Bioinformatics (Akiyama) Exercise #04

Student ID Name

PHYLOGENETIC TREE

 Reconstruct a phylogenetic tree for sequence A, B, C, and D. Use UPGMA method. A distance matrix is given below.

/	А	В	С	D
А	/	0.1	0.12	0.21
В	0.1	/	0.04	0.13
С	0.12	0.04	/	0.11
D	0.21	0.13	0.11	

(a) At first, search the minimum distance pair. In this case, it is B and C.Fill the vacant columns in the following new distance table.Note that a distance between clusters is calculated (in UPGMA) as the average between all elements. (The distance between point A and cluster {B, C} is the average of A-B and A-C).

\backslash	А	{B,C}	D
А	/		0.21
{B, C}		/	
D	0.21		/

(b) Now next closest pair is A and $\{B, C\}$. Let's make a new cluster named $\{A, \{B, C\}\}$. Fill the new distance table below.

	{A, {B,C}}	D
{A, {B,C}}		
D		

(c) Draw a final phylogenetic tree for sequences A,B,C, and D, based on calculations performed above.

Not only show the tree topology, but also indicate the length of each edge. (Remember how to define the height of each branch in UPGMA).