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# **Teaching Evolutionary Principles with AI Image Generators**

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### **Teaching Evolutionary Principles with AI Image Generators**

#### **Purpose:**

The purpose of this assignment is for students to practice constructing phylogenies using the principle of parsimony. In this activity, students will use an AI Image Generator to create a grid of images of the same organism and identify a series of traits that vary to build a possible phylogenetic tree.

### **Learning Objectives:**

Describe the concept of parsimony.

Understand the difference between homology and homoplasy.

Explain why shared derived characters are useful in establishing a phylogeny, while shared ancestral characters are not.

## **Additional Material:**

Teaching Resource on Parsimony: <u>https://evolution.berkeley.edu/using-parsimony/</u>

## Activity:

1. Create a 3x3 grid of an organism of choice (e.g., birds) (left). Each box in the grid will be labelled Species A-I (right). Students can be creative by selecting different artistic styles or other components.

Prompt: Create a 3x3 grid of different birds in the style of Van Gogh



Species A	Species B	Species C
Species D	Species E	Species F
Species G	Species H	Species I

- 2. Identify 5 traits among the organisms in the grid.
- 3. Species
  - a. In this example, possible traits could include beak length (long/short), wing/breast/head/tail colouration, striped wings, number of talons, etc.
- 4. Assume that the **outgroup** does not possess any of the traits above.
- Create a table of trait absence/presence among the species (absent = 0, present = 1)

	Long Beak	Three Talons	Wings	Striped Wings	Grey Eyes
Outgroup	0	0	0	0	0
Species A	1	0	1	1	1
Species B	1	1	1	1	0
Species C	0	1	1	1	1
Species D	0	0	1	0	1
Species E	0	0	1	1	0
Species F	1	1	1	1	1
Species G	1	1	1	1	1
Species H	1	1	1	1	0
Species I	0	1	1	0	1

6. From this table, construct **two possible phylogenetic trees** and map the evolution of trait presence and absence, such as this figure from the additional resource listed above.



7. Students will then evaluate the two trees. How many evolutionary steps are required in each tree? Which one is most parsimonious?