Biology 164 Lab

Using Bioinformatics to Determine the Evolution of Darwin’s Finches

Darwin’s finches and the Galapagos Islands have played a major role in our understanding of evolutionary phenomena. In particular, morphological and ecological differences that exist among Darwin’s finches, especially their beak shapes, plumage colorations, and feeding behaviors, have been offered as examples of adaptive radiation, in which a population diversifies into a number of subsidiary types adapted to more restricted niches within the range of the larger group.

The group of birds known as Darwin’s finches consists of fourteen species (Fig. 1), of which thirteen are found among the islands of the Galapagos archipelago. The remaining species is found on Cocos Island, which lies 600 kilometers northeast of the Galapagos (Fig. 2). The remote island setting in which these birds are found offers extreme ecological isolation; Darwin’s finches have evolved in the absence of predators and competing bird species that occur on the mainland.

Figure 1: Fourteen species of Darwin’s finches arranged to show similarities and differences among beak morphology and plumage coloration.
Darwin’s finches are considered to be descendants of a mainland species that migrated to the islands several million years ago. It is known that the Darwin’s finch lineage diverged that long ago because there are no bird species on the mainland today that even remotely resemble Darwin’s finches.

Figure 2. Location of the Galapagos archipelago and Cocos Island with respect to mainland.

Because of the great distances that separate the Galapagos from the mainland, the specific migration route of the ancestral founding species is in dispute. Some evolutionary biologists consider 1000 kilometers, the distance between the Galapagos and the mainland, as too great for a finch-like bird to have reached the Galapagos directly from the mainland. They propose that Cocos Island, which lies 500 kilometers from the mainland, was colonized first, followed by subsequent dispersal from Cocos to the Galapagos. In this scenario, the Cocos Island finch would be considered ancestral to the finches of the Galapagos. Note that in the phylogeny developed by Lack (1945) the Cocos Island finch is placed closest to the presumed mainland ancestral species (Fig. 3). Lack’s phylogeny was based primarily on feeding behavior, beak morphology and plumage coloration.

Other evolutionary biologists propose that the Galapagos were colonized directly from the mainland, followed by subsequent dispersal to Cocos Island. In this scenario the Cocos Island finch would not be more or less ancestral than any of the other Darwin’s finches. You will attempt to settle the dispute by constructing a phylogeny of Darwin’s finches using genetic distances computed by comparing the degree of similarity of the nucleotide sequences of their mitochondrial DNA.

Figure 3. Suggested phylogeny of Darwin’s finches proposed by Lack in 1947.
To resolve the evolutionary pathway of Darwin’s finches, you will construct a phylogeny based on sequence data developed from blood samples taken from the finches. To save time, you will be provided with the finch sequence data in FASTA format.

Rather than using protein sequence data this time, we will be using DNA sequences from a specific region of the mitochondrial Cytochrome B gene. The file containing these DNA sequences is named “finch_cytb.txt.”

Make a copy of “finch_cytb.txt.” and place your copy in a folder bearing your name.

Open your copy of “finch_cytb.txt.” Note how the DNA sequences look different from the protein sequences you were using in the Euglena study. First, they consist only of four letters, A, T, C, and G, and second, the sequences are quite a bit longer than the protein sequences of the Euglena study.

In order to develop your phylogeny you will need to find a corresponding DNA sequence from a suitable outgroup species. In research conducted by Sato et al. (2001), a phylogeny was developed to determine how a number of neotropical bird species were related to Darwin’s finch species. The list of bird species they evaluated, along with the phylogeny, are shown in Figs. 4 and 5 respectively. In Fig. 5 the abbreviation DF denotes Darwin’s Finches.

Once you have decided on an appropriate outgroup species, you will need to search the NCBI database to determine if corresponding DNA sequence data exists for that species. In order to determine if a specific sequence is usable, you will need to download it in FASTA format and inspect it visually to make sure the descriptive information and the number of nucleotides in the sequence are similar to your finch data.

When searching NCBI make sure you are looking in the NUCLEOTIDE database.

After you have found a usable sequence for an appropriate outgroup species, add it to your list of finch sequences.
The tree you develop from the data will be less cluttered if you replace the descriptive information in your sequences with the common name of the organism. Clustalx does not allow spaces in names so make sure to use an underscore instead of a space. Remember to leave the leading “>” in front of each sequence since this symbol is used by Clustalx to recognize the beginning of a sequence.

Perform a Clustalx alignment procedure on your sequences.

While still in Clustalx, generate N-J Tree data.

Open N-J Plot to actually draw the tree.

**Lab Report**

Prepare a lab report that includes a Results and Discussion section for your study. The Results section will include a properly labeled figure (your phylogeny) and text that summarizes the grouping of finches that exists within the phylogeny. Your Discussion should address the following questions:

1) Where does your phylogeny place the Cocos Island finch in relation to the other finches?

2) To which group of finches is the Cocos Island finch most closely related?

3) How closely related is the Cocos Island finch to it’s closest relatives? What do you think is responsible for this genetic distance?

4) Which finch species is most ancestral in your phylogeny?

5) For which hypothesis regarding the evolution of Darwin’s finches do the CytB sequence data offer greater support?

**Literature Cited**
