## PHYLOGENETIC TREE

1) Reconstruct a phylogenetic tree for sequence $A, B, C$, and $D$.

Use UPGMA method. A distance matrix is given below.

| - | A | B | C | D |
| :---: | :---: | :---: | :---: | :---: |
| A |  | 0.1 | 0.12 | 0.21 |
| B | 0.1 | , | 0.04 | 0.13 |
| C | 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 $A-C$ ).

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

(c) Draw a final phylogenetic tree for sequences $\mathrm{A}, \mathrm{B}, \mathrm{C}$, 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).

