Homework 2

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1.

Chose gene and add it to
https://docs.google.com/spreadsheets/d/1a4EPqfJqUfNl1E2iZy1tRvHzw1NX43LeMtP74i
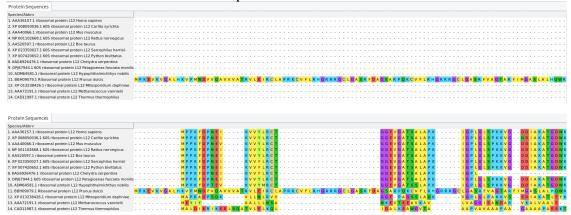15ugo/edit?usp=sharing.

You can find .fasta file with 14 different species here.

##2.

Make multiple alignment by clustalW and Muscle using MEGA.

You can find file after ClustalW here and after Muscle here.

The difference is obvious. For example we can find it on these screenshots:

(beginings of sequences)

##3.

Construct phylogenetic tree by different methods. You can find all combinations here.

After ClustalW alignment:

UPGMA

NJ

maximal likelihood

After Muscle alignment:

UPGMA

NJ

maximal likelihood

Results

1. In comparison with ClustalW method, the Muscle is better, because the trees, constructed by using muscle-alignment is more close to modern evolution tree.

2. We can find, that trees are really different. And sometimes most closed to each other species in first tree are really far in another. In other words, topology of trees is completely different.

3. According to bootstrap values, we can see the similar sutiation: there is a huge difference.

4. In the resulting trees human and primates rarely closer than human and rat or bovine. That's is absurd in general, but it will be normal if we says that we compare organism only by one gene.

But also we can see, that plants, archaea, bacteria, fungi, animals are divided near the root in general. Thats is confirmed by modern theory of evolution.