

Phylogeny – TME2

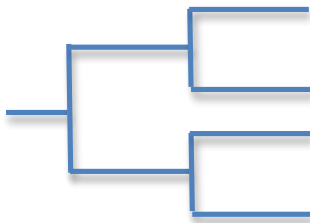
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You have to send your answers to this e-mail address, subject [PHYL] TME2. Your report must be a single pdf file, it have to be simple, clear and well organized. The first page should be a summary indicating the page of each answer.

Exercise 1: Parsimony

1. What is the main idea of parsimony methods? Give an example.
2. What are the small and large parsimony problems? Which problem is harder and why?
3. Given the following sequences and the bellow topology apply the Fitch and Sankoff's algorithms to calculate the scores. Use the cost matrix from Alessandra slides.

A = ATCCTG B = ATCCGG C = ACGGCC D = AGGGCA



4. What is the main idea of nearest neighbor interchange algorithm? Why it is considered as a Heuristic method? Is it exact?

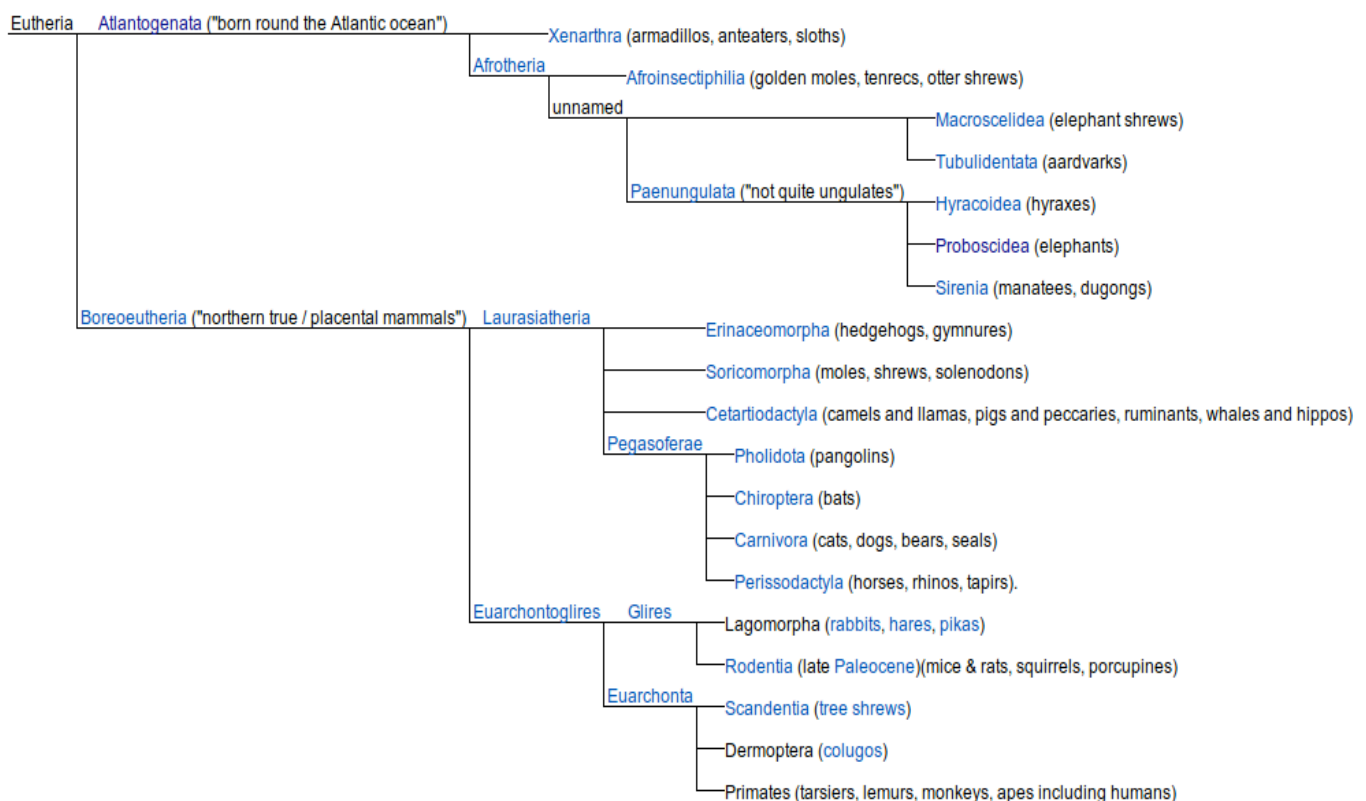
Exercise 2: Reconstruction using reversal distances

1. Go to this website: <http://cinteny.cchmc.org/>, select human and mouse and click start. Then select “whole genome analysis” (using human genome as reference). For human, genes are colored by chromosome, and for mouse they are colored by chromosome of homologous gene in human. Include both figures in your report.
2. Now go back and start again with human and mouse. Then select chromosome versus chromosome for chromosome 1 in human and 4 in mouse. What is reversal distance? Why a big part of each chromosome was left in white? Include the figure in your report.
3. Now start again with human, mouse, cow, chimpanzee. Choose a whole genome analysis and write the matrix of reversal distances. Include this matrix in your report.
4. Use <http://mobyli.pasteur.fr> in phylogeny → distance → neighbor to compute an NJ and UPGMA tree from this matrix (use advanced options to select UPGMA). Are these trees correct?
5. Now we want to do the same with all mammals. I have already written the matrix (just like in previous question), you can download it here <http://www.lcqb.upmc.fr/julianab/teaching/PHYL/TME2.zip> as matrix2.txt.
Compute both UPGMA and NJ trees.
Select “drawtree” (to draw unrooted tree) and “further analysis” to draw the NJ tree.
Select “drawgram” (to draw rooted tree) and “further analysis” to draw the UPGMA tree.
Include these two trees in your report
6. Are these trees correct? What is the limitation of our approach?

Exercise 3: Reconstruction using characters

	Has placenta	Lives in water	Lays eggs	Single pair of incisors	Opposable thumb	Enlarged malleolus
Zebrafish	No	Yes	Yes	No	No	No
Opossum	No	No	No	No	Yes	No
Whale	Yes	Yes	No	No	No	Yes
Mouse	Yes	No	No	Yes	No	Yes
Rat	Yes	No	No	Yes	No	Yes
Chimp	Yes	No	No	No	Yes	Yes
Human	Yes	No	No	No	Yes	Yes

1. Use <http://mobyle.pasteur.fr> in phylogeny → parsimony → pars with the matrix above to compute a tree based on characters. Attach the tree to your report. Is it correct?
2. Remove the last column (enlarged malleolus) and run the analysis again. What happens? Which character is responsible for this incorrect tree?
3. The presence of a character in two species can be explained either by a common ancestor having this character, or by convergent evolution. Find all cases of convergent evolution in the table.



The correct phylogenetic tree of placental mammals (the opossum is not there because it is not a **placental** mammal).