The goal: To familiarize with genomic differences as regards their phylogenetic signal.

Datafile data_3.txt is a set of complete mitochondrial sequences from a set of mammals. Datafile data_4.txt is one gene, cytochrome B, cut from this data.

- Write an interpretation about phylogenetic relationships of the species
  a) on the basis of the whole mt-genome data
  b) on the basis of cytochrome B

  For a) do only neighbor-joining phylogeny; the data is so big that other analyses will be really slow.

  For b) do the same analyses as you did for Assignment 1 (the bacteria data). In addition to writing an interpretation of the results, write about comparison between one-gene-data and whole-mt-genome-data (on the basis of neighbor-joining).

- Inspect visually the whole mt-genome alignment and write about differences you notice between protein coding genes and D-loop: how useful are these two types of sequences in providing information for species comparisons by using phylogenetics (for which sequence alignment, which you are now asked to inspect, is the first step). Next page shows the coordinates for different genes and other pieces in the mt-genome. A verbal story is here enough.

- NOTE: In MEGA, with cytB, you have to define the code: it is NOT “standard”, but “vertebrate mitochondrial”. When you work with the whole mt-genome data your answer to question “protein coding data” is NO because the data (although it contains protein coding genes, see the table next page) is not a clear 123 123 123.... (=the codons for amino acids). For example the first gene in the data is a transfer-RNA etc.
<table>
<thead>
<tr>
<th></th>
<th>Nucleotides in AB499817, the first sequence in datafile</th>
<th>Nucleotides taking into account gaps in aligned file</th>
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<tbody>
<tr>
<td>tRNA-Phe</td>
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<td>12S ribosomal RNA</td>
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<td>tRNA-Val</td>
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