

Systematic Botany Lab 12.

Phylogenetic trees

November 17, 2011

1 How to make phylogenetic tree

1 The goal of analysis is creation of evolutionary history tree (“cladogram”) which become a basis of classification

2 We need to start with determining “players”—all subtaxa of bigger group. In our case, it will be three families:

Alphaceae

Betaceae

Gammaceae

3 Assess descriptions of these three groups:

Alphaceae: Flowers red, petioles short, leaves whole, spines absent

Betaceae: Flowers red, petioles long, leaves whole, spines absent

Gammaceae: Flowers green, petioles short, leaves dissected, spines present

4 Separate individual characters (we will need $2N + 1$ characters where N is a number of studied taxa):

(1) **Flower color**

(2) **Petiole size**

(3) **Dissection of leaves**

(4) **Presence of spines**

5 **Polarization of characters:** every characters should have at least two characters states where 0 is a primitive, **plesiomorphic** state, 1 is advanced, **apomorphic** state:

(1) Flower color green—0; red—1

(2) Petiole size small—0; big—1

(3) Dissection of leaves absent—0; present—1

(4) Absence of spines—0; spines present—1

5a These states are usually applied on the base of:

(a) Historical evidence (e.g., from fossils)

(b) Developmental evidence

(c) Comparative evidence (from all available taxa)

5b If we do not have this information, we need to find **outgroup** which is primitive by definition. In our case, we will employ outgroup:

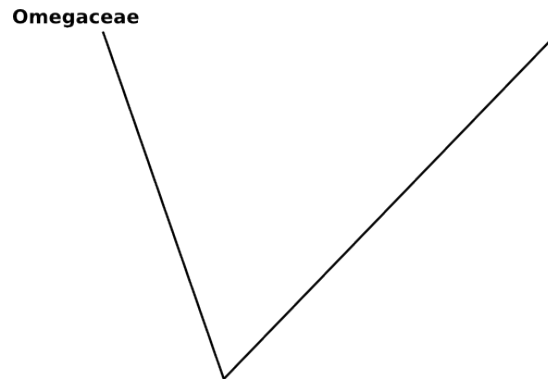
Omegaceae: Flowers green, petioles short, leaves whole, spines absent.

6 Character table

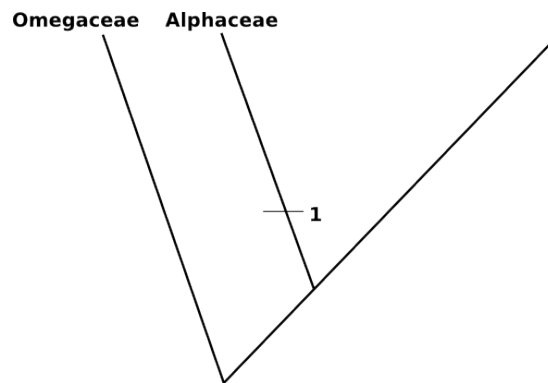
	1	2	3	4
Alphaceae	1	0	0	0
Betaceae	1	1	0	0
Gammaceae	0	0	1	1

[Omegaceae has all zeroes]

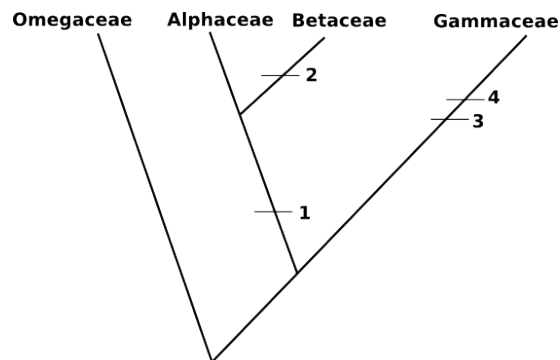
7 Our tree will start from outgroup:



8 Then, the most primitive ingroup (Alphaceae) is attached as a first branch:

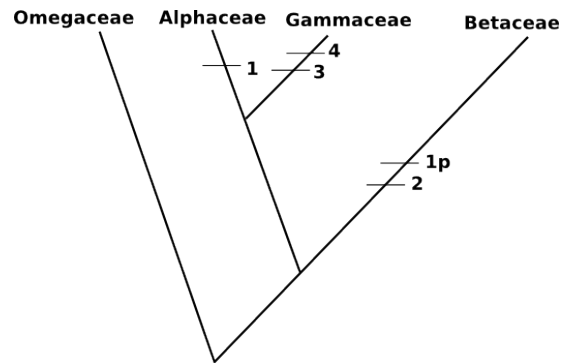


9a Next, the more and more advanced taxa are attached. If there is a choice, we can end up with multiple trees. In our case, Betaceae and Gammaceae have equal number of synapomorphies but Betaceae have only one character different from Alphaceae so we attach it there, and finally we attach Gammaceae:



The tree has 4 evolutionary events (length= 4)

- 9a If we attach taxa in other way (saying, Gammaceae to Alphaceae), the resulted tree will be one step longer:



“p” are parallel characters (homoplasies). There are five events (length= 5).

- 10 We need to choose the shortest, most **parsimonous** tree. Second tree has 5 events, first tree has 4 events. Consequently, we prefer the first tree. Many computer programs produce all possible trees and then choose shortest.
- 11 We can now use chosen tree as a source of classification, e.g.:

Order Alphales

1. Family Alphaceae
2. Family Betaceae

Order Gammales

1. Family Gammaceae

2 Assignment

We will use the following table of taxa and characters:

	1	2	3	4
A	1	0	0	0
B	1	1	1	1
C	1	0	1	1
D	0	1	1	0

1. Download and install R software. Hints: search “R” in Google, go to R Web site, choose CRAN, choose nearest mirror, e.g., Iowa State.
2. Open R, type command (be careful with letter cases, commas, quotes and brackets!):

```
install.packages(c("rpanel", "phangorn"))
```

and press **Enter**. In the dialog which will open, choose the mirror closest to us (KS or IA).

3. Open Web browser and download script **pfpt.r** from the course Web site and copy it to some working directory
4. Inside R, change working directory (from menu: **File -> Change dir...**) to the directory where you put **pfpt.r**.
5. In the R command window, type a command:

```
source("pfpt.r")
```

and hit **Enter**

6. In the right window, change number 1 to 1 (yes, 1 to 1) and press **Enter**. You will see a tree in the left window. Repeat it several time. Tree will change because tree search is based on a random processes. However, please note that C and D never appear together. *Why? Please answer.*
7. **THE GOAL:** change numbers to make D and C appear together (in most cases). *Report the resulted table.*

If something goes wrong, close R, open it again, change working directory and type **source** command.