

Exercise walk-through

Concept and uses of classification systems ■ 1.2

eXercise

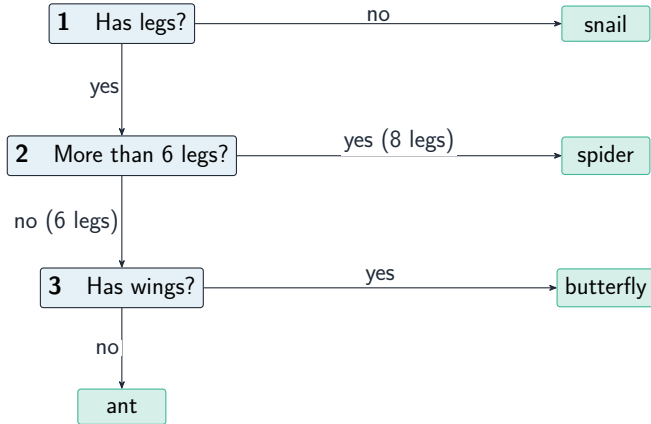
You must be able to

- define a species and use the binomial naming rules
- use and construct a dichotomous key
- explain how DNA base sequences show how closely related organisms are

Method — Keys and naming

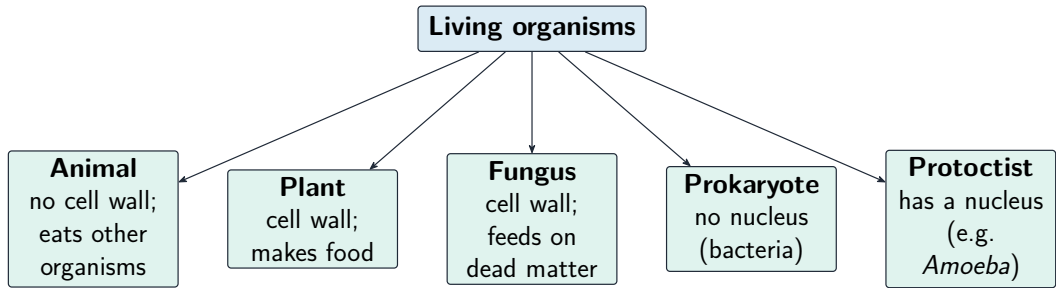
- **species:** a group that can reproduce to make fertile offspring.
- **binomial:** *Genus species* — Genus capital, species lower-case, both italic.
- more similar DNA base sequence → more closely related (more recent ancestor).

Method — Keys and naming



A dichotomous key flowchart: each step splits into two choices

Method — Keys and naming



A key sorts organisms into the five kingdoms

Practice 2.1 ■ 1 mark

Define a species.

Solution 2.1

Worked steps

a group of organisms that can reproduce to make fertile offspring **B1**.

Practice 2.2 ■ 1 mark

In the name *Homo sapiens*, state which word is the genus.

Solution 2.2

Worked steps

Homo B1.

Exam-style 3.1 ■ 1 mark

Two organisms with very similar DNA base sequences are:

- A** distantly related
- B** closely related
- C** the same individual
- D** not related

Solution 3.1

Method: Keys and naming

A distantly related

B closely related 

C the same individual

D not related

Worked steps

B. Similar DNA base sequences mean closely related.

Exam-style 3.2 ■ 2 marks

A student writes a scientific name as “homo Sapiens”.

- (a) State the two mistakes in this name.
- (b) State one feature you should use when building a dichotomous key, and one you should avoid.

Solution 3.2

Worked steps

- (a) the genus should have a capital letter (Homo); the species should be lower-case (sapiens) **B1** **B1**.
- (b) use a clear visible feature (e.g. has wings / no wings) **M1**; avoid a feature that changes, such as size **A1**.

Exam-style 3.3 ■ 2 marks

Explain how DNA base sequences can be used to find out how closely two species are related.

Solution 3.3

Method: Keys and naming

Worked steps

compare the base sequences of the two species **M1**; the more similar the sequences, the more closely related they are (they share a more recent ancestor) **A1**.