

made by German Ilya

1.

Chose gene and add it to

<https://docs.google.com/spreadsheets/d/1a4EPqfJqUfNl1E2iZy1tRvHzw1NX43LeMtP74i15ugo/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:

Protein Sequences	
Species/Abbrv	
1. AAA36157.1 ribosomal protein L12 Homo sapiens	
2. XP_008050036.1 605 ribosomal protein L12 Carloti syrichta	
3. AAA40466.1 ribosomal protein L12 Mus musculus	
4. NP_001024681.1 605 ribosomal protein L12 Rattus norvegicus	
5. AAS20597.1 ribosomal protein L12 Bos taurus	
6. XP_023350027.1 605 ribosomal protein L12 Sacrophilus harrisi	
7. XP_0240652.1 605 ribosomal protein L12 Python bivittatus	
8. KAC6926476.1 ribosomal protein L12 Chelydra serpentina	
9. OP679441.605 ribosomal protein L12 Petaioglossa fasciata monilis	
10. AD864581.1 ribosomal protein L12 Hypophthalmichthys nobilis	
11. BBH09079.1 Ribosomal protein L12 Prunus dulcis	M P K E V K V G A L H K V P M D I F A V V V A R V L I E I C L A P R K C V F L H G R R R C L A S R I G A A P K C V F L H G R R C L A S R F V A G I A R F I N G A L A L H D W
12. XP_012338426.1 ribosomal protein L12 Mitosporidium daphniae	
13. AAA72191.1 ribosomal protein L12 Methanococcus vannielii	
14. CAD11987.1 ribosomal protein L12 Thermus thermophilus	

(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 situation: 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. That's is confirmed by modern theory of evolution.