

### Assignment 3 – Due on October 9

Write a Parser in Python that reads in Balati\_COI.fst and writes a fasta file to the standard output (stdout) in which every sequence was cropped by 10 nucleotides from the 5' end (beginning of sequence) and 5 nucleotides from the 3' end (end of sequence).

You may use BioPython or a dictionary (see the example scripts we worked through).

In addition to cropping the 5' and 3' ends of each sequence, rename each sequence. Every sequence should be labeled in the following manner: 'Genus\_Species\_AccessionNumber' (e.g., >Holothuria\_mammata\_GQ214743.1). Recall that strings can be converted to lists with the *split* method/function. Lists, in turn, can be converted into strings using the *join* function.

<http://www.pythonforbeginners.com/data-types/python-join-examples> - follow the examples in the tutorial and then apply what you learned to your script. Note that you can do better than the examples in the link: tabs are encoded by \t and newlines by \n.

Hint: strings are indexed in the same way lists are.