

Introduction to Bioinformatics (autumn 2005)

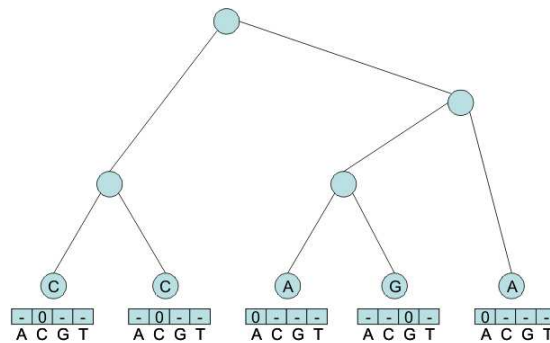
Exercise 8

Group	time	place
Riikka Kaven / Veli Mäkinen	Wednesday 7.12 at 10.15–12.00	D122

- (Problem 10.6 in J & P) How do you calculate the trimming parameter δ in ADDITIVEPHYLOGENY (SUMMAUTUVAFYLOGENIA).
- Let D be the following distance matrix:

	i	j	k	ℓ
i	0	1	3	3
j	1	0	3	2
k	3	3	0	2
ℓ	3	2	2	0

- Does D contain a degenerative triple?
 - Is D additive (summautuva)?
- Solve the Small Parsimony problem using Sankoff's algorithm and Hamming distance on the following tree:



- A pair-HMM is a Hidden Markov Model that models pairwise alignment. It has a match state M , deletion state D , and an insertion state I . Match state M emits characters from both input sequences (with some predefined probability assigned to each character pair), deletion and insertion states emit only characters from one of the sequences with some fixed probability (not dependent on the character). The transition probabilities between the states are fixed to some constants. Visualize the described pair-HMM. Can it be used to compute pairwise alignment under affine gap-penalties? What is the difference (if any)?
- Answer the course feedback form:
<https://ilmo.cs.helsinki.fi/kurssit/servlet/Valinta>