

**C. Internet can be used for the following task. Write answers accordingly, 10 point x 1 questions = 10 points)**

1. Search the tree of Human Cytochrome C oxidase subunit IV
2. Query sequence  

```
>sp|Q96KJ9|COX42_HUMAN Cytochrome c oxidase subunit 4
isoform 2, mitochondrial OS=Homo sapiens
MLPRAAWSLVLRKGGGRRGMHSSEGTTTRGGGKMSPYTNCYAQRYYPMPEEPFCTEL
NAE
EQALKEKEKGSWTQLTHAEKVALYRLQFNETFAEMNRRSNEWKTVMGCVFFFIFGFAA
LVI WWQRVYVFPKPIITLTDERKAQQLQRLMDMKVNPVQGLASRWDYEEKQWKK
```
3. Collecting additional sequences. Using the above query sequence do BLAST search against Uniprot or Swissprot or NCBI protein databases.
  - a. Discuss briefly the scores and values that you have observed from the BLAST results?
  - b. How many sequences did your query sequence match with default settings in BLAST ? Select approximately 10 – 20 or more sequences in fasta format. (save the file = yourname\_input.fas)
4. Do multiple sequence alignment. Save it in clustalW or aligned fasta format. This file is a part from answer. (yourname\_clustal.aln)
  - a. Convert the above clustal alignment to phylip format using (<http://insilico.ehu.es/tophylip/>) (save the file = phylip\_somenumber.aln) Note : you have to include the clustal header in the alignment
  - b. What is the length of the alignment?
5. **Optional** you can compute a bootstrapped tree with at least 100 bootstraps to get the statistical significance.
6. Compute a phylogenetic tree using your method.
  - a. you can use <http://bioweb2.pasteur.fr/phylogeny/intro-en.html>
  - b. **protpars** can be used on the phylip format
  - c. Alternatively you can compute distance by using **protdist** to get a distance matrix, then use the distance matrix and view in any phylip program (phylip, neighbor, quicktree, bionj, puzzle etc)
7. Use the above tree output and view in phylogenetic tree printer <http://iubio.bio.indiana.edu/treeapp/treeprint-form.html>
8. Which tree style did you use and why?
9. Discuss the results? Where is your query sequence located? Which group is closer to query sequence?
10. Save all the files that you are generating and a snapshot or a image format of the tree file.

Mail the results to me [balaji@ut.ee](mailto:balaji@ut.ee)