

CHAPTER 2

CLASSIFYING

BIODIVERSITY

By the end of this chapter you will have covered the following material.

Science Understanding

- Biological classification is hierarchical and based on different levels of similarity of physical features, methods of reproduction and molecular sequences (ACSBL016)
- Biological classification systems reflect evolutionary relatedness between groups of organisms (ACSBL017)





Alamy/The Art Archive

Figure 2.1 ▲
One of John Gould's illustrations of a cassowary



JOHN GOULD

Learn more about John Gould and his contribution to biology.

A scientific theory is not the same as a guess. It is an explanation based on observations and usually takes time to develop, based on experimentation, evidence and discussion in the scientific community.

At the time of the exploration and settlement of Australia by Europeans, the science of natural history was at its height. The naturalists who described, collected and classified plants and animals were amazed by the sheer number of new species discovered in Australia. It is from the diverse plant life found there that Captain Cook's landing point at Botany Bay takes its name. The exploration of Australia provided opportunities, as well as challenges, for the naturalists of the 18th and 19th centuries.

One such challenge was how to make sense of the flora and fauna in Australia. Initially, European explorers described Australian animals in terms of those they were familiar with. They wrote of wolves (actually dingoes), badgers (wombats) and raccoons (wallabies). Eventually, naturalists realised that the plants and animals of Australia were so different from those of Europe that they needed their own names.

Some naturalists based their work on specimens and sketches brought back from Australia. Others, however, made the voyages out themselves. British ornithologist John Gould made this journey with his wife Elizabeth – a sketch artist. Over a period of 2 years spent in Australia, the Goulds described around 300 new species of birds. While initially focusing on birds, John Gould became so interested in Australian mammals during his stay he also spent considerable time describing and classifying them. The Goulds' contribution to the classification of Australian wildlife was phenomenal.

Why do we classify organisms?

Classification systems are a method of sorting, so that similar or related organisms are grouped together. Throughout this chapter you will learn how biologists use similarities and differences to classify organisms, but why we do need to do this?

Classification of organisms is done for several reasons. Firstly, the diversity of life on Earth is so enormous that classifying organisms is a way of organising information. Organisation of information about organisms then allows for patterns and trends to be observed, and relationships between organisms to be better understood. As such, the second reason to classify organisms is to allow biologists to analyse information about organisms.

Finally, classifying organisms allows biologists to communicate with one another. Classification systems allow biologists to identify organisms that have already been discovered. Using standardised systems around the world allows biologists to compare their findings with one another. Because science is a field that relies heavily on worldwide collaboration, a standardised classification is of the utmost importance.

Classification systems as scientific tools

Classification systems are tools used by scientists to help make it possible to see patterns and relationships. Classification systems do this by simplifying information that would otherwise be too complex to analyse. While this is the reason that classification systems work, it is also a limitation of these systems. As you continue in your biology studies, keep in mind that the classification systems used are artificial structures and are not perfect.

One way to view classification systems is as complicated theories about the way that organisms are related. These proposed explanations can change when new data comes to light. Throughout this chapter you will encounter several examples of classification changing as a result of new evidence.

QUESTION SET 2.1

Remembering

- 1 List three reasons why biologists use classification systems.

Understanding

- 2 Explain why biological classification systems can be thought of as theories.

Applying

- 3 Humans use classification systems in many aspects of life, not just in biology.
 - a List two other situations in which classification systems are used.
 - b Using what you have learned about why biologists classify, explain why classification systems are used in these situations.
- 4
 - a Classification systems can be useful but also have limitations. Describe some limitations of classification systems.
 - b Do you think that these limitations outweigh the usefulness of these systems? Justify your response.

Levels of classification

Scientists classify organisms into a number of groups that form a hierarchy or series of nested levels. These groups are known as **taxa** or **taxonomic levels**. The names of the major taxa, from largest to smallest, are Domain, Kingdom, Phylum, Class, Order, Family, Genus and Species. At each taxonomic level, organisms can be further grouped according to features that they share. Each organism is therefore able to be defined by the taxa to which it belongs.

The higher taxonomic levels are larger groupings and show more diversity between individuals than lower levels. For example, the Class Amphibia, to which all frogs belong, is a large group of more than 7000 species that also contains other organisms such as toads and salamanders. The Genus *Rana* is a smaller taxa within the Class Amphibia and contains around 90 different species of frog.

Initially, organisms are classified into very large groups called domains. The domains are then divided up into kingdoms. Organisms within a kingdom can be further grouped according to the features that they share. This grouping is called a phylum; for example, the Phylum Chordata includes all living things that at some stage of their development possess a dorsal notochord ('dorsal' = back, 'notochord' = primitive backbone), gill slits and a hollow dorsal nerve cord. Humans belong to this phylum.

Organisms within a phylum can be further grouped according to similar features. These smaller groupings are called classes. For example, any members of the Phylum Chordata that nourish their young on milk produced by the female (such as dogs, humans and kangaroos) are grouped within the Class Mammalia.

Organisms within a class can be further grouped into orders according to similar features. Humans are grouped within the Order Primate along with monkeys, orangutans, chimpanzees and gorillas. Orders are subdivided into families, which can be further subdivided into genera (singular, genus). Finally, genera are further subdivided in species. The order of this hierarchy is shown in Figure 2.2.

Organisms are classified into a hierarchy of groups called taxa. The names of the taxa are Domain, Kingdom, Phylum, Class, Order, Family, Genus and Species.

WOW

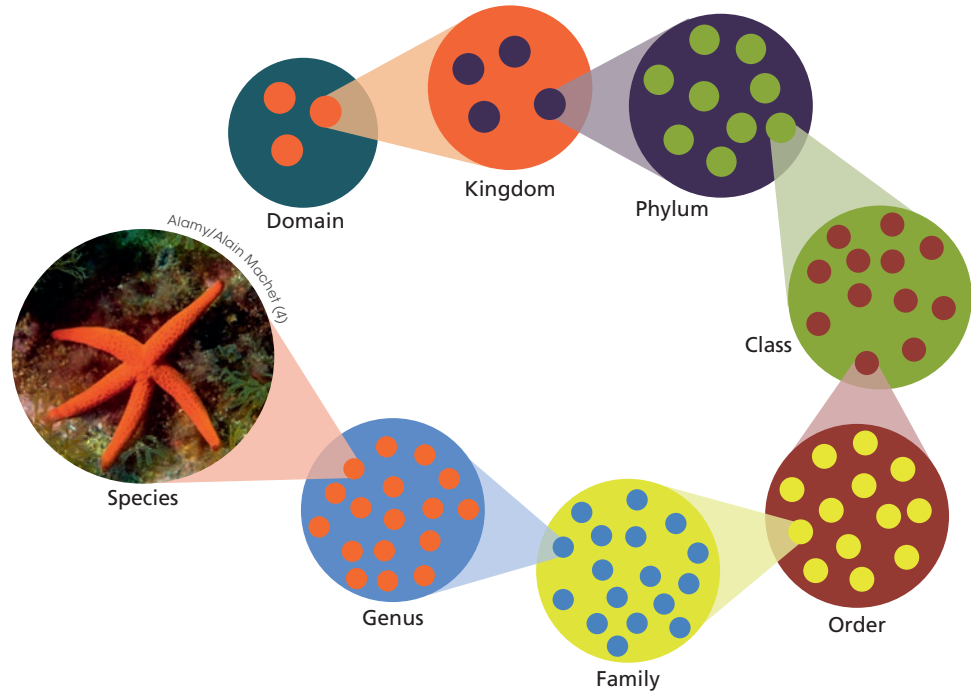
A platypus prank?

When the first platypus specimen was sent from Australia to England it was thought to be a hoax. The combination of a duck's bill and a mammal's body was so bizarre to European naturalists that they considered it could not be real. Fake 'mermaid' samples made from stitching together fish tails and other animals had been sent from Asia and it was thought the platypus was a similar trick. It took several more years before scientists truly accepted that this odd-looking creature existed!

More information about classification into species is given in Chapter 1 and on page 17.

Figure 2.2 ▶

The hierarchy of the taxa. Each taxonomic level can be divided into multiple groups in the level below.



The initial division of life into three domains (Figure 2.3) is based on cellular **characteristics**. Members of Domain Eukarya, called **eukaryotes**, contain their **DNA** (deoxyribonucleic acid) within a nucleus and have other membrane-bound compartments called **organelles** within their cells. Domains Archaea and Bacteria contain **prokaryotes**: organisms that lack these features. Prokaryotes are microscopic, single-celled organisms. Despite this superficial similarity, organisms in Domains Archaea and Bacteria have differences in the way DNA is stored and how proteins are synthesised, which means that they are classified in separate domains. Many of the members of Domain Archaea live in extreme environments (such as areas of high salt or temperature).

The differences between prokaryotes (Domains Bacteria and Archaea) and eukaryotes (Domain Eukarya) are discussed further in Chapter 7 on pages 158–62.

Figure 2.3 ▶

The initial divisions of life: the domains and kingdoms

	Eukaryotes Contain DNA within a nucleus and membrane-bound organelles				Prokaryotes No nucleus or membrane-bound organelles	
Domain	Eukarya				Archaea	Bacteria
Kingdom	Animalia Includes mammals, insects and sea sponges	Plantae Includes mosses, ferns and flowering plants	Protista Includes amoebae	Fungi Includes yeasts, moulds and mushrooms	Archaea Microscopic single-celled organisms known for living in extreme environments	Bacteria Microscopic single-celled organisms

There is controversy over whether viruses are considered to be alive. As such, viruses are not currently included in the kingdoms of life and instead have a separate classification system.



A BRIEF HISTORY OF THE KINGDOMS OF LIFE

An explanation of how classification systems changed over the years and some of the newer proposed systems.

There are four kingdoms in Domain Eukarya: Animalia, Plantae, Protista and Fungi. You may be familiar with many of the organisms within these kingdoms. Kingdom Animalia contains all of the animals, including some that are single-celled. Plants (Kingdom Plantae) have cell walls that contain cellulose and obtain energy from the sun using organelles called chloroplasts. Yeasts, mushrooms and moulds all belong to Kingdom Fungi and are characterised by having cell walls made of a specific polysaccharide (chitin). The protists (Kingdom Protista) are a diverse group of organisms that are mostly single-celled and live in aqueous environments.

Interestingly, there is still debate among **taxonomists** as to how these groups should be divided. The Archaea and Bacteria used to be considered as part of a single kingdom, the Monera, and this terminology is sometimes still used. Other taxonomists have suggested different kingdoms.

Extremely fragile specimens

While many museums have botanical collections of dried flowers, the Harvard Natural History Museum's flowers are unique. Made entirely from glass, the collection of more than 3000 floral specimens are not only beautiful, but scientifically accurate. The flowers were made by father and son Leopold and Rudolf Blasckha in Germany over a period of 50 years.

Naming organisms: the binomial system

There are multiple ways of naming organisms. Most organisms have at least two names: a common name and a scientific name. Common names (such as grasswren or echidna) may refer to individual species or to larger taxonomic groups. They can vary between languages and are not always used consistently. The scientific name (or binomial name) is used by scientists around the world and refers to a single species.

A binomial name consists of two parts: a generic name and a specific name. The first part (generic name) denotes the genus and is common to all organisms within that genus, whereas the second part is unique to a single species. For example, Golden Wattle, Australia's floral emblem, has the name *Acacia pycnantha*. Related species of wattle such as black wattle (*Acacia mearnsii*) and tan wattle (*Acacia hemiteles*) share the same first part of their name: *Acacia*. However, the different second part of the name (specific name) indicates that these are different species.

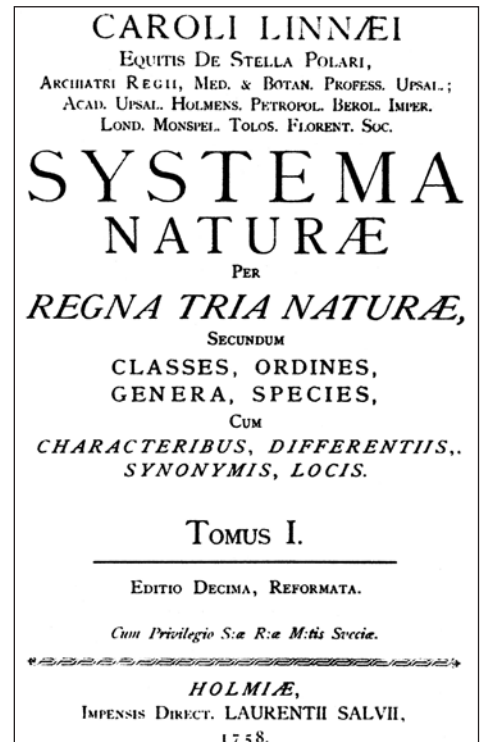
All organisms have a binomial (scientific) name. Binomial names consist of two parts: the first denotes the genus and the second is specific to the species.

Binomial names are written using Latin grammar, but can come from various sources. Sometimes they describe features of the organism. For example, the binomial name for the short-beaked echidna (*Tachyglossus aculeatus*) means 'fast-tongued and covered with spines'. In other cases species may be named after a distinguished person, a location or a mythological character. The binomial name for humans, *Homo sapiens*, comes from the Latin phrase for 'wise man'.

The **binomial system** of naming organisms was developed by 18th century Swedish botanist and zoologist, Carl Linnaeus. Before Linnaeus introduced the binomial system, organisms had descriptive Latin names that could be very long. His system revolutionised the way that scientists describe and communicate about organisms. Considered the father of modern taxonomy, Linnaeus first used this system in his book *Systema Naturae* in which he classified organisms into kingdoms, classes, organisms, genera and species. These taxa are different to the ones we use today, but Linnaeus' work formed the basis of the system we still use. Over his lifetime, Linnaeus named and described more than 10000 species of animals and plants. In recognition of his substantial scientific contributions, Linnaeus was made a member of the nobility in 1761 and changed his name to Carl von Linné.

▼ Figure 2.4

The title page from Linnaeus' pivotal 10th edition of *Systema Naturae*



The human type specimen

When a species is described and named, a particular specimen is designated as the 'type specimen'. A type specimen is usually kept in a museum or herbarium research collection and is used as a reference worldwide for that species. There are a series of strict rules stating which specimen can become the type specimen. These include (a) that the specimen has to have been examined by the person who named the species, (b) that the specimen has to be available for scientists to examine and (c) that the specimen has to have been named as the type specimen in a scientific publication. Based on these criteria, the type specimen for humans (*Homo sapiens*) appears to be Carl Linnaeus himself! A fitting honour for the father of taxonomy.

There are conventions for writing scientific names. The name is usually written in italics and the first part of the name, but not the second part, is capitalised. When the name of a species has already been mentioned, the first part can be abbreviated. For example, the name of the bacterium *Escherichia coli* can be abbreviated to *E. coli* when it is written for the second time. Sometimes you may see sp. (singular) or spp. (plural) in place of the second part of the name. These are used when the author is not referring to a particular species. For example, *Lasiiorhinus* sp. means 'a member of Genus *Lasiiorhinus* (hairy-nosed wombats)' and *Macropus* spp. refers to 'members of Genus *Macropus* (kangaroos)'.

WOW

What's in a name?

While many species are named after a distinguishing feature or discovering scientist, some species carry more bizarre names. A recently discovered fungus was named *Spongiforma squarepantsii* for its similarity to the cartoon character SpongeBob SquarePants. Other species have been named after Darth Vader (*Agathidium vaderi*; a slime-mold beetle), the singer Beyonce (*Scaptia beyonceae*; a horse fly) and, using his catchphrase 'Bazinga!', Dr Sheldon Cooper from *The Big Bang Theory* (*Euglossa bazinga*; a bee).

QUESTION SET 2.2

Remembering

- 1 Describe Linnaeus' contribution to biological classification.
- 2 List the kingdoms that make up Domain Eukarya.
- 3 Define 'taxonomic level'.

Understanding

- 4 Explain the relationship between a phylum and a class.
- 5 Using a specific example, explain what the two parts of the binomial name of an organism represent.

Classification is based on the characteristics of organisms

Classification never stops. Taxonomist's opinions differ; some will lump species together and others will reclassify a species to split it into new species. At the same time, new species are regularly being discovered. We will now go on to explore the characteristics that taxonomists use to group organisms.

Characteristics are features that can be used to describe an organism. Classification is based on the idea that members of the same group share characteristics that are not present in members outside the group. Platypuses, for example, have a backbone, are covered in fur and lay eggs. All of these are characteristics that are used to classify platypuses into Phylum Chordata (with other vertebrates), Class Mammalia (with other animals with fur) and Order Monotremata (with echidnas; the other egg-laying mammals). Order Monotremata is further divided based on the characteristics of its members. Echidnas and platypuses have many different characteristics, so they have their own families and genera.

These characteristics are also used in the construction of phylogenetic trees, which is discussed on page 29.

How many species are left to find?

It is impossible to know with certainty how many species exist. Recent estimates suggest that there are more than 10 million different species on Earth. This means that roughly 87% of these species remain undiscovered. If the discovery of species continues at the same rate as today, it will take scientists nearly 500 years to discover all of them!

Physical characteristics

When creating the classification system presented in *Systema Naturae*, Linnaeus used the physical characteristics of organisms as the basis for his groups. Taxonomists today still use physical characteristics to classify organisms. Almost any aspects of an organism that you can describe could be used in this way.

Can you think of some of the physical characteristics that could be used to define humans? Examples include the fact that humans have cells that contain a nucleus, possess a backbone and have hair. You will learn later on how these physical features are used to classify humans.

Reproductive methods

The ability to reproduce is a fundamental characteristic of life on Earth. It is unsurprising that there is considerable variation in how organisms do this. Methods of reproduction are an important characteristic that can be used to classify organisms.

One major difference is between organisms that reproduce sexually (with mixing of gametes from two individuals) or asexually. There are species of both plants and animals that reproduce each way. Some species are able to reproduce both sexually and asexually depending on environmental conditions.

Among mammals (animals that produce milk for their young and have fur), the method of reproduction is used to separate three main groups. Eutherian (or placental) mammals give birth to live young after a gestation period during which the foetus develops inside the mother. The majority of mammals are included in this group. Marsupials give birth to live young at a very early developmental stage. This group of animals, which are predominantly found in Australia, includes kangaroos, koalas and possums. These young then develop in a pouch on the belly of the mother until they are mature enough to survive outside. Monotremes are a very small group of mammals made up of echidnas and platypuses that lay eggs.

Molecular sequences

More recently, the sequences of molecules such as DNA and protein have also been used to classify organisms. Even though they cannot be directly seen, molecular sequences are still distinct characteristics. Now that technology allows for the measurement of these sequences, they can also be used in classification.

DNA is made up of a sequence of four bases: adenine (A), thymine (T), cytosine (C) and guanine (G). The order of these bases determines the physical features of an organism. Individuals within a species have some differences in the order of these bases. However, these differences are much smaller than the differences in sequence between organisms of different species. By looking at the similarities and differences between DNA sequences, scientists can help to classify organisms.

DNA evidence has been particularly useful when morphological evidence is not clear. The classification of the red panda (*Ailurus fulgens*) was a topic of debate for many years. At different points in time it had been considered part of the Family Ursidae (bears) and



WHAT MAKES A PRIMATE A PRIMATE?

Learn about the characteristics that define humans and our closest relatives: the primates.



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▲ Figure 2.5

A kangaroo suckling her joey. Like all other mammals, kangaroos have fur and produce milk.

Learn more about how technology has impacted taxonomy on page 35.

Unit 3 Biology goes into more detail about the structure and function of DNA.



Family Procyonidae (raccoons) because it shared physical characteristics with members of both families. DNA evidence has suggested that the red panda is sufficiently different to be considered in its own family, called Ailuridae.

Similar to DNA, information about protein structure can also be used in classification. Proteins are made up of sequences of **amino acids** and the order of these amino acids can be used to help classify organisms. Table 2.1 shows the sequence of the first 38–40 amino acids in the protein cytochrome c for five different animals. These sequences have been aligned so you can compare them. Each letter stands for a different amino acid. You can see that when an animal has a different amino acid to that in the human sequence, it has been coloured red.

◀ **Figure 2.6**

The red panda is in a family all on its own: Family Ailuridae.

Table 2.1 The first 38–40 amino acids in the protein cytochrome c

Human (<i>Homo sapiens</i>)	MG--DVEKGGK	KIFIMKCSQC	HTVEKGGGKHK	TGPNLHGLFG
Chimpanzee (<i>Pan troglodytes</i>)	MG--DVEKGGK	KIFIMKCSQC	HTVEKGGGKHK	TGPNLHGLFG
Emu (<i>Dromaius novae-hollandiae</i>)	MG--D I EKGGK	KIF VQ KCSQC	HTVEKGGGKHK	TGPNL N GLFG
Lamprey (<i>Lampetra tridentata</i>)	MG--DVEKGGK	KVFVQ KCSQC	HTVEK A GKHK	TGPNL S GLFG
Fruit fly (<i>Drosophila melanogaster</i>)	MGS GDA EN GK	KIF VQ KCA QC	HT Y E V GGGKHK	V GP N L G G V V G

Molecular sequences can be used to classify organisms because those with similar sequences are closely related. How understanding the relationships between organisms helps with classification is discussed on page 29.

You will notice that the amino acid sequences for humans and chimpanzees are identical. This supports the classification of humans and chimpanzees into the same order (Primates). Humans are less similar to emus than they are to chimpanzees. As such, although they are in the same phylum (Chordata), they are in different classes. Emus have four amino acids that differ from humans in this sequence, supporting their difference in classification. Fruit flies have 13 amino acids that differ from humans. This supports the fact that, unlike all the other animals listed, fruit flies are in Phylum Arthropoda.

The study of bioinformatics combines mathematical modelling, computer science and biology to compare molecular sequences on a very large scale. The development of specialised computer programs has been very important in enabling scientists to further explore the relationships between organisms.

All living organisms can be classified based on physical traits, reproductive method and/or molecular sequences.

Case study

A microbiological sleuth: Dr Adam Jenney

Staphylococcus aureus or 'golden staph' is a bacterium that can cause serious infections of the skin, blood, bones and other organs. Some strains of *S. aureus* are resistant to commonly used antibiotics and need to be treated differently to other bacteria. It can be difficult to tell which bacterium is causing an infection because different bacteria can cause similar symptoms in patients. So how do doctors know what bacterium they need to treat?

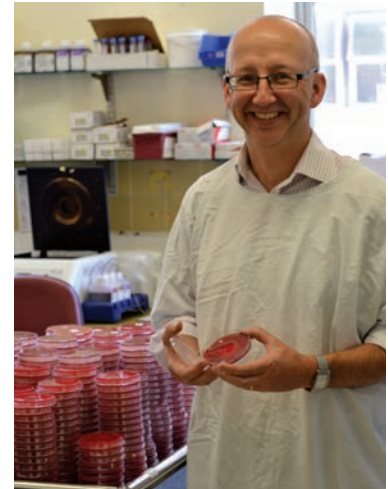
Dr Adam Jenney is a clinical microbiologist at the Alfred Hospital in Melbourne. He works with other doctors and scientists to help them identify bacteria that are causing disease in patients. According to Dr Jenney, 'identifying organisms allows you to predict how the pathology associated with that infection may evolve'. Most importantly, accurate identification is necessary because 'we treat different species in different ways. An example of that is *S. aureus* versus other types of *Staphylococcus*'.

One of the first steps in identifying these bacteria is to grow the organisms in the laboratory. 'Let's take, for example, a specimen of sputum from someone who the clinician thinks has got pneumonia ... we take a sterile swab and will put some of that sputum onto culture media.' The next step, describes Dr Jenney, is to 'spread the sputum over the plate to allow us to achieve, if there is something to grow, single colonies so we can identify the organisms causing the infection.'

Until recently, organisms were identified using **classification keys** based on physical and biochemical properties. 'We would take a tiny amount from a colony that we think might be a pathogen, spread it on a glass slide and make a gram stain of it,' explains Dr Jenney. 'Gram stain allows us to fix colour into organisms to determine whether it is Gram positive or negative, which is still very important in the identification process.' The results of the Gram stain help to direct further tests to be performed. 'For instance, if the slide showed Gram-positive cocci [spherical-shaped bacteria], we could take another small dab of the colony and mix it with some hydrogen peroxide on a clean glass slide. If this produced bubbles, it indicates oxygen is being released. This is a positive catalase test indicative of staphylococci rather than the other common Gram-positive cocci we see, namely streptococci.'

New technologies, however, have changed the way that bacteria are identified. The laboratory at the Alfred now uses a MALDI-TOF machine to identify bacterial colonies. 'You take a normal, though sterile, toothpick and pick off a little bit of that colony and place it on a slide,' outlines Dr Jenney. 'Then the MALDI-TOF machine fires lasers at the colony forcing proteins to be released. Those proteins have a characteristic size and they are able to be identified using a mass spectrometer.' Mass spectrometry measures the size of particles by converting them to ions and separating them by size and charge. Each bacterial species is made up of a different set of proteins, so a computer can use this information to identify the species of bacteria. The MALDI-TOF can quickly diagnose a *S. aureus* infection, the significance of which is often considerably greater than other species of staphylococcus.

As well as helping with identification, Dr Jenney also works with organisations to help track and prevent the spread of infections within hospitals and the community. He became interested in microbiology during his training as a doctor specialising in infectious diseases. 'I realised that such a vast amount of clinical infectious diseases relies on clinical microbiology so I did that as well.' Dr Jenney's advice for science students considering a career in science: 'Do it! Science is forever expanding and is becoming more interesting and is constantly challenging.'



▲ **Figure 2.7**
Dr Adam Jenney with a plate of *S. aureus* grown from a clinical sample

MALDI-TOF stands for Matrix-Assisted Laser Desorption/Ionisation - Time of Flight. What a mouthful.

Questions

- 1 Explain why it is important for doctors to be able to identify species of bacterium.
- 2 Construct a flow chart to show how bacteria are identified in the laboratory.
- 3 Distinguish between the characteristics of bacteria used in identification using traditional microbiological techniques, such as growing them on a plate, and the MALDI-TOF machine.
- 4 Explain how collaboration between scientists from different fields has changed the way that bacterial identification occurs.

Classification keys



Tim Alexander

Figure 2.8 ▲

This species of sea snail is commonly found in Australian waters. How would you identify it?

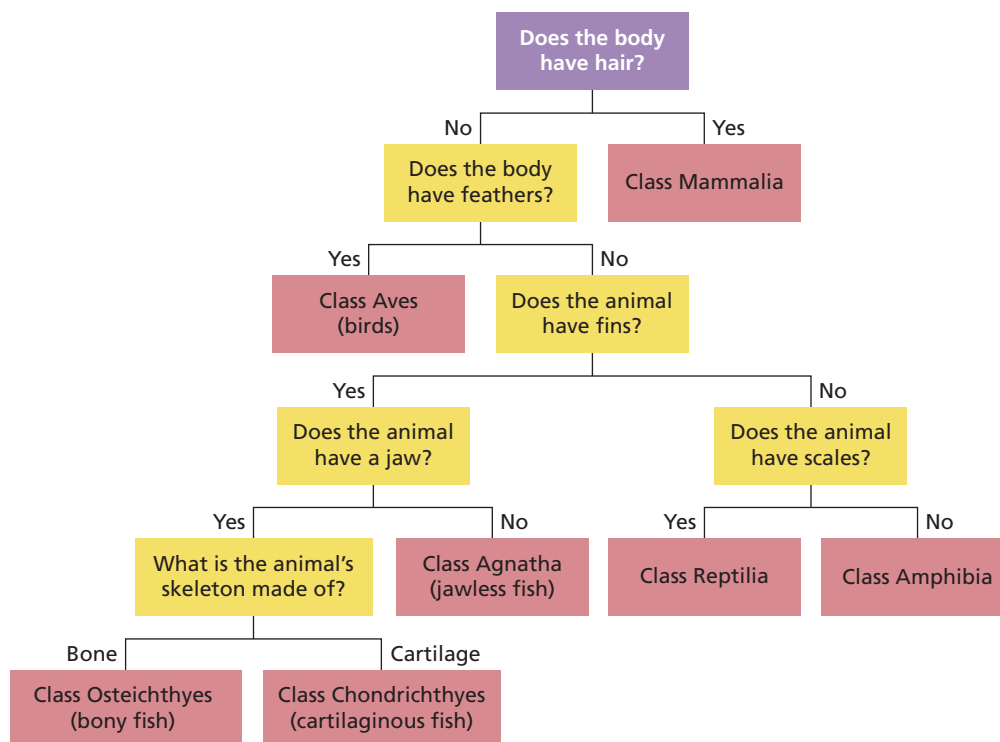
Imagine you are exploring a rockpool and find a sea snail that you want to learn more about. The first step is to identify the snail, but how would you do this? One way would be to use a **field guide**, a book containing pictures and descriptions of plants and animals in a particular area. If there are a lot of options, it can be hard to be confident that you have found the correct organism. Furthermore, field guides often only identify organisms down to order. A more scientific option is to use a classification key. These are tools used by scientists to identify organisms that have already been discovered. Using information about the physical features and habitats of organisms, classification keys guide scientists through the identification process.

At the start of a classification key the user is given a choice between several options that describe the organism to be identified. Each choice leads to more options to choose between. The user continues to make choices until they reach an endpoint. Most classification keys are **dichotomous** meaning that at each step the user has to choose between two options (Figure 2.9).

Dichotomous keys are tools used to identify organisms. They involve choosing between a series of two options until an organism is identified.

Figure 2.9 ►

A dichotomous key for identifying the class of vertebrate animals



Imagine that Figure 2.9 had hundreds of branches. Dichotomous keys can be very long so it is not always practical to present them this way. Most keys are presented as a list with the pairs of choices numbered. A simple dichotomous key for classifying animals into phyla is shown on page 23.



IPHONE FIELD GUIDE

The Melbourne Museum has a free iPhone/iPad field guide app that provides information about animals in Victoria.

1a	Body symmetrical	go to 2
1b	Body asymmetrical with no structure/organs	Phylum Porifera
2a	Body with multiple planes of symmetry (radial symmetry)	go to 3
2b	Body with a single plane of symmetry (bilateral symmetry)	go to 4
3a	Tentacles present, body soft	Phylum Cnidaria
3b	No tentacles, body hard and rough	Phylum Echinodermata
4a	Body divided up into segments (segmented)	go to 5
4b	Body unsegmented	go to 6
5a	Body divided into 2–3 segments; jointed legs present	Phylum Arthropoda
5b	Body divided into many segments; jointed legs absent	Phylum Annelida
6a	Body with internal or external shell	Phylum Mollusca
6b	Body without shell	go to 7
7a	Body flat and worm-like	Phylum Platyhelminthes
7b	Body not worm-like	Phylum Chordata

We can use this key to identify the phylum of our sea snail (Figure 2.8). The body is symmetrical with a single plane of symmetry so we choose option 1a and then 2b. The body is unsegmented so we choose option 4b, which directs us to pair 6. The sea snail has a shell so we choose option 6a, which identifies our sea snail as belonging to Phylum Mollusca. A more detailed key is needed to identify the further taxa.

One of the difficulties with dichotomous keys is that if the user cannot distinguish between two options, they become ‘stuck’ and cannot keep going. To help overcome this problem, many keys are now available on the Internet or as computer software. These digital keys allow users to input information about the organism’s features in any order. The program eliminates options until enough information has been entered to uniquely identify the organism.



THE PEA KEY

A digital key that allows you to distinguish between 1500 species of Australian pea plants.

ACTIVITY 2.1

DIFFERENT TYPES OF SYMMETRY

Aim

To discover the difference between radial and bilateral symmetry

You will need

- modelling clay or playdough
- butter knife
- sheet of paper

What to do

- 1 Make clay models of some of the following organisms: starfish, snail, turtle, sea urchin and cat.
- 2 Using the butter knife, determine how many ways you could cut each organism in half so that the two pieces are mirrored versions of one another.
- 3 Create a table listing each of the organisms under the headings bilateral symmetry (only able to cut the organism once) and radial symmetry (able to cut the organism more than one way).

What did you discover?

- 1 Describe the difference between radial and bilateral symmetry.
- 2 Are humans radially or bilaterally symmetrical?

ACTIVITY 2.2

MAKING YOUR OWN DICHOTOMOUS KEY

Aim

To produce a dichotomous key to identify different leaves

You will need

- selection of leaves from different plants
- hand lens
- blank sheet of paper

What to do

- 1 Start by dividing the leaves into two groups that have a characteristic in common (some of the terms used to describe leaf characteristics are shown in Figure 2.10. If your leaves don't fit these terms, describe the characteristics instead). This is the first branch in your key.
- 2 Divide each group into two further groups.
- 3 Continue to divide the groups in this manner until each leaf is in its own group.
- 4 Write the dichotomous key in two formats: as a branching diagram (e.g. Figure 2.9) and as a list.
- 5 Ask a friend to identify some of the leaves using your key.

What did you discover?

- 1 Was your friend able to identify the leaves using your key? Explain why or why not.
- 2 Explain whether the leaves have more or less in common as you go down the key.
- 3 Which format (a list or flow chart) for the key do you prefer? Justify your response.

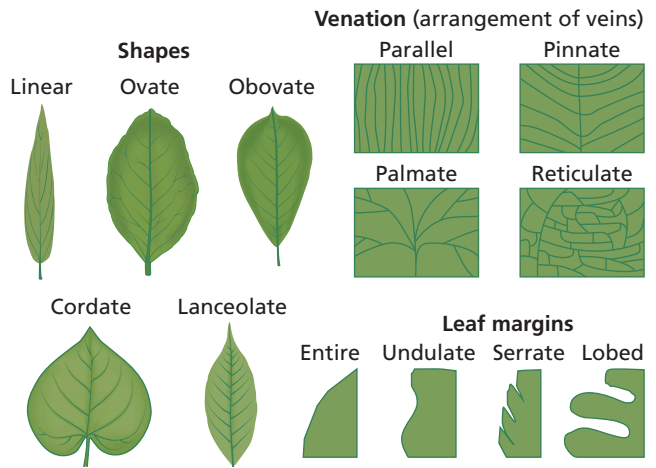


Figure 2.10 ▲
Selected terms that can be used to describe the characteristics of leaves

EXPERIMENT 2.1

IDENTIFYING INSECTS

In this experiment you will use two types of keys to aid in the identification of some Australian insects. You will use a dichotomous key, as well as a digital key, to identify these insects. These keys will allow you to identify the insects down to order. Further keys would be needed to identify the family, genus and species.

Aim

To practice using classification keys

Materials

- preserved insect specimens and/or
- appropriate photos and diagrams of insects
- stereo (dissecting) microscope
- computer with access to the weblink
- forceps
- dissecting needle
- hand lens

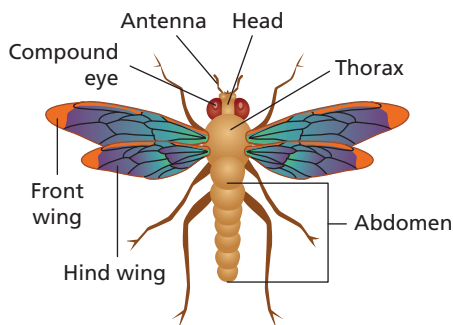


**WHAT GROUP
DO I HAVE?
INSECT
ORDERS OF
AUSTRALIA**

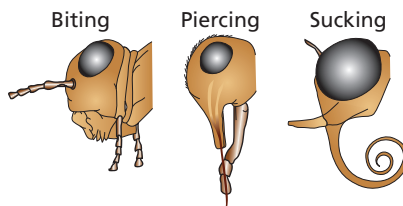
A matrix key to identify Australian insects down to their order.

Procedure

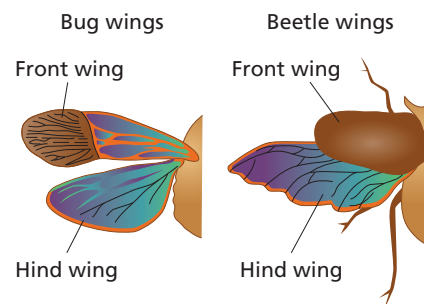
- 1 Familiarise yourself with some of the terms used to describe insect parts (shown in Figures 2.11, 2.12 and 2.13). The digital key contains further images that help explain the terms used.
- 2 Using the written key shown below, 'key out' each specimen to identify the order to which they belong. You can use the stereo microscope, forceps and dissecting needle to help you look more closely at the insects.
- 3 Repeat the process using the digital key. To use the digital key, you should select any features you can identify. Orders that the insect could belong are shown in 'entities remaining'. Continue to select features until only a single order remains.
- 4 Record your results in a table such as that shown as Table 2.2 on page 28.



▲ **Figure 2.11**
The main parts of a typical insect



▲ **Figure 2.12**
Insect mouth parts



▲ **Figure 2.13**
A comparison of beetle wings and bug wings

- | | | |
|----|---|------------------|
| 1a | Winged insects | go to 2 |
| 1b | Wingless adult insects | go to 25 |
| 2a | Two pairs of wings, one of the pairs being either partly or wholly hardened, or parchment-like (papery) and opaque (non-transparent) | go to 3 |
| 2b | One pair of wings or two pairs resembling one another in appearance and texture | go to 12 |
| 3a | Front wings forming a pair of hard covers meeting in a straight line down the centre of the back. Mouthparts of biting type (unsuitable for sucking) | go to 4 |
| 3b | Front wings overlapping (not meeting in a straight line down the back). Hind wings membranous and often fan-like | go to 6 |
| 4a | Front wings very short, covering less than half the abdomen | go to 5 |
| 4b | Front wings covering all or most of the abdomen. Beetles | Order Coleoptera |
| 5a | Abdomen with two hardened pincer-like (or forceps-like) extensions behind. Earwigs | Order Dermaptera |
| 5b | Abdomen without a pair of pincer-like (or forceps-like) extensions behind, though often with a pair of short segmented processes. Some beetles | Order Coleoptera |
| 6a | Each front wing divided into two sections sharply marked off from each other, the fore-section being leathery and opaque, the hind-section membranous. Mouthparts in the form of a jointed piercing tube (suitable for sucking). Bugs | Order Hemiptera |
| 6b | Front wings parchment-like, more or less uniform in texture | go to 7 |
| 7a | Mouthparts of piercing type. Hind wings not fan-like. Most planthoppers and froghoppers | Order Hemiptera |
| 7b | Mouthparts of biting type. Hind wings fan-like | go to 8 |
| 8a | Hind legs much longer than other legs, suited to leaping. Grasshoppers and crickets | Order Orthoptera |
| 8b | All legs more or less equal in length | go to 9 |
| 9a | Broad, flattened insects with legs pressed close to the body. Usually rapid runners. Head partly or completely hidden when viewed from above. Cockroaches | Order Blattodea |
| 9b | Elongated, slow-moving insects with extended legs and a clearly visible head | go to 10 |

10a	Front legs markedly different in shape from the other legs	go to 11
10b	Front legs similar to other legs; the first segment of the thorax (the segment bearing the front legs) very short; second segment of the thorax very long. Stick insects, phasmatids	Order Phasmatodea
11a	Front legs greatly broadened and adapted for digging. Front wings very short and round. Mole-crickets	Order Orthoptera
11b	Front legs adapted for securing prey. First segment of thorax (segment bearing the front legs) very long. Mantids	Order Mantodea
12a	One pair of wings. (Hind wings are reduced to a pair of balancers, which are often obscured by a pair of scale-like processes arising from the side of the thorax.) True flies	Order Diptera
12b	Two pairs of wings	go to 13
13a	Wings and body completely covered with fine scales or hairs visible at low magnification (though occasionally part of whole of the wing may lack scales)	go to 14
13b	No scales or hairs visible at low magnification	go to 16
14a	Insects resembling moths, but with hairy wings (scales rub off). Mouthparts never in the form of a sucking tube	go to 15
14b	Insects with fine scales covering the wings and body. (The wings of a few species are partly or wholly transparent.) Mouthparts often in the form of a long sucking tube held coiled like a watch spring. Butterflies and moths	Order Lepidoptera
15a	Distinct, biting mouthparts. Wings with numerous short cross-veins leading from one of the main wing veins to the front margin of the wings. Pattern of wing veins very complex with much branching and numerous cross-veins. Some lacewings	Order Neuroptera
15b	Mouthparts non-functional. Wing veins much simpler, without the series of cross-veins between the long wing vein and the front margin of the wings. Caddisflies	Order Trichoptera
16a	Mouthparts in the form of a piercing tube only (often folded underneath)	go to 17
16b	Distinct, separate mouthparts suited for biting, or some mouthparts forming a sucking tube and some used for manipulation	go to 18
17a	Very small elongated insects, with a short, piercing beak and very narrow wings with long fringes of hairs. Nearly always found on the buds and flowers of plants. Thrips	Order Thysanoptera
17b	Small, medium or large insects with mouthparts in the form of a long, piercing beak; wings of normal width, without long fringes of hairs. Aphids, psyllids (lerps), cicadas etc.	Order Hemiptera
18a	Stiff wings, with thick wing veins. Hind wings linked to front wings by a row of hooks (use a hand lens). Abdomen connected to the thorax by a 'waist', which is often very narrow. Sawflies, wasps, ants, bees	Order Hymenoptera
18b	Wings not linked by a row of hooks	go to 19
19a	Insects with long, segmented filaments extending from the end of the body	go to 20
19b	Insects without long, segmented filaments extending from the end of the body	go to 21
20a	Front wings distinctly narrower than the hind wings, which are partly or almost entirely fan-like; antennae long. Stoneflies	Order Plecoptera
20b	Front wings much broader than hind wings; antennae extremely short and bristle-like. Mayflies	Order Ephemeroptera
21a	Wing veins very simple with few cross-veins. Pale, soft-bodied insects with very weak flight. Termites	Order Isoptera
21b	Wing veins more complex with numerous cross-veins and much branching	go to 22
22a	Antennae extremely short and bristle-like; eyes very large, taking up most of the head. Wing venation extremely complex. Wings held stiffly to the sides (dragonflies), or held over the abdomen (damselflies) when the insect is at rest. Dragonflies and damselflies	Order Odonata
22b	Antennae of more normal length, often very long. (If they are short, they are never bristle-like.) Eyes of more normal size	go to 23



23a	Wings without a series of cross-veins linking the long wing veins to the front margin of the wings. Wings long and thin; legs usually very long; head elongated into a snout. Scorpionflies	Order Mecoptera
23b	Wings with numerous short veins linking one of the main long wing veins to the front margin of the wings. Wing venation usually very complex with much branching and numerous cross-veins	go to 24
24a	Main veins in wings branch near ends. Wings held tent-like over abdomen when insect is at rest. Lacewings and ant-lions	Order Neuroptera
24b	Main veins in wings unbranched near ends. Wings folded flat over abdomen when at rest. Alderflies or dobsonflies	Order Megaloptera
25a	Minute insects with a 'spring' present at the tip of the abdomen, enabling the insect to spring strongly. Springtails	Order Collembola
25b	Insects not possessing this spring	go to 26
26a	Insects with pincer-like or forcep-like processes extending from the tip of the abdomen	go to 27
26b	Abdomen without processes, or with processes coming from the tips of the abdomen and divided into segments	go to 28
27a	Segments of the abdomen clearly separated from each other by membranous sections. Body very soft. Mouthparts internal, not visible externally. Japygids	Order Diplura
27b	Abdominal segments telescoped to some extent so that membranous parts between segments not visible dorsally. Mouthparts of biting type and clearly visible. Earwigs	Order Dermaptera
28a	Abdomen with long, segmented, thread-like processes (filaments) extending from the tip	go to 29
28b	Tip of abdomen without processes, or with short ones	go to 30
29a	Three filaments; body often covered with silvery scales (which rub off). Silverfish	Order Thysanura
29b	Two filaments; body bare (without scales)	Order Diplura
30a	Soft-bodied, pale insects parasitic on the feathers of birds or the hair of mammals. Lice	Order Phthiraptera
30b	Other insects. If parasitic on the bodies of birds or mammals then not particularly soft-bodied or pale	go to 31
31a	Body strongly compressed from side to side; hind legs long and suited to leaping. Parasitic on the bodies of birds or mammals. Fleas	Order Siphonaptera
31b	Body not strongly compressed from side to side; not parasitic on birds and mammals	go to 32
32a	Minute insects, with pale, soft bodies, found amongst old books and papers or neglected museum specimens; rapid runners. Booklice	Order Psocoptera
32b	Larger insects of different appearance and habits	go to 33
33a	Abdomen constricted to form a 'wasp waist'. Ants and wingless wasps	Order Hymenoptera
33b	Abdomen broadly joined to thorax (no 'wasp waist')	go to 34
34a	Mouthparts of biting type	go to 35
34b	Mouthparts not of biting type	go to 38
35a	Hind legs much longer than other legs, and suited to leaping. Wingless grasshoppers	Order Orthoptera
35b	All legs more or less equal in length	go to 36
36a	Pale, soft-bodied, slow-moving insects tunnelling in soil or timber, often living in colonies made up of several distinct castes. Termites	Order Isoptera
36b	Insects differing in appearance and habits from 36a	go to 37



- | | | |
|-----|--|-------------------|
| 37a | Large, broadly flattened insects with legs pressed close to the body; usually rapid runners. Head partly or completely hidden when viewed from above. Wingless cockroaches | Order Blattodea |
| 37b | Elongated stick-like insects with the first segment of the thorax (the segment bearing the front legs) short and the second segment of thorax very long. Phasmatids | Order Phasmatodea |
| 38a | Very furry, slow-moving insects with an abdomen much larger than head and thorax. Some female moths | Order Lepidoptera |
| 38b | Insects without a hairy covering | go to 39 |
| 39a | Very small, slow moving insects with long thin legs. Abdomen with a pair of short tubes on the back through which wax is secreted. Aphids | Order Hemiptera |
| 39b | Insects of different form, without tubes on the back | go to 40 |
| 40a | Head with a distinct neck. Wingless flies | Order Diptera |
| 40b | Head usually set into thorax. Many bugs | Order Hemiptera |

Results

Table 2.2 Insects identified using the keys

Specimen number	Order identified (written key)	Order identified (digital key)

Analysis of results

- 1 Were you able to identify all specimens using both keys? If not, identify where you became 'stuck'.
- 2 Did both keys identify the insects as belonging to the same order? If not, suggest some reasons why this might have occurred.

Discussion

- 1 List three of the features that were used to identify the insects.
- 2 If you wanted to confirm your identification, suggest some other resources you could use to do this.
- 3 Compare and contrast the features of the written key and digital key you used. Do you prefer one over the other?

Taking it further

- 1 The weblink on page 24 also contains keys that allow you to identify the family of insects within a particular order. Identify what family your insects belong to.

QUESTION SET 2.3

Remembering

- 1 List three different types of characteristics that can be used to classify organisms.
- 2 Describe what a dichotomous key is.

Understanding

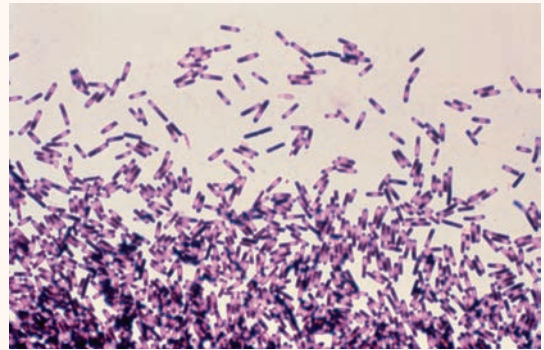
- 3 Explain how protein structure can be used to classify organisms.

Applying

4 Shown below is a simplified dichotomous key for identifying several species of bacteria that can cause disease in humans. Using this key involves performing a Gram stain, which is a staining process that groups bacteria into two groups based on characteristics of their cell wall.

- | | | |
|----|---|---------------------------------|
| 1a | Gram positive (stains purple with a Gram stain) | go to 2 |
| 1b | Gram negative (stains pink with a Gram stain) | go to 4 |
| 2a | Bacteria are cocci (sphere-shaped) | go to 3 |
| 2b | Bacteria are bacilli (shaped like rods) | <i>Clostridium difficile</i> |
| 3a | Cocci are arranged in chains | <i>Streptococcus pneumoniae</i> |
| 3b | Cocci are arranged in bunches | <i>Staphylococcus aureus</i> |
| 4a | Bacteria are cocci (sphere-shaped) | <i>Neisseria</i> spp. |
| 4b | Bacteria are bacilli (shaped like rods) | <i>Escherichia coli</i> |

- State which of the listed species are sphere-shaped.
- Using the dichotomous key, determine what species of bacterium is shown in Figure 2.14.
- Using this key, not all bacteria can be identified to the species level. Which group are you unable to identify? Provide a reason for your answer.



Getty Images/CDC/SPL

▲ **Figure 2.14**
A light micrograph of a species of bacterium stained with a Gram stain

Classification reflects evolutionary relationships

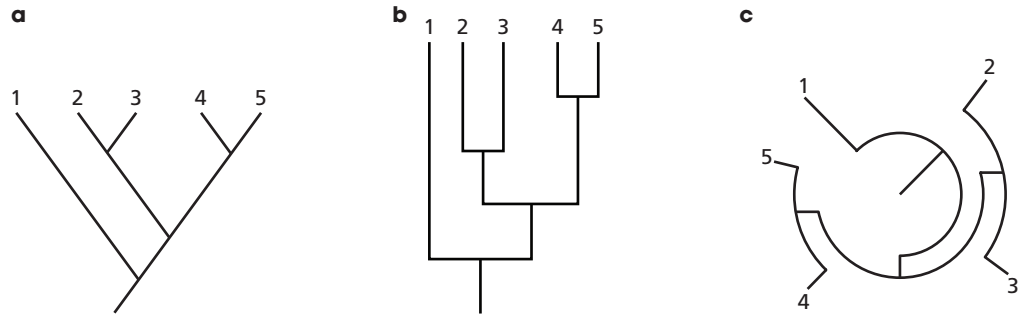
All organisms on Earth are related to one another, meaning that at some point in time they shared a **common ancestor**. Over generations, populations change as organisms adapt to their environments. These slow, incremental changes are referred to as evolution and can result in the formation of new species. Consequently, multiple species can develop from the same common ancestor. The more recently that two species shared a common ancestor, the more closely related they are and the more features they will have in common. When we classify organisms, we are also figuring out how they are related to one another. Two birds within the same genus, for example, are more closely related to one another than either bird is to animals in a different class.

These relationships can be shown in diagrams called **phylogenetic trees**. Like trees, these diagrams follow a branching pattern. You can think of each organism as a leaf on the tree and each branch point representing the most recent ancestor shared by two organisms. The more closely related two species are, the more recently they shared a common ancestor. Higher taxonomic levels branch off from one another earlier than lower levels. Figure 2.15 shows some of the different ways phylogenetic trees can be drawn. This tree shows that species 2 and 3 are closely related and that both of these are more closely related to species 4 and 5 than to species 1. You can see that even though each of these shows the same branching pattern, they look quite different.

Unit 3 Biology discusses the process of evolution and how organisms are related.

You will notice that dichotomous keys also show a branching pattern. Unlike phylogenetic trees, the branches in a dichotomous key do not necessarily reflect how organisms are related.

Figure 2.15 ▶ Three different ways of drawing phylogenetic trees. Type c is useful when trees are very large.



Cladistics

Phylogenetic trees are commonly constructed using a technique called **cladistics**. Phylogenetic trees made using this technique are known as **cladograms**. Cladistics relies on several assumptions.

- The more closely related two organisms are, the more characteristics they will share.
- Some characteristics that are shared by a group will not be present in more distantly related groups.
- When there are multiple possible ways that organisms can be related, the simplest explanation is the most likely to be correct. This is because if a feature is shared between organisms, it is more likely that this feature evolved once in a common ancestor than independently for each organism. You will see an example of this in the following text.

Organisms are classified into groups that reflect their evolutionary history. This classification is based on the fact that related organisms share characteristics.

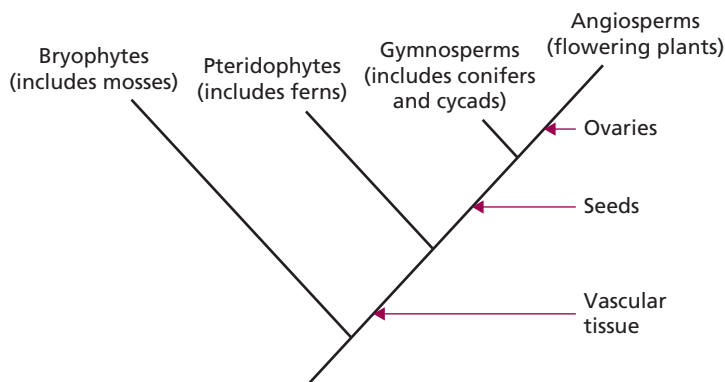
Table 2.3 Character matrix of major plant groups

	Bryophytes (includes mosses)	Pteridophytes (includes ferns)	Gymnosperms (includes conifers and cycads)	Angiosperms (flowering plants)
Performs photosynthesis	+	+	+	+
Has vascular tissue (xylem and phloem)	–	+	+	+
Makes seeds	–	–	+	+
Seeds enclosed in an ovary	–	–	–	+

Figure 2.16 is an example of a cladogram and shows the relationship between major plant groups. The first step in constructing a cladogram is to create a table of the characteristics to be

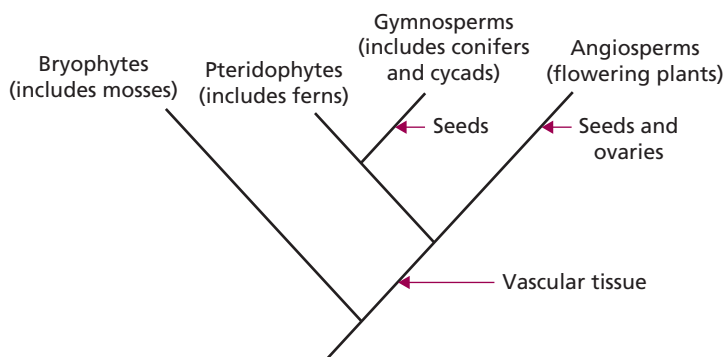
used. This table is known as a **character matrix**. In the character matrix used to build this cladogram (Table 2.3) you can see that a + is used to indicate when a characteristic is present and a – when it is absent.

The groups can then be arranged in different ways until the simplest cladogram is found. An alternative way of arranging the major plant groups based on the same character matrix (Table 2.3) is shown in Figure 2.17. For this cladogram to be correct, the presence of seeds would have had to evolve twice, once for the gymnosperms and separately for the angiosperms. This is unlikely and as such, Figure 2.16 is considered to be the most likely arrangement.



◀ **Figure 2.16**

A cladogram showing the evolutionary relationship between major plant groups. The arrows indicate when each characteristic evolved.



◀ **Figure 2.17**

An alternative cladogram showing the relationship between major plant groups. This option is far less likely to have occurred.

Taxonomists try to ensure that classification reflects the evolutionary relationships between organisms. Ideally, each taxonomic group contains all of the organisms descended from the same common ancestor. When looking at a cladogram, this means that a group contains all of the organisms on a branch. When this occurs, that group is called a **clade** (or can be referred to as **monophyletic**).

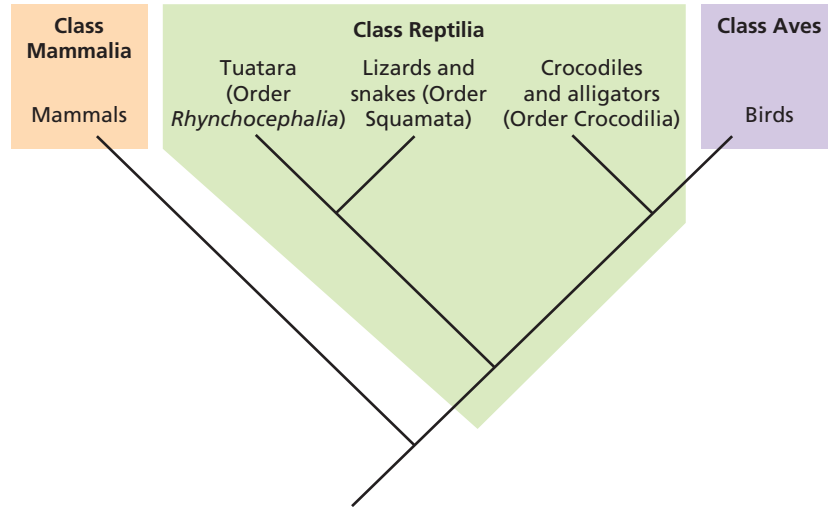
Three classes of animals are shown in the cladogram in Figure 2.18. You can see that both Class Aves and Class Mammalia are clades because they contain all of the animals on that branch. Class Reptilia, however, is not a clade. This is because it does not contain birds, which also descended from a reptilian ancestor. Class Reptilia can be called a **paraphyletic** group. This arrangement has occurred because birds and reptiles were classified into separate classes before their evolutionary relationships were known. More recently, it has been determined that birds evolved from dinosaurs and as such, share a recent common ancestor with crocodiles and alligators. Some scientists have suggested that these taxonomic groups need to be reclassified to ensure that all are clades.



SORTING SEASHELLS

An interactive activity that guides you through sorting shells based on their physical characteristics to build a cladogram.

Figure 2.18 ►
Cladogram showing the major classes of amniotes. Classes Aves and Mammalia are monophyletic/clades; Class Reptilia is paraphyletic.



ACTIVITY 2.3

CONSTRUCTING A CLADOGRAM

Aim

To complete a character matrix and use it to construct a cladogram

You will need

- photos of each of the following: starfish, snail, bee, cow, duck and turtle

What to do

- 1 Create a character matrix that can be used to distinguish between the organisms. Use a + to indicate a feature is present and a - if it is absent. Table 2.4 shows some suggested characteristics, but you will need to decide on some others to use.

Table 2.4 Character matrix

	Starfish	Snail	Bee	Cow	Duck	Turtle
Bilateral symmetry						
Has a backbone						
Gives birth to live young						

- 2 Find an animal that differs from another by only one (or very few) characteristics. Place these as an initial branch.
- 3 Place the rest of the animals on the cladogram into the simplest arrangement (the arrangement that is most likely to have evolved).
- 4 Check your arrangement by marking at each branch point what characteristics have evolved in that branch. Remember, you are aiming to have an arrangement that means no characters needed to evolve twice.

What did you discover?

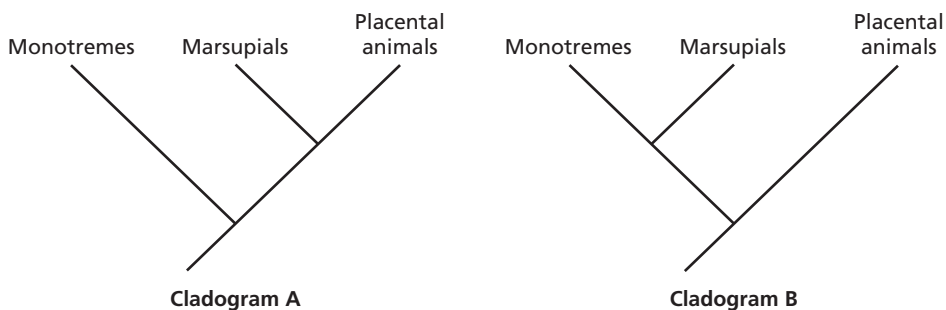
- 1 Circle a clade (monophyletic group) on your cladogram.
- 2 Were there multiple ways you could construct the cladogram? How did you choose your arrangement?
- 3 How has this activity improved your understanding of what a cladogram represents?

One of the limitations of cladistics occurs when unrelated organisms have evolved similar characteristics independently. This can occur with organisms that inhabit similar niches in different parts of the world, as in the case of marsupial moles and African golden moles. Marsupial moles (*Notoryctes typhlops*) that live in central Australian sandy deserts look remarkably like African golden moles (*Chlorotalpa* spp.). They have almost identical size and body shape. Both are blind and lack external ears, have several spade-like claws on their front feet, a horny shield protecting the snout, a stubby tail and silky fur (Figure 2.19). Should marsupial moles and golden moles be grouped together? Not if we think about their method of reproduction. Like other marsupials, marsupial moles give birth to live young at an extremely young age. These young then develop in a specialised pouch until they are mature enough to survive outside. Golden moles are placental mammals meaning that their young develop inside the mother until the time of birth. Golden moles cannot be grouped with marsupials even though, externally, marsupial moles and golden moles are almost identical to look at.



◀ **Figure 2.19**
a) Marsupial moles and b) golden moles are superficially similar, but have evolved their characteristics independently.

It is important to understand that cladograms are theories about the way that organisms are related. Like all scientific theories, they can be confirmed or challenged when more evidence is available. Cladograms can, and do, change as our understanding of these relationships improves. Figure 2.20 shows two possible cladograms for the evolution of the three groups of mammals: placental mammals, marsupials and monotremes. Most evidence based on the physical characteristics supports cladogram A. However, there is some evidence based on teeth and molecular data that suggests that monotremes and marsupials are more similar to one another than either is to placental mammals. This would support cladogram B. Has there been a verdict? Yes – molecular sequencing of DNA supports cladogram A, which is now widely accepted to be the most likely evolutionary relationship.



◀ **Figure 2.20**
Two different cladograms showing the evolution of monotremes, marsupials and placental mammals. Cladogram A is currently regarded as correct.

Scientific literacy: Wattle lot of fuss over a name

In 2011 the name of the genus of African plants previously known as *Acacia* was changed to *Vachellia*. Below is an extract from *The Age* just before this historic decision was finalised.

It is rare that controversy strikes the botanical world. However, 6 years ago, when the International Botanical Congress met in Vienna to vote on what plants could carry the name *Acacia*, the simple question of what's in a name divided the usually unified global group.

Essentially the world's botanists were at odds over changing the rules so that the name *Acacia* would apply only to Australia's 1000-plus species, meaning a smaller number of species, mainly from Africa, would have to change their name to *Vachellia*.

The alternative – which for some was too problematic to even contemplate – was to rename Australia's acacias, including the wattle, *Racosperma*.

'Given the iconic status of acacias both in Australia and in Africa it was probably inevitable that there was going to be this controversy,' said Bill Aitchison, leader of the acacia study group section of the Australian Plants Society.

While the wattle is Australia's botanical emblem and informs our national colours, the silhouette of the flat-topped thorn tree against a rust-red sunset is symbolic of Africa. Both, botanically speaking, are acacias. Until now.

The International Botanical Congress meets in Melbourne from today and it is anticipated that 'the acacia issue' – one of the most contested botanical cases debated to date – will finally be resolved ... come this Friday, a final vote in favour of Australia using the name *Acacia* is expected to be little more than a formality. Meanwhile, 163 species formally classed as *Acacia* will now be known as *Vachellia*.

A proposal to compromise by adding a prefix to the name *Acacia* – so *Austroacacia* would refer to Australian acacias and *Acanthacacia* to species in Africa, India, the Middle East, South and Central America – was rejected by 70 per cent of voters.

'Africa is the home of the acacia, in that it is where the first *Acacia* species was described. But Australia is the hot spot for acacia because there are more than 1000 species here – none of which were known at the time the acacia was first described. So you can see why it's been so controversial.'

Smith, B. (2011) 'Wattle it be? Name claim for Africa or Australia'. *The Age*, 25 July.



Shutterstock.com/Lev Krupotov

Figure 2.21 ▲

The floral emblem of Australia: Golden wattle (*Acacia pycnantha*). The name *Acacia* has symbolic value in both Africa and Australia.

Questions

- 1 List the three potential solutions to 'the acacia issue' that the article discusses.
- 2 Explain why the Australian and African groups cannot both have the name *Acacia*.
- 3 Which group of plants (Australian or African) do you think should keep the name *Acacia*? Justify your answer.

The impact of new technologies on taxonomy

New technologies have transformed cladistics and taxonomy. One of the most important developments has been the use of DNA technology to provide new and highly detailed information about evolutionary relationships. In some cases DNA evidence has supported previous hypotheses about these relationships, but in other cases it has led to reclassification of organisms. Additionally, because some changes in DNA occur at a predictable rate, DNA technology has allowed scientists to understand when certain groups evolved.

The information provided from DNA evidence is so detailed that classification systems have changed to reflect this. It is now possible to classify organisms down to many more levels than the traditionally recognised taxa. The prefixes super- (above) and sub- (below) can be added to existing taxa to create additional ranks (e.g. subphylum) and some newer taxa (e.g. tribe) are also recognised. Some scientists have argued that because of this complexity, the taxa are no longer relevant and have suggested replacing it with a system called the PhyloCode. The PhyloCode assigns a name to a clade along with a definition of the members, but does not assign a rank to these names. For example, Mammalia could be defined as the clade originating with the most recent common ancestor of humans and platypuses.

Phylogenetic trees can be extremely large and complex so the ability to display these in digital form, rather than in print, makes viewing these easier. An ambitious project to create a phylogenetic tree that maps all of the life on Earth is underway. Called the Tree of Life Web Project, the tree is available to explore online. It is a collaborative project with contributions by scientists from all around the world and updated to reflect recent developments.

The production of such detailed phylogenetic trees could not have occurred without developments in computer technology. Modern computers can produce cladograms from very large data sets, something that would be impossible to do manually.

DNA technology is covered in Unit 3 Biology.



EXPLORE THE TREE OF LIFE

You can browse the branching phylogenetic tree and find information about the organisms it contains.

QUESTION SET 2.4

Remembering

- 1 List the three assumptions that are used in the construction of cladograms.
- 2 Define 'monophyletic'.

Understanding

- 3 Explain why some taxonomists have suggested that the taxa containing birds and reptiles should be reorganised.
- 4 Sometimes multiple cladograms could be constructed for a character matrix. Explain how scientists decide between these different cladograms.

CHAPTER SUMMARY

- Scientists classify organisms into groups to help organise, analyse and communicate information about species.
- Organisms are classified into a hierarchy of groups called taxa. From order of the largest to smallest groups, the taxa are known as Domains, Kingdoms, Phyla, Classes, Orders, Families, Genera and Species.
- Organisms are given scientific names using the binomial system. This means that names have two parts; the first part is the genus name and the second part identifies the species.
- Classification is based on the characteristics of organisms that include physical features, reproductive methods and molecular sequences.
- Tools known as classification keys are used to identify organisms. Most commonly in biology, dichotomous keys are used.
- The classification of organisms into groups reflects the evolutionary relationship between organisms. These relationships can be shown using phylogenetic trees.
- Classification and phylogenetic trees can change as new evidence becomes available. In particular, technological advancement has made new evidence available and changed the way these trees are constructed.

CHAPTER GLOSSARY

amino acid a nitrogen-containing compound that is the building block of proteins

binomial system a system of naming organisms using two parts: a generic name and a specific name

character matrix a table that lists the characteristic of organisms and that is used to construct cladograms

characteristic a feature or quality of an organism that can be used to classify and identify it

clade a taxonomic group that contains all of the descendants of a common ancestor

cladistics a method of classifying organisms based on the characteristics they share

cladogram a diagram constructed using cladistics that shows the evolutionary relationship between organisms

classification key a tool used to identify organisms based on their characteristics

common ancestor an organism from which two different species both evolved

DNA (deoxyribonucleic acid) an information molecule that is the universal basis of an organism's genetic material; it contains instructions, written in a chemical code, for the production of proteins by the cell

dichotomous a classification system where each branch has two options

eukaryote a complex type of cell with a nucleus and membrane-bound organelles; a member of Domain Eukarya

field guide a book used to identify organisms using photos and descriptions

monophyletic organisms that are grouped together as a clade

organelle a specialised structure or compartment within a cell that has a specific function

paraphyletic a group that does not contain all of the organisms descended from the most recent common ancestor

phylogenetic tree a system of classification based on common ancestry, often determined through genetic analysis; a diagram that shows the evolutionary relationship between organisms

prokaryote a simple type of cell that lacks a nucleus and membrane-bound organelles; a member of Domains Archaea or Bacteria

taxa/taxonomic level a group of organisms; the major taxa are known as Domains, Kingdoms, Phyla, Classes, Orders, Families, Genera and Species

taxonomist a scientist who studies organisms and places them into taxa

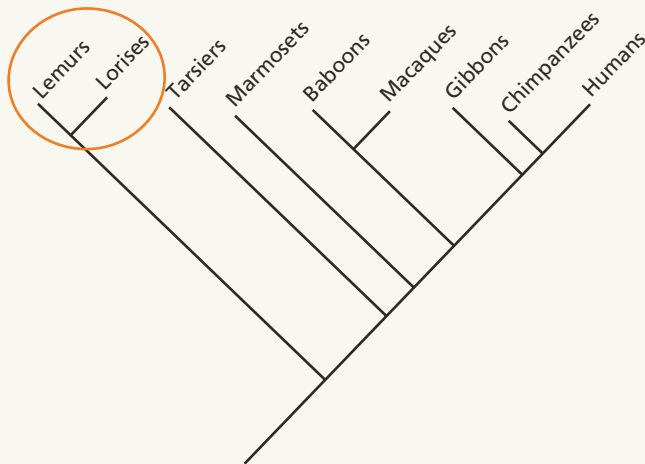
CHAPTER REVIEW QUESTIONS

Remembering

- 1 Describe the characteristic that defines members of Domain Eukarya.
- 2 Name the eight major taxonomic levels.
- 3 Describe what a common ancestor is.

Understanding

- 4 Define 'binomial system'.
- 5 Summarise the reasons why biologists classify organisms into groups.
- 6 Explain why the biological classification system is described as hierarchical.
- 7 The following questions relate to Figure 2.22. Copy the diagram and answer the questions.
 - a State whether the circled group (known as strepsirhines) is monophyletic or paraphyletic.
 - b On your diagram, circle the clade that contains macaques and gibbons but not marmosets.
 - c State which other primate in the figure is also descended from the most recent common ancestor of humans and gibbons.



◀ **Figure 2.22**

A cladogram showing the relationship between several primates

- 8 Explain what a cladogram represents.
- 9 Explain why some organisms that share physical similarities (e.g. the marsupial mole and the African golden mole) are classified separately.

Applying

- 10 Using the data in Table 2.1 on page 20, construct a cladogram that shows the relationship between the five species listed. (Hint: Consider each amino acid as a characteristic.)
- 11 Irukandji jellyfish (*Carukia barnesi*) live in the waters around the north of Australia. Even though they are only a couple of centimeters long, the highly venomous sting of this jellyfish can cause symptoms of severe pain, vomiting and blood pressure changes. Rarely, the sting can be fatal.
 - a List three characteristics of the Irukandji jellyfish that could be used to help classify it.
 - b Identify what domain, kingdom and genus the Irukandji jellyfish belongs to.
 - c Using the dichotomous key on page 23, determine what phylum the Irukandji jellyfish belongs to. You will need to look up a photo of the Irukandji jellyfish.

Analysing

- 12 The Southern Corroboree frog (*Pseudophryne corroboree*) is a critically endangered species of frog that is found in a small region in NSW. Individuals are small (2.5–3 cm long), poisonous and are marked with a bright yellow and black pattern.
 - a List five characteristics of the Southern Corroboree frog that could be used to classify this species.

- b Use the dichotomous key in Figure 2.9 to determine the class to which the Southern Corroboree frog belongs.
 - c There is a large conservation program, including captive breeding, trying to save the Southern Corroboree frog from extinction. Explain why accurate identification is important for this program.
- 13 Identify two advantages of using the binomial system rather than common names to describe species.
- 14 Outline how technology has impacted on scientific classification. You may like to present your answer as a flow chart.

Evaluating

- 15 Taxa, dichotomous keys and cladograms are all based on the characteristics of organisms. Create a table that compares these three scientific tools.
- 16 Distinguish between members of Domain Eukarya and members of Domains Bacteria and Archaea by referring to the specific characteristics of each domain.
- 17 Do you think that the binomial name, common name or both should be used to describe an organism? Justify your response.
- 18 'Dinosaurs are not extinct because many species of birds exist today.' Do you agree with this statement? Justify your response.

Creating

- 19 Use the information in the character matrix shown below to create a cladogram, marking in which characteristics evolved at each branch.

Table 2.5 Character matrix showing several groups of aquatic vertebrates

	Lamprey (Order Petromyzontiformes)	Shark (Class Chondrichthyes)	Lobe-finned fish (Class Sarcopterygii)	Ray finned fish (Class Actinopterygii)
Jaw	–	+	+	+
Fins attached to body on a fleshy stalk	–	–	+	–
Skeleton made of bone	–	–	+	+

Reflecting

- 20 We often classify things without even being aware of it. Reflect on whether this topic has made you more aware of the way you group things.
- 21 Think about which type of identification tool (field guide, written dichotomous key, branching diagram or digital key) you prefer using. Explain which one you prefer and why.