa

- The differences between sequence data can also be used to produce a **quantitative estimate** for **how long ago** two species diverged from each other
  - Differences in sequence data come about due to mutations in the DNA
  - Evidence suggests that **mutations occur at a constant rate**
  - This means that the **number of mutations** that have occurred gives an indication of the **amount of time that has passed** since two species diverged
    - Scientists refer to the constant rate of mutation as the **molecular clock**

- Analysing the differences in sequence data allows evolutionary biologists to determine the **order** in which different species **diverged from a common ancestor**, and therefore **how closely related** species are
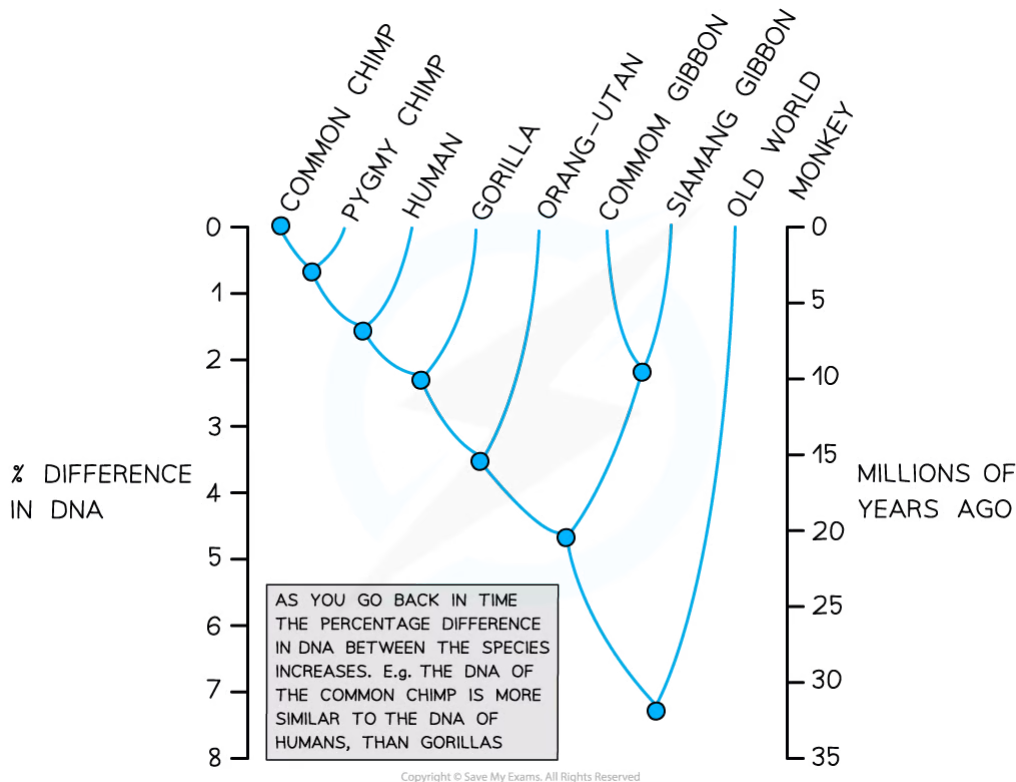

Differences in DNA sequence data show how much time has passed since species diverged from each other, enabling the relationships between species to be established

Analogous & Homologous Traits

- **Homologous traits** can be defined as
  - Characteristics that may differ in form and function in different species but that have shared evolutionary origins

- Homologous traits, or characteristics, **indicate common ancestry**, and are useful for classifying organisms into **true clades**
  - An example of a homologous characteristic is the **pentadactyl limb**; limbs in different species of animal differ significantly in their shape and role, but similarities in overall structure indicate common ancestry

- The difficulty with using homologous traits in classification is that it is not always obvious whether characteristics are **homologous** or **analogous**
- **Analogous traits** can be defined as
  - Characteristics with the same function but which do not share an evolutionary origin

- Such characteristics have **evolved independently of each other** from **different ancestors**, enabling organisms to **adapt to similar environments**
  - This is known as **convergent evolution**

- Analogous characteristics **look similar**, hence the danger of confusing them with homologous characteristics
- Classifying organisms on the basis of analogous characteristics will **not produce an accurate clade**
  - This has led to **errors** of classification in the past
  - For this reason, **sequencing data** is now used for classification instead of observable characteristics

SHARK

BUTTERFLY

DOLPHIN

BAT

STREAMLINED BODY SHAPE AND FINS

WINGS ADAPTED FOR FLIGHT
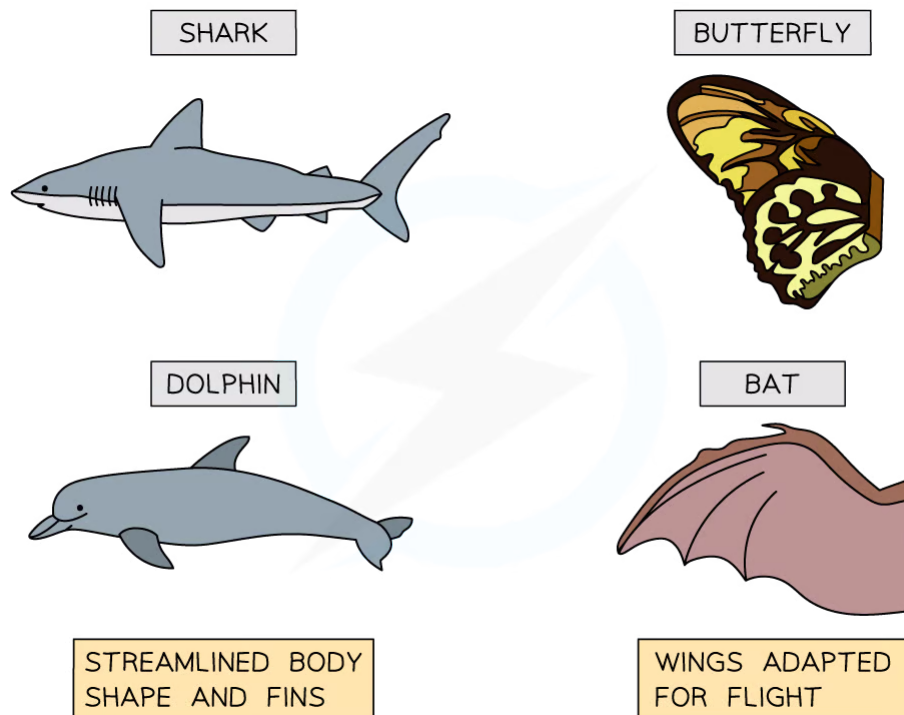
The body shape of sharks/dolphins and the wings of butterflies/bats are both examples of analogous structures
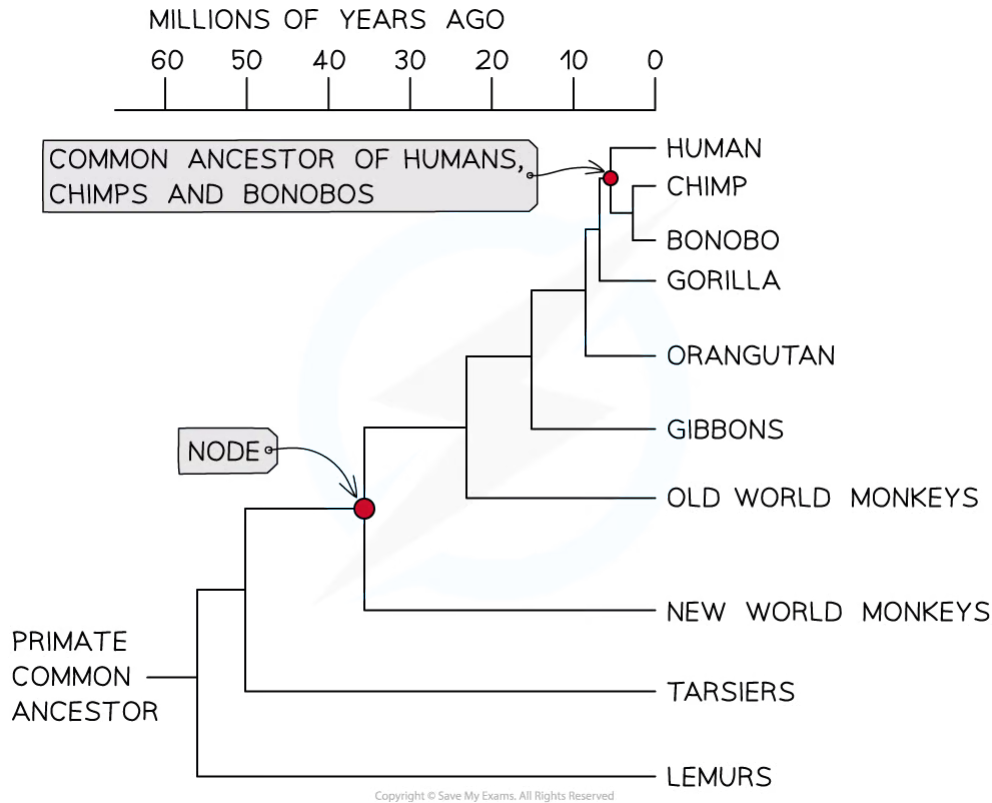
Cladograms

- **Evolutionary relationships** between species can be represented visually using a diagram called a **cladogram**
- Cladograms are **evolutionary trees** that show probable **order of divergence from ancestral species** and therefore probable **relationships between species**
  - The point at which two branches separate is known as a **node**
  - Nodes represent **common ancestor** species

- The information used to build cladograms most often comes from **sequence data** due to difficulties in the use of observable characteristics
  - It can be difficult to be sure whether observable traits are **homologous** or **analogous**

- Sequence data can provide information about **how different species are** from each other, as well as **how much time has passed** since divergence from a common ancestor took place
  - The constant rate at which mutations accumulate can be used as a **molecular clock**

- **Computers** use the information from sequence data to **build the most likely cladogram**
  - This is done using the principle of **parsimony**, which states that the simplest explanation is preferred
    - The computer builds the **shortest possible cladogram** with the **smallest number of divergence events** to fit the available data

  - We say that cladograms show the **most probable** divergence times and relationships rather than providing **definite** conclusions

Cladograms that include humans and other primates

- Analysis of **sequence data** for humans and other primate groups show that **humans are most closely related to chimps and bonobos**, and that the **next closest relative is the gorilla**
- Humans are thought to have **diverged** from chimps and bonobos between 5–7 million years ago

A cladogram showing humans and other primates

5.2.6 Reclassification

Cladistics & Reclassification

- The development of **DNA sequencing technology** means that classification can now be carried out on the basis of **evolutionary relationship**
  - Organisms classified in this way are grouped into clades

- Historically, organisms would have been classified on the basis of **observed traits**, which often led to organisms being classified into groups that were **not true clades**
  - This resulted from analogous characteristics being incorrectly thought to be homologous

- The use of DNA sequencing to classify organisms has led to discoveries of classification errors and the need to **reclassify** organisms
  - Some species have been reclassified into **different groups** of organisms
  - Some groups of organisms have been **split**
  - Some groups have been **merged**

- Classifying organisms correctly **according to their clade** is important to ensure that groups of organisms are **close evolutionary relatives**
  - This means that the characteristics of one group member can be **predicted** on the basis of the characteristics of another

Example of Reclassification

Reclassification of the figwort family

- The **figwort** (pronounced 'figwurt') **family**, also known as the **Scrophulariaceae**, was at one point the 8th largest family in the **angiosperm** phylum
- When the group was originally classified in the late 1700s it contained 16 genera, which later expanded to 275 genera
  - The classification of the figworts was based on **observable traits** such as a tube-shaped flower structure
  - Examples of members of the original figwort family include foxgloves and yellow rattle

- When **DNA sequence analysis** began, plant scientists discovered that the shared features of the figwort family were in fact **analogous** and not evidence of **shared ancestry**
  - Three chloroplast **genes** were analysed
  - It was discovered that the original figwort family was **not a true clade**
  - The figworts were found to contain **several separate plant families**
    - **New families** were created
    - Several genera were moved into other **existing families**
    - The remaining genera were grouped together with two previously missed genera to form the **new figwort family**, still known as the Scrophulariaceae

- The new figwort family is **less than half** its original size and is only the 36th largest in the angiosperms, where it had previously been 8th

FOXGLOVES ARE NOW IN THE PLANTAGINACEAE FAMILY

YELLOW RATTLE IS NOW IN THE OROBANCHACEAE FAMILY

FIGWORT REMAINS IN THE NEW SCROPHULARIACEAE FAMILY

DNA sequencing data led to the reclassification of many species within the original figwort family

NOS: Falsification of theories with one theory being superseded by another; plant families have been reclassified as a result of evidence from cladistics

- A **theory** is an **explanation of observed phenomena** that is **supported by evidence**
- This means that when **new evidence** is found that **no longer supports the theory**, it needs to be **changed** to take the new evidence into account
- Reclassification of organisms on the basis of DNA sequencing data is a good example of this
    - Scientists **theorise** that a group of plants should be classified together on the basis of **existing evidence**; historically this would have been the **evidence of observable traits** such as flower shape
    - **New evidence from DNA sequence analysis** shows that existing plant groups are not true clades, and so are not descendants of a common ancestor
    - The historical classification **theory has therefore been falsified** and needs to be changed to take the new evidence into account
    - **New evidence** from **DNA** and **computer analysis** is used to calculate the most likely plant evolutionary relationships, and this **evidence** is used to form a **new theory** regarding the classification of plants

- Analysis of new DNA data continues all the time, and if **evidence** is found that doesn't fit with current classification theories then more **falsification** and reclassification will take place

**5.2.7 Skills: Classification & Cladistics**

Dichotomous Keys

- For anyone who doesn't specialise in studying a particular group of organisms, it can be very **difficult to identify, or ID, a species** when working in the field
  - Correctly identifying species may be important for a researcher studying biodiversity or looking at the impacts of a changing environment on a community of organisms

- Someone seeking to identify species with which they are not already familiar may use a tool known as a **dichotomous key**
- A dichotomous key contains a series of **paired statements**
  - The term 'dichotomous' refers to these pairs of statements
  - An example of such a pair of statements might read:
    - The organism shows radial symmetry
    - The organism shows bilateral symmetry

  - Or:
    - The organism has one pair of wings
    - The organism has two pairs of wings

- To work through a dichotomous key, you start with the first pair of statements and apply them to the unknown species; one statement will be **clearly false**, while the other will be a **correct description** of the species
- The correct statement leads to **another pair of statements**, and so on until the final correct statement leads to the name of the species

YOUR NOTES
↓

❓ Worked Example

Use the dichotomous key provided to identify the type of organism below

The organism has an exoskeleton, a segmented body, and 4 pairs of legs. It has no tail and cannot produce silk

SEGMENTED BODY
HARD EXOSKELETON
4 PAIRS OF LEGS
CANNOT PRODUCE SILK FIBRES
NO TAIL
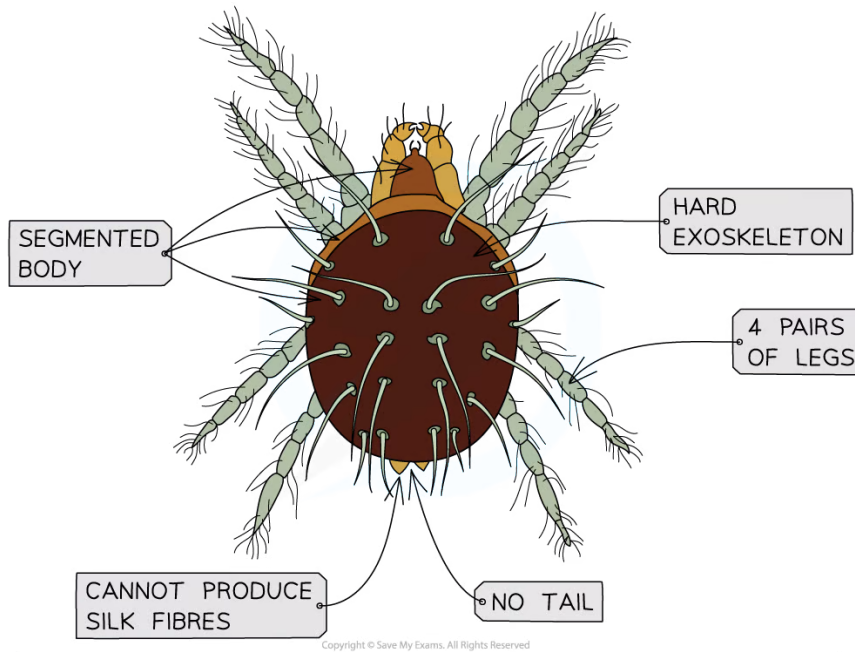
1	Hard exoskeleton absent...................................2
	Hard exoskeleton present..................................3
2	Hard shell absent.................................Slug
	Hard shell present.................................Snail
3	3 pairs of legs 5
	4 pairs of legs 4
4	Tail absent...6
	Tail present.................................Scorpion
5	Body colour uniform ....Ant
	Body striped black and yellow.................Wasp
6	Silk producing organ present ....Spider
	Silk producing organ absent ....Mite

Step 1: Decide which of the first pair of statements applies

The organism has an exoskeleton, so we can ignore the first statement in pair 1 and move onto the third pair of statements as instructed in the key

Step 2: Decide which of the third pair of statements applies

The organism has 4 pairs of legs, so we move on to the fourth pair of statements as instructed

Step 3: Decide which of the fourth pair of statements applies

The organism has no tail, so we know that it is not a scorpion, and we move onto the sixth pair of statements as instructed

### Step 4: Decide which of the sixth pair of statements applies

The organism cannot produce silk, so it must be a species of **mite**

Constructing a dichotomous key

- When **constructing a key**, the following should be considered
  - Each pair of statements should contain features that are **clearly identifiable** and **not subject to opinion** e.g. the organism has 3 pairs of legs, rather than e.g. the organism is small
    - A leg count gives an objective number, but size is relative and depends on what the species is being compared to

  - Statements must be 'yes' or 'no' in style
  - Each pair of statements should **divide the organisms being identified into two distinct groups**
  - Each subsequent pair of statements should divide the organisms into **smaller and smaller groups**
  - Each statement should be followed by either a **number** to continue the process of narrowing down the options, or should **name the organism** to which it applies
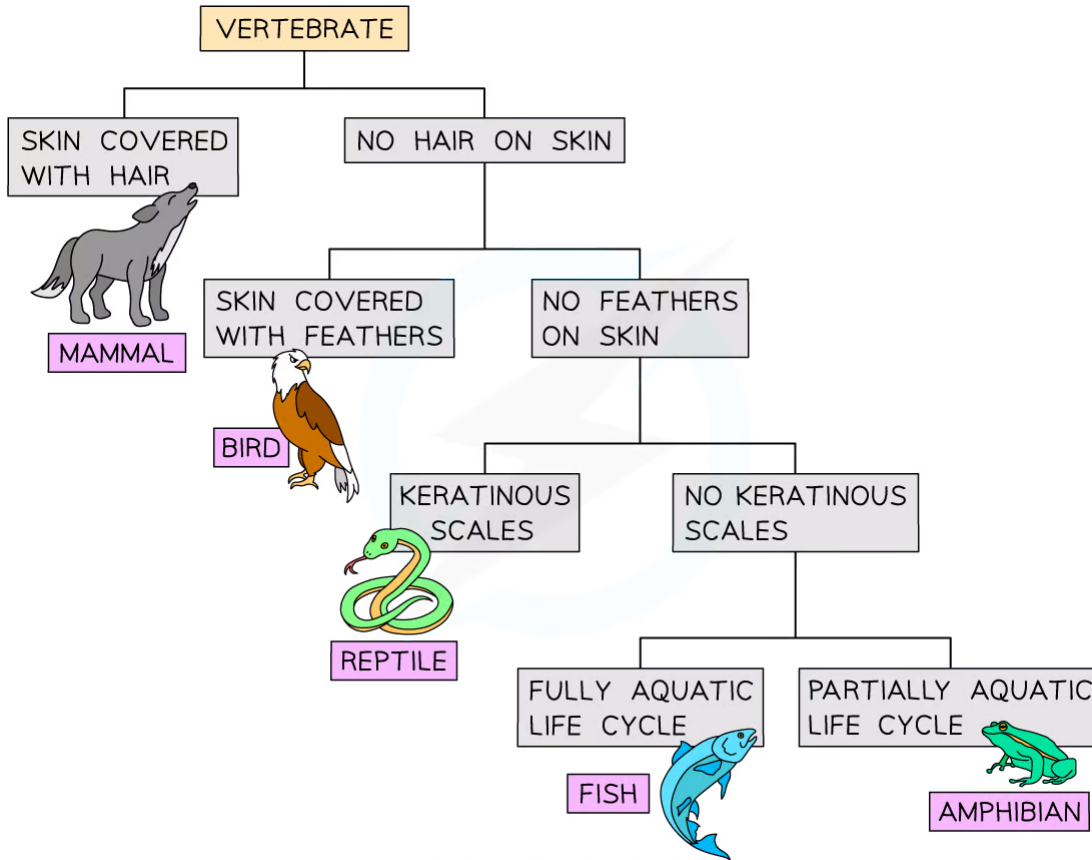
Dichotomous keys can also be represented using a branched diagram as shown here. This visual representation can be easier to understand, but it is limited in the number of organisms it can include

💡 **Exam Tip**

Get some practice at using a dichotomous key by identifying the remaining organisms featured in the key, all of which are described below. Note: they are all quite easily recognisable animals so you should be able to tell whether you have used the key correctly or not.

1. The organism has an exoskeleton, a segmented body, and 4 pairs of legs. It has a tail with a sting
2. The organism has an exoskeleton, a segmented body, and 3 pairs of legs. Its body is uniform in colour
3. The organism has an exoskeleton, a segmented body, and 3 pairs of legs. It's body is striped black and yellow
4. The organism is soft bodied with a muscular foot and a hard shell
5. The organism has an exoskeleton, a segmented body, and 4 pairs of legs. It has no tail but can produce silk fibres from a specialised organ on its abdomen
6. The organism is soft bodied with a muscular foot and no hard shell

Analysis of Cladograms

- **Evolutionary relationships** between species can be represented visually using a diagram called a **cladogram**
- Cladograms are **evolutionary trees** that show probable **order of divergence from ancestral species** and therefore probable **relationships between species**
- Analysis of a cladogram can provide several pieces of information
  - The point at which two branches separate is known as a **node**, and represents **common ancestor** species
    - A node **immediately adjacent** to a pair of clades indicates that these two clades share a **recent common ancestor**
    - This shows that the two clades are **more closely related to each other than they are to any other clade** in the cladogram
    - If **several nodes need to be traced back** before two clades can be joined, this indicates a **more distant relationship** between two clades
  - Cladograms sometimes show **numbers** along the branches; these indicate the **number of base or amino acid changes** that have occurred between one node and the next or between a node and an emerging clade or species
    - The constant rate at which mutations accumulate means that these numbers can be used as a **molecular clock** to calculate how much time has passed
  - Some cladograms have a **time scale** to show how many millions have years have passed

- **Computers** use the information from sequence data to **build the most likely cladogram**
  - This is done using the principle of **parsimony** which states that the **simplest explanation** is preferred
    - The computer builds the **shortest possible cladogram** with the **smallest number of divergence events** to fit the available data

- Cladograms provide the **most likely estimate** of the evolutionary progress of organisms
  - The **reliability of a cladogram may vary** depending on the **amount of sequence data** used to construct it
    - A cladogram based on the sequencing of one gene will be less reliable than a cladogram based on the sequencing of several genes
  - Cladograms are **subject to change** when new sequence data becomes available
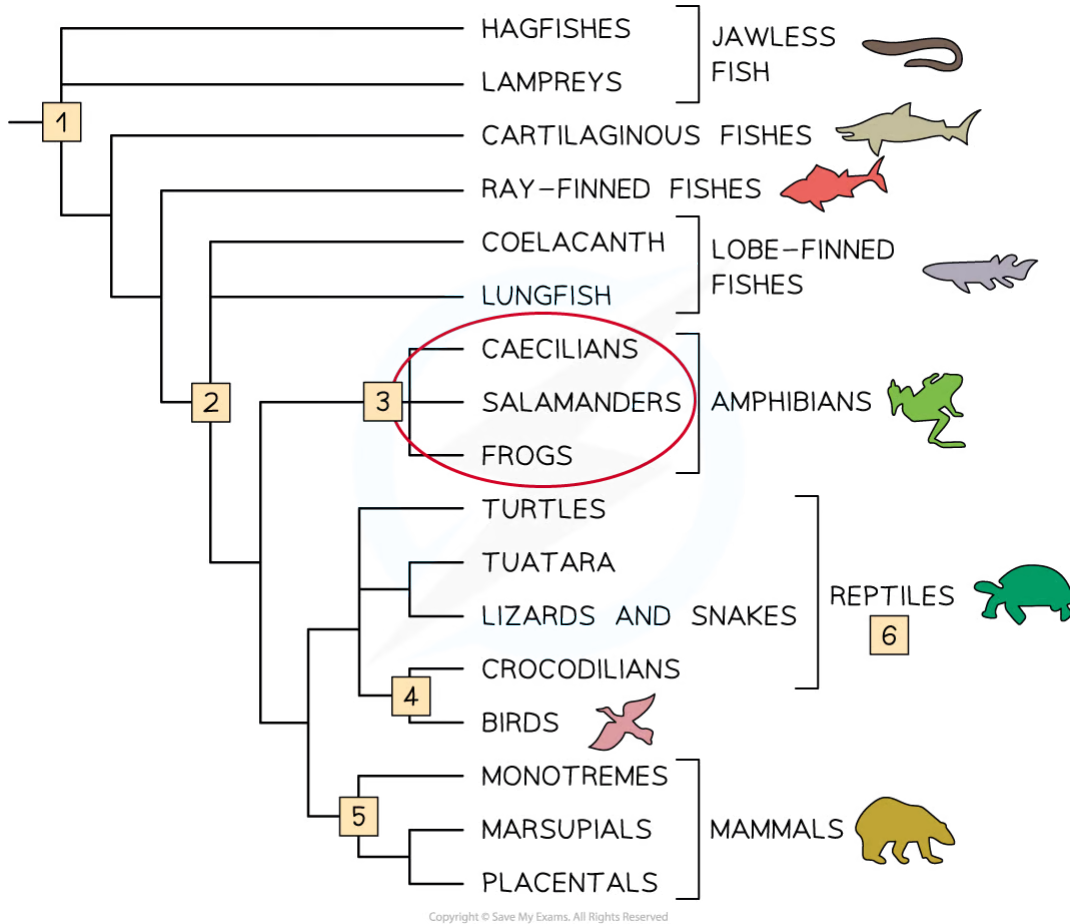
1 NODE REPRESENTING COMMON ANCESTOR OF ALL VERTEBRATES

2 FIVE NODES NEED TO BE TRACED BACK TO LINK PLACENTAL MAMMALS WITH COELACANTHS, INDICATING A MORE DISTANT RELATIONSHIP

3 THREE CLADES DIRECTLY LINKED TO ONE COMMON ANCESTOR INDICATES THAT THIS CLADOGRAM WAS BUILT WITHOUT ENOUGH DATA TO DETERMINE WHICH OF THESE THREE CLADES ARE MORE CLOSELY RELATED

4 ONLY ONE NODE NEEDS TO BE TRACED BACK TO LINK CROCODILIANS AND BIRDS, SO THEY ARE MORE CLOSELY RELATED TO EACH OTHER THAN TO ANY OTHER CLADE

5 NODE REPRESENTING COMMON ANCESTOR OF ALL MAMMALS

6 NOTE THAT THE REPTILES ARE NOT A TRUE CLADE, AS THEY DO NOT INCLUDE THE BIRDS, WHICH SHARE A COMMON ANCESTOR WITH THEM

A cladogram with notes to indicate some of the conclusions that can be drawn from it. Note that this cladogram contains no numbers or time scale, so it does not show the number of base or amino acid changes that have occurred between one node and the next, or how much time has passed between nodes.