"Endangered Birds"

1) Select a bird species that is endangered, critically endangered or extinct in the wild using the IUCN Red List. (www.iucnredlist.org/)

2) Select 10 nearest-neighbor species from the Tree of Life as shown in OneZoom (onezoom.org) centering on your endangered bird species. (You will explore these species in your term project, but not in this homework assignment.)

3) Use mitochondrial cytochrome C oxidase DNA sequences to make a multiple sequence alignment and tree for your ten species. Before aligning them, remove introns using any tool you can find online and/or using the information in the GenBank files. (You may want to write a script to do this.) Align the nucleotide sequences (exonic regions only) using any alignment tool, including but not limited to COBALT, UGENE, PhyML, MUSCLE. Describe your methods for processing and aligning sequences.

4) First, prune any terminal ragged ends and internal hotspots (large indels), if they occur. Then, generate a tree with bootstrap values using the tools of your choice. Ideally you should have a block alignment (no indels). Again describe your methods. Show the resulting tree as a unrooted phylogram with species labels and bootstrap values.

5) Generate a distance matrix based on your nucleotide alignment using the J-C correction.

Turn in your species list, GenBank accession numbers, phylogram, distance matrix and a short description of your methods on paper, Nov 30. Thanks!