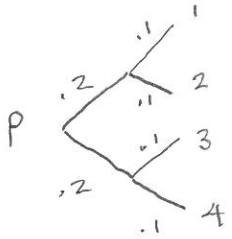
Graph:

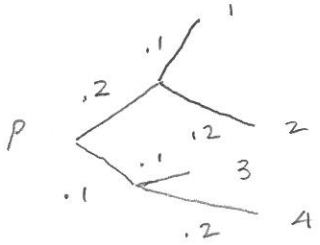


Given a rooted phylogenetic X-tree with weights or edge lengths, we can compute pairwise distances

T_1

	1	2	3	4
1		.2	.6	.6
2			.6	.6
3				.2

Now consider the tree T_2 in comparison to T_1



T_2 suggests that "more" mutation occurred in taxon 2's descent from a common ancestor than taxon 1's.

≡ Differing amounts of mutation

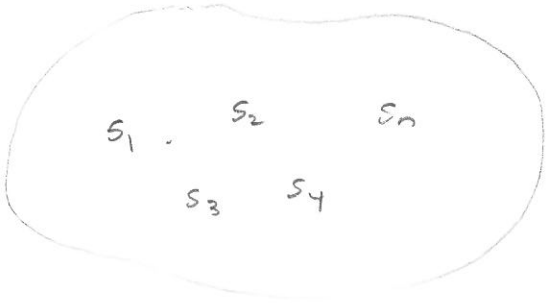
This might be caused by a change (speeding up or slowing down) of the mutation rate for instance.

Defn: A rooted metric tree is called ULTRAMETRIC or we have a MOLECULAR CLOCK if all tips/leaves are equidistant from the root.

i.e. for all $l_1, l_2 \in \mathcal{L}$ leaves, $d(\rho, l_1) = d(\rho, l_2)$

One benefit of a molecular clock at work is that one might assume that the mutation rate is constant so that edge lengths are proportional to time.

It turns out that many software packages for phylogenetic inference, return unrooted trees, though a rooted tree is desired. To root an unrooted tree, one might include an OUTGROUP



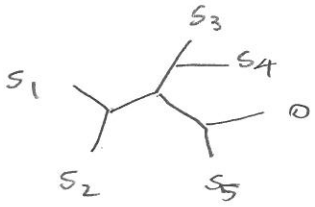
n taxa of interest

distantly related taxon

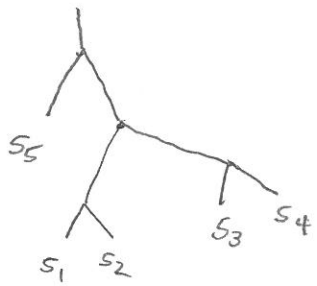
construct a tree for $s_1, \ldots, s_n, o$

delete o and root tree where the branch leading to o came in

Eg.



n=5



Finally, trees are represented in NEWICK FORMAT

$(s_5, (\,(s_3, s_4)\,,\,(s_1, s_2)\,))$

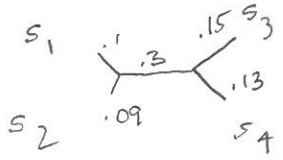
↑
root

Rooted version

$(s_1, s_2, (\,(s_3, s_4)\,,\,(o, s_5)\,)\,)$

Unrooted version

To include distances, use colons

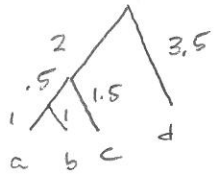


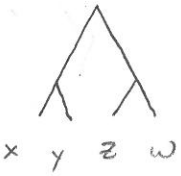
$$\left(s_1 : .1 , s_2 : 09 , (s_3 : .15 , s_4 : 13) : 03 \right)$$

Exercise: Sketch

$$T_1 = \left((a : 1 , b : 1) : .5 , c : 1.5 \right) : 2 , d : 3.5 \right)$$

Ans:



Write  in Newick format

Ans: $((x,y),(z,w))$

Questions etc.