

Exercise 2

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Background

When examining the cultural evolution of narratives, researchers have used phylogenetic techniques to examine the transmission histories of stories. Phylogenetic analyses of narrative material entail identifying mutations in the plot of a group of related stories and reconstructing their transmission histories.

In this exercise, you will focus on reconstructing relationships among five variants of ATU 333 (Grandmother Tiger, The False Grandmother, The Story of Grandmother, Little Red Riding Hood and Little Red Cap), which are provided in the ATU 333 Stories document.

Step 1 - Coding

Below are listed 11 "sites" of variation in these stories. These are known as "characters" in phylogenetic parlance (not to be confused with characters in the story!) and are expressed as different "character states" (for example, present or absent). The different states for each character are shown in the square brackets, with each one assigned a numerical code (0,1).

List of characters

1. Villain is: [0 = a wolf] [1 = tiger] [2 = ogre]
2. Victim is: [0 = animal] [1 = human]
3. Victim is [0 = siblings] [1 = a single girl]
4. Victim's clothing: [0 = doesn't wear a red hood] [1 = wears a red hood]
5. Villain poses as [0 = mother] [1 = grandmother]
6. Victim alone because [0 = mother goes out] [1 = victim goes out]
7. Mother warns victim not to stray from path [0 = no] [1 = yes]
8. The first encounter of the villain and the victim: [0 = in the house] [1 = victim encounters the villain in the woods on the way]
9. Victim uses toilet excuse to escape [0 = no] [1 = yes]
10. Victim is eaten by the villain [0 = no] [1 = yes]
11. Victim is rescued by the huntsman [0 = no] [1 = yes]

When there is a change in a character from one state to another (i.e. a mutation, also known as a "derived trait"), and the changed state is exhibited by two or more taxa, it provides evidence that they are descended from a common ancestor. Changes are identified using a reference taxon known as an Outgroup, which is a distant relative and/or known ancestor that would not be expected to share any derived character states with the in-group. For the purposes of this analysis, we are using an old Aesopic version of a tale that is related to – but distinct from – ATU 333, 'The Wolf, the Goat and the Kids' (ATU 123).

Using the character state codes, fill out the matrix provided in the Exercise 2 work sheet to code the states taken by each character in each variant of ATU 333. As an example, the character states for the Outgroup and the Brothers Grimm tale 'Little Red Cap' are coded as:

	1	2	3	4	5	6	7	8	9	10	11
Aesop	0	0	0	0	0	0	0	0	0	0	0
Grimm	0	1	1	1	1	1	1	1	0	1	1

Step 2 - Determining groups

Once you have completed the matrix, you can start building a phylogeny for the tale variants. Work out how variants group together for each individual character. Remember to only group them based on shared derived traits – i.e. changes in character state (where the state differs from the Outgroup taxon, WolfGoat). For example:

3 Characters, 4 taxa (+ 1 Outgroup, X):

Character 1 links taxa A, B, C and D

Character 2 links A, B and C

Character 3 links A and B

Enter the tales linked by each character state in the table in the Exercise 2 work sheet, and enter the number of tales to determine the size of each group.

Step 3 - Constructing the tree

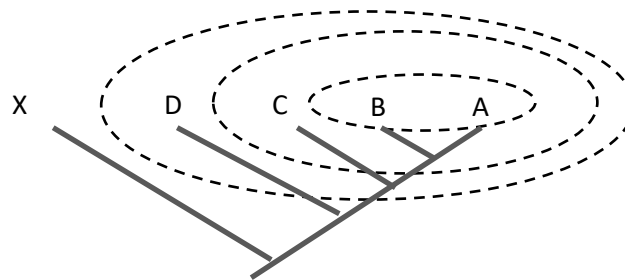
Once you've determined the groups, you can nest the smaller groups within the larger ones to construct a branching evolutionary tree, as per the hypothetical example below:

3 Characters, 4 taxa (+ 1 Outgroup, X):

Character 1 links taxa A, B, C and D

Character 2 links A, B and C

Character 3 links A and B



In cases where different characters support conflicting groups, you should choose the group that is the most compatible with the other groups (unless you have a good reason to give special treatment to the other one). For instance, if we added another character, 4, to the above that grouped A and D, conflicting with character 1, we would choose the reconstruction suggested by character 1 because it is compatible with character 2, whereas 4 is not. These kinds of problems are common in phylogenetics due to the fact that not all similarities among taxa are due to descent (e.g. because of independent evolution and borrowing/blending among lineages) – especially when you're dealing with folktales!

After completing the exercise steps, you can then compare your coding and tree to the model answer.