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Building a phylogenetic tree

Aim

This activity shows how phylogenetic trees are constructed using the morphological characteristics of organisms. It is an introduction to modern systematics that classify organisms according to their evolutionary relatedness.

Introduction

Modern taxonomy tries to classify organisms according to their relatedness. Earlier taxonomic systems used morphological or anatomical similarities that did not always reflect true evolutionary relationships. The tree of life may be built with either morphological and anatomical structures or molecular data.

Several artificial organisms are shown on the cards. These drawings have been prepared so that it is easy to find differences and to distinguish between the characteristics of each organism. No numerical data are needed to distinguish between characteristics such as long and short birds' tails. In contrast, with real organisms a researcher must usually collect numerical data and subjectively decide how to group characteristics or, alternatively, use advanced mathematical tools. Such problems do not exist when analysing molecular data. Phylogenetic trees for even distantly-related organisms may be prepared using amino acid or nucleotide sequence data. The differences between the sequences in different organisms indicate evolutionary distances.

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In the following introductory exercise, each of three groups of students draw a phylogenetic tree for set of organisms on the cards: plants, birds or butterflies.

Materials

Required by each student or group

- Cards with pictures of the organisms (printed in colour).
- Worksheet with tables to fill in
- Paper
- Pencil

Procedure

Each person or group should analyse a different set of organisms — plants, birds or butterflies. Examples of the features used for the analysis include: number of petals, length of a tail or colour of body or abdomen.

1. Look at the organisms shown on the cards and identify *seven* features that differ between them. List those features in the first row of the table. Fill in the table, recording data for each of organisms, A → F.

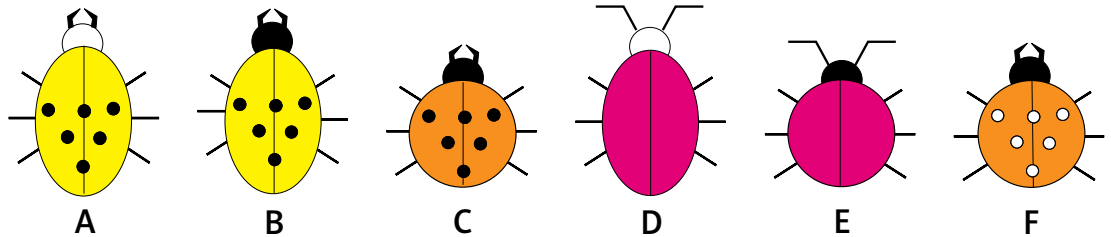| Feature / Organism							
A							
B							
C							
D							
E							
F							

2. Now compare each pair of organisms and, in the small table, record the total number of differences between each pair. *This is the data matrix that will be used to build the phylogenetic tree in the next step.*

3. The numbers in the data matrix can now be used to draw a phylogenetic tree showing the relatedness of all six organisms. The example on the following pages demonstrates how to do this.

	B	C	D	E	F
A					
B	▓				
C	▓	▓			
D	▓	▓	▓		
E	▓	▓	▓	▓	

How to draw a phylogenetic tree

In this example, there are six beetle-like organisms, labelled A to F.

A table has been completed, listing the features of each organism:

Feature	Body shape	Colour	Head colour	Antennae present?	Jaws visible?	Spots on back?	Colour of spots
A	Oval	Yellow	White	No	Yes	Yes	Black
B	Oval	Yellow	Black	No	Yes	Yes	Black
C	Round	Orange	Black	No	Yes	Yes	Black
D	Oval	Pink	White	Yes	No	No	None
E	Round	Pink	Black	Yes	No	No	None
F	Round	Orange	Black	No	Yes	Yes	White

Using the records from the first table, a data matrix, recording the number of differences between pairs of organisms, has also been produced:

|	B	C	D	E	F
A	1	3	5	7	4
B		2	6	6	3
C			7	5	1
D				2	7
E					5

Currently living (extant) organisms will be placed at the top of the tree — all of the organisms analysed live in the present.

Coming down the tree, we are moving into the past. The last common ancestor of the organisms will be shown on the very bottom of the tree.

Last common ancestor
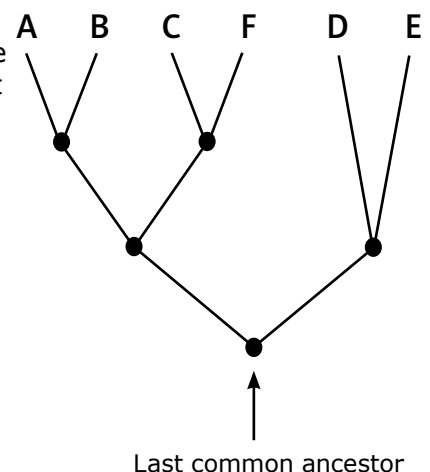
To create the tree, proceed as follows:

1. Start by finding the closest relatives — the pair or pairs of organisms that have the *fewest* differences between them. In this example, beetles A and B have only one difference, so they are the closest relatives. C and F also have just one difference so they are the closest relatives as well. Place these pairs at the top of the tree. The last common ancestor of A and B lived relatively recently. Mark a dot under A and B, showing the separation of evolutionary lines leading to the contemporary forms of A and B. Repeat this for C and F (Figure 1).

2. Next, find organisms that have *more than one* difference. B differs from C by *two* features, so the last common ancestor of this pair lived before the common ancestor of A and B and C and F. Draw a dot to represent the common ancestor of both of these pairs and link them together (Figure 2, left).

3. Organisms D and E also differ by just two features, so they are closely related to each other, but not to the other organisms. D and E are paired up by linking them with a common ancestor (Figure 2, right).

Fig. 1   Fig. 2   Fig. 3
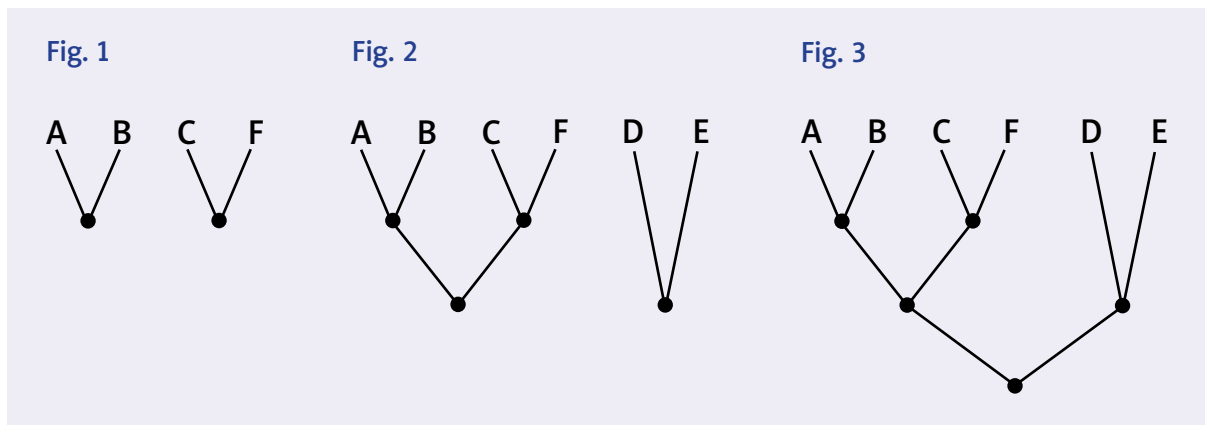
4. Establish which organisms differ by *three* or *four* characteristics. In this way, we can confirm the earlier assumption of the relationship between A, B, C and F.

5. Next, look for organisms that differ by *five* features. These are beetles A and D, C and E and E and F. When there groups are linked by a common ancestor, the tree is complete (Figure 3).

Additional questions

Can you invent names for the main groups which are visible on the tree you have created? Suggest systematic names based on the main common characteristic for each group — for example five- and seven-petalled flowers.

Identify those characteristics that are convergent. Convergence is the independent evolution of the same feature in two unrelated or distantly-related groups of organisms. For example, in the plants analysed here, some of the plants lost thorns independently, and did not inherit this thornless feature from their ancestors. Convergent evolution is usually hard to unearth. With phylogenetic analysis, however, we can easily distinguish between features that are due to evolutionary relatedness (like five or seven petals) and those, like the thorns, which have appeared due to convergent evolution.

What do you think of splitting the organisms into groups such as long and short beaked birds, black and grey bodied butterflies or plants with and without petals? Is this method of grouping consistent with the relatedness shown in the phylogenetic trees?
Can you analyse relatedness between other organisms or even different objects like cakes or coins in the same way?

Additional sources of information

The Tree of Life Project: http://tolweb.org/tree/phylogeny.html

Wellcome Trust Tree of Life: http://www.wellcome-treeoflife.org

EMBL Interactive Tree of Life: http://itol.embl.de

Acknowledgments

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C

F

B

E

A

D