Blast Lab
Bio B

Introduction:

The BLAST database, compiled by the National Institutes of Health, is an incredibly powerful tool which represents the collaborative nature of science. Any scientist who performs a study that involves sequencing a portion of an organisms genome is required to submit that sequence to the database. The database is funded by public money and is thus freely accessible.

Procedure:

1. Open a blank word document. You will be using this document to copy and paste the genetic sequences you find.

2. Select 8 animals that interest you. Record your choices in the space provided below. Do not worry about filling in the scientific names at this point.

3. Using the concepts discussed at the beginning of class, create a phylogenetic tree that predicts the evolutionary relationship between these animals in the space provided under "Predictions."

4. Open a web browser and go to http://www.ncbi.nlm.nih.gov/. Find the search bar at the top of the page. Select "Nucleotide" in the drop-down menu to the left of the search bar. Type the common name of your first animal and the phrase "cytochrome b" into the search bar (if your first animal was an emperor penguin, you would type "emperor penguin cytochrome b") and then click search.

5. Your results will be labeled by scientific name rather than common name. At this point, the partner with an unused computer should open a browser window to double check that the scientific name corresponds to the desired animal. Take note of the scientific name and the specific common name that corresponds to that scientific name in the space provided.

*Note: The number of results for your search will vary based on the specificity of the common name you supply for your animal ("penguin cytochrome b" will have a lot more hits than "emperor penguin cytochrome b"). If you are having trouble finding the animal you are looking for, the results are categorized by species off to the right under the heading "Results by taxon."

6. Once you have found a result that corresponds to your animal, double check that it contains the right information. The database is huge and cytochrome b is a commonly documented gene, but it does not have all genetic information for all animals. A valid result will have "cytb" or "cytochrome b" somewhere in the title. Generally speaking, select the top result for your animal. Do not worry if the result is says "clone" or "haplotype," and do not worry about the difference between a "partial cds" and a "complete cds." It is representative of that species regardless. If you have any question as to whether the result you would like to pick is valid, feel free to ask.

7. Click on the “FASTA” on the last line of the result you have selected. This will bring up the FASTA format of the animal's cytochrome b gene sequence. Copy and paste the entire sequence (including the scientific name) into the blank word document.

8. Repeat steps 3 through 6 for your other 7 animals.

9. Go to phylogeny.lirmm.fr/. Click on “One-Click Mode.” Copy and paste the contents of your word document, now containing the FASTA sequences of the 8 animals cytochrome b gene, into the dialogue box. The default settings are fine for our purposes, so click “Submit” and be prepared to wait. This is an excellent time to start working on the discussion questions.
10. After 5-10 minutes, you will end up with a phylogenetic tree demonstrating the relatedness of the genes you entered. Copy this phylogenetic tree down in the space provided under “Results.” Be neat and pay attention to the relative length of the lines. Label the animals by their specific common name rather than their scientific name. Be sure to include the numbers on the phylogenetic tree as well.

11. **(Optional)** Briefly prepare a 3 minute presentation explaining your predictions and your results. Focus on aspects of both predictions and results that you found to be particularly interesting or surprising (especially similarities and differences between your them). If space and time allows, draw your phylogenetic tree on the whiteboard before your presentation. If not, one group member should draw it while the another is speaking.